

10B13

SEARCH REQUEST FORM

4-400

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: 4-22-98
Searcher: maek
Terminal time: 6
Elapsed time: Manda 11
CPU time: _____
Total time: 17
Number of Searches: 1
Number of Databases: 7

Search Site

☐ STIC
☒ CM-1
☐ Pre-S

Type of Search

☒ N.A. Sequence
☒ A.A. Sequence
☐ Structure
☐ Bibliographic

Vendors

☒ IG MPSRCH
☐ STN
☐ Dialog
☐ APS
☐ Geninfo
☐ SDC
☐ DARC/Questel
☐ Other

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Mpserch_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 21 00:00:18 1998; MasPar time 145.06 Seconds

Tabular output not generated. 795.535 Million cell updates/sec

Title: >US-08-292-694A-11

Description: (1-1000) from US08292694A.seq

Perfect Score: 994 1 AAGAAGCAAAATCAGTAATC.....CCAGTATGACTAGTCGTGGA 1000

N.A. Sequence: Comp: TTCCTCGTTTATGTCATTAG.....GGTCACTACTGATCAGCACCT

Scoring table: TABLE default

Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: n-geneseq30

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.090; Variance 5.438; scale 1.671

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	992	99.8	1000	13	Q75931	Human kappa opioid re	0.00e+00
2	857	86.2	1142	20	T12550	Human kappa opioid re	0.00e+00
3	670	67.4	1410	13	Q75926	Mouse kappa opioid re	0.00e+00
4	660	66.4	2481	15	Q86725	Mammalian kappa opioi	0.00e+00
5	282	28.4	1610	14	Q89226	Human mu opioid recep	3.87e-173
6	282	28.4	2160	15	Q93102	Human mu opiate recep	3.87e-173
7	279	28.1	2070	12	Q79199	Rat mu opioid recepto	5.01e-171
8	277	27.9	1618	14	Q89222	Rat mu-subtype opioi	1.28e-169
9	277	27.9	1618	14	Q89223	Transcription regulat	1.28e-169
10	265	26.7	1821	10	Q56705	Sequence of murine de	3.52e-161
11	265	26.7	1981	10	Q56705	Partial sequence of t	3.52e-161
12	265	26.7	2272	13	Q75927	Mouse delta opioid re	3.52e-161
13	248	24.9	2216	11	Q66656	Murine delta opioid r	3.01e-149
14	245	24.6	829	10	Q56703	Partial sequence of t	3.82e-147
15	245	24.6	2447	10	Q56702	Partial sequence of t	3.82e-147

16	210	21.1	1567	14	Q89233	Rat opioid receptor c	1.10e-122
17	208	20.9	2706	15	Q92972	Rat opiorph receptor	2.72e-121
18	202	20.3	1330	13	Q75928	Mouse opioid receptor	4.07e-117
19	191	19.2	2600	14	Q90096	Mouse kappa-3 opioid	1.78e-109
20	74	7.4	1047	2	Q10572	Human Natriuretic Pep	2.35e-30
21	73	7.3	1518	14	Q83682	Epsilon opioid recept	1.03e-29
22	70	7.0	1047	2	Q10572	Human Natriuretic Pep	8.61e-28
23	70	7.0	1634	7	Q45653	Human somatostatin re	8.61e-28
24	69	6.9	1265	7	Q45654	Murine somatostatin r	3.74e-27
25	63	6.3	1244	7	Q45656	Murine somatostatin r	2.36e-23
26	61	6.1	726	31	T77788	G-protein coupled rec	4.25e-22
27	61	6.1	1110	5	Q29155	Pituitary somatostati	4.25e-22
28	61	6.1	1130	23	T09250	Human somatostatin re	4.25e-22
29	61	6.1	1351	7	Q45655	Human somatostatin re	4.25e-22
30	52	5.2	1054	14	Q83681	Epsilon opioid recept	1.55e-16
31	51	5.1	1796	7	Q45658	Murine somatostatin r	6.28e-16
32	47	4.7	1296	7	Q45657	Human somatostatin r	1.60e-13
33	44	4.4	130	10	Q56701	Partial sequence (seq	9.61e-12
34	43	4.3	91	9	Q51746	Oligonucleotide probe	3.71e-11
35	42	4.2	204	1	N81164	Base substituted E.co	1.42e-10
36	42	4.2	204	1	N81164	Base substituted E.co	1.42e-10
37	41	4.1	723	31	T77787	G-protein coupled rec	5.40e-10
38	40	4.0	91	9	Q51746	Oligonucleotide probe	2.04e-09
39	40	4.0	563	9	Q55055	Sequence of mouse som	2.04e-09
40	40	4.0	678	9	Q55056	Sequence of mouse som	2.04e-09
41	39	3.9	114	12	Q70468	Brain somatostatin re	7.61e-09
42	38	3.8	822	5	Q25156	Generic DNA sequence	2.82e-08
43	37	3.7	114	12	Q70466	Generic DNA sequence	1.04e-07
44	36	3.6	114	12	Q70467	Generic DNA sequence	3.76e-07
45	36	3.6	1378	17	T10666	Human bradykinin B2 r	3.76e-07

ALIGNMENTS

RESULT 1
ID Q75931 standard; DNA; 1000 bp.
AC Q75931;
DT 18-AUG-1995 (first entry)
DE Human kappa opioid receptor partial cDNA fragment.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW Transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe; ss.
OS Homo sapiens.
FH Key
FT CDS Location/Qualifiers
FT CDS /*tag= a 102..989
FT /product= partial human kappa opioid receptor
FT PN W09428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI: 95-022804/03.
DR P-PSDB; R67672.
PT Polynucleotides and peptides derived from opioid receptor
PT Polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 10; Page 236-239; 300pp; English.
CC The partial nucleotide sequence of the novel human kappa opioid receptor
CC gene. The gene was isolated from a human brain hippocampus cDNA library
CC using a probe from the mouse kappa opioid receptor gene (Q75926). The
CC gene is missing the N-terminal sequence. The C-terminal sequence is
CC very similar to the mouse kappa opioid receptor sequence. Of the
CC C-terminal 293 amino acids, 281 residues are identical and 6 residues
CC have conservative substitutions. The gene encoding the human opioid
CC receptor can be placed in a suitable expression vector for production of
CC the protein in a cell. The opioid receptors thus produced are useful for
CC the development of novel assays designed to select or improve substances,
CC capable of interacting with the opioid receptor proteins, for use in
CC diagnosis, drug design and therapeutic applications.

SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T;

Query Match 99.8%; Score 992; DB 13; Length 1000;
Best Local Similarity 99.9%; Pred. No. 0.00e+00;
Matches 999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 aagaagcaaatcagtaatccaaggctatcacaaacacattcacctlatggttgac 60
QY 1 AAGAAGCAAATCAGTAATCCAAGGCTATCACAAACACACTTACCTTATGGGTTGAC 60
Db 61 ttgaataatggaggaatgtctattgtttcttcttttagatatacaaaagatgaagacag 120
QY 61 TTGAATAATGGAAGGAATGCTATTGTTCTTTCTTTTAGATACACAAAGATGAAGACAG 120
Db 121 caaccaacatttacatatttaacctggttttgagagatgctttagttactacaacctgac 180
QY 121 CAACCAACAATTACATATTTAACCTGGCTTTGGCAGATGCTTTAGTTACTACAAACCATGC 180
Db 181 ccttcagagtaacggtctacttgataattcctggccttttggggagatgtgtgtgcaaga 240
QY 181 CCTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCTTTTGGGAGATGTGCTGTGCAAGA 240
Db 241 tagtaattccattgattactacaaacatgttcaaccagcatcttcaaccttgaccatgatga 300
QY 241 TAGTAATTCCATTGATTACTACAAACATGTTCAACCAGCATCTTCACTTGAACCATGATGA 300
Db 301 gcggtgacgcgtacatattgcccgtgtgcccaccccgtgaagccttggacttcgcacacccct 360
QY 301 GCGGTGACCGCTACATTTGCCGTGTGCCACCCCGTGAAGGCTTTGGACTTCCGCACACCCCT 360
Db 361 tgaagcacaagaatcatcaatatctgcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 420
QY 361 TGAAGGCAAGATCATCAATATCTGCATCTGGCTGCTGTCATCTGTTGGCATCTCTG 420
Db 421 caatagtccttggaaggaaccaaaagtcaaggaaaggtgtcgaatgtcattgtatgtctgttc 480
QY 421 CAATAGTCCTTGGAAGGACCAAAAGTCAAGGAAGGTGTGCGATGTCAITGAGTGTGCTTGC 480
Db 481 agtccacagatgatgactactcctgtgtgtggaaccttccatgaagatcgtccttcatct 540
QY 481 AGTCCACAGATGATGACTACTCCTGTGTGGACCTTTCATGAAGATCTGCGTCTTCATCT 540
Db 541 ttgccttcgtcatccctgtctcctcatcatcatcgtctgtctacacacctgatctcgtc 600
QY 541 TTGCCTTCGTGATCCCTGTCTCTCATCATCATCTGCTGTACACCCGTGATGATCCTGCGTGC 600
Db 601 tcaaganngtccggtctccttctgtgtctcccgagagaagaatlnnaacctgtgtagatca 660
QY 601 TCAAGANNGTCCGGCTCTTCTTGTGGCTCCCGAGAGAAAGATNNCAACCTGCGTAGGATCA 660
Db 661 ccagactggtcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
QY 661 CCAGACTGTCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 721 tcaatcctgtgtgaagcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 780
QY 721 TCATCCTGTGTGAGGCTCTGTGGGAGACCTCCACAGACAGAGCTGCTCTCTCCAGCTATT 780
Db 781 acttcgtcatcgccttgaagctataaccaacagtagcctgaatcccatctctacgaccttc 840
QY 781 ACTTCTGCATCGCCTTAGGCTTATACCAACAGTAGCCTGAATCCCATTTCTTACGCTTTC 840
Db 841 ttgatgaaacttcaagcgtgtttcccgagactctgttttccactgaagatgagatgag 900
QY 841 TTGATGAAACTTCAAGCGGTGTTCCCGGAGCTTGTGCTTCCACTGAAGATGAGNATGG 900
Db 901 agcgcnagagcactagcagagtcggaataatacagttcagagatccctgtctacactgagagaga 960
QY 901 AGCGCNAGAGCACTAGCAGAGTCCGAATATACAGTTCAGGATCCTGTACCTGAGGAGAGA 960
Db 961 tgcgatgggatgatgataaataaacagatgatgactagtgtgtga 1000
QY 961 TCGATGGGATGATGATAATAAACAGATATGACTAGTGTGTGA 1000
```

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RESULT 2
ID T12550 standard; cDNA; 1142 BP.
AC T12550;
DE 03-SEP-1996 (first entry)
DE Human kappa opioid receptor cDNA.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
OS neurology; diagnosis; ds.
FH Homo sapiens.
FT Key Location/Qualifiers
FT CDS 1..1142
FT /tag= a
FT /product= kappa_opioid_receptor
FT /note= "Incomplete termination codon"
PN WO9601898-A1.
PD 25-JAN-1996.
PF 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B, Simonin F;
PI WPI; 96-097628/10.
DR P-PSDB; R88722.
PT New nucleic acid encoding the human Kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 3; Page 13-15; 30pp; French.
CC This sequence codes for the human kappa opioid receptor and was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

Query Match 86.2%; Score 857; DB 20; Length 1142;
Best Local Similarity 98.7%; Pred. No. 0.00e+00;
Matches 862; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 257 gatacacaagaatgaagacagcaaccaacattacatatattaacctgtgtggcagatg 316
QY 100 GATACACAAGATGAAGACAGCAACCAACATTTACATATTTAACCTGGCTTGGCAGATG 159
Db 317 cttagtactacaacatgccccttcagagtagcgtctactgtatgtaattcctgtgccct 376
QY 160 CTTAGTTACTACAACCATGCCCCCTTTCAGAGTAGCGGTCTACTTGATGAATTCTTGCCCTT 219
Db 377 ttgggatgtgtgtgaagatagtaatttccattgattactacaacatgttcaaccagca 436
QY 220 TTGGGATGTGCTGTGCAAGATAGTAATTTCCATGTATTACTACAACATGTTCAACGCA 279
Db 437 tottaccttgaccatgatgagcgttggaccgtctacattgcccgtgtgtccacccogtgaag 496
QY 280 TCTTACCTTGACCAATGATGAGCGTGGACCGCTACATTTGCCGTGTGCCACCCGTGAAGG 339
Db 497 ctttgacctccgcaaccccttgaagcgaagatcatcaatatctgcatctgtgtgtgt 556
QY 340 CTTTGGACTTCCGACACCCCTTGAAGGCAAGATCATCATATCTGCATCTGGCTGTGTGT 399
Db 557 cgtcatctgttggcatctctgtcaaatagtccttggaggagcaccaaagtcaaggagagctgc 616
QY 400 CGTCATCTGTTGGCATCTCTGTCAATAGTCCCTTGGAGGACCAACAAAGTCAAGGAGGTGTCG 459
Db 617 atgtcattgagtgctccttgcaagttcccaagatgatactactcctgtgtggagaccttca 676
QY 460 ATGTCAATTGAGTGTGCTGTGCAAGTTCACAGATGATGACTACTCTGTGTGGAGCTTCTCA 519
Db 677 tgaagatctgcgtcttcatcttttgcccttgatccctgtcctcatcatcatcgtctgtct 736
QY 520 TGAGATCTGCGTCTTCATCTTTGCCCTTGTGATGCCCTGTCTCATCATCATCTGTCTGCT 579
```


Db 737 acaccctgatgatccctgcgtctcaagagcgctccggtcccttctgtgctcccgagagaag 796
QY 580 ACAACCGTATGATGCTGCGTCTCAAGANNNGCCGCTCCTTCTGTGCTCCGAGAGAAAG 639
Db 797 atcgcaacctgcgtagatcacaccagactgctctgtgtgtgtgagcgtcttctgtct 856
QY 640 ATNNCAACCTGCGGTAGGATCACACAGACTGCTCTGCTGTGTGGCAGTCTTCTGCTCT 699
Db 857 gctgacttccattcacatattcactgtgtgaggtctgtgagagcactccacagca 916
QY 700 GCTGACTTCCATTCACAIATTCATCTGCTGTGAGGCTCTGGGAGCACCTCCACAGCA 759
Db 917 cagctgtctctccagctattactctgtcatcgcccttaggtctataccaacagtagcctga 976
QY 760 CAGCTGCTCTCTCCAGCIATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGA 819
Db 977 atcccatctctacagccttctgtatgaaacttcaagcggtgttccgggactctgtct 1036
QY 820 ATCCCAITCTCTACGCCCTTCTGTGATAAACTTCAAGCGGTGTTTCCGGGACTTCTGCT 879
Db 1037 ttccactgaagatgagatgtgagcgccagagcactagcagagtcggaataacagttcag 1096
QY 880 TTCCACTGAAGATGAGNATGAGCGGCGNAGAGCACTAGCAGAGTCCGAAATACAGTTTCA 939
Db 1097 atcctgttaccctgagggacatgagtgatga 1129
QY 940 ATCCTGCTTACCTGAGGGAGATGATGGGATGA 972

RESULT 3
ID Q75926 standard; DNA; 1410 BP.
AC Q75926;
DT 17-AUG-1995 (first entry)
DE Mouse kappa opioid receptor MORK1 cDNA.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
transmembrane domain; somatostatin; receptor; human; expression vector;
truncate; chimeraic; assay; probe; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 186..1328
FT /*tag= a
FT /product= mouse kappa opioid receptor
PN W09428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100594.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR P-PSDB; R67669.
PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 10; Page 207-211; 300pp; English.
CC The nucleotide sequence of the novel mouse kappa opioid receptor gene
CC MORK1. The gene was isolated from a mouse brain cDNA library using a
CC fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRIF) receptor
CC subtypes SST1, SST2 and SST3. The 1.2 kb PstI fragment from the mouse
CC kappa opioid receptor clone, lambda msl-1, was subcloned into the mouse
CC promoter-based expression vector PCMV-6b. The resultant construct
CC PCMV-msl-1 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete,
CC truncated or chimeraic opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T;

Query Match 67.4%; Score 670; DB 13; Length 1410;
Best Local Similarity 87.7%; Pred. No. 0.00e+00;
Matches 790; Conservative 0; Mismatches 108; Indels 3; Gaps 2;

Db 442 gatacagaagatgaagaccgcaaccaatcatcatatttaacctggttggcagatg 501
QY 100 GATACACAAGATGAAGACAGCAACCAACATTACATATTAACTGGCTTGGCAGATG 159
Db 502 ctltgttactaacactatgccccttcaagatgctgtctacttgaattccttgccct 561
QY 160 CTTTAGTTACTACAACCATGCCCCCTTCAAGATACGCTCTACTTGATGAATTCTCGCCTT 219
Db 562 ttgagatgtgtctatgcaagatgtgtcatttccatttgactactacaacatgtttaccagca 621
QY 220 TTGGGATGTGCTGTGCAAGATAGTAATTTCATTTGATTACTACAACATGTTCAACAGCA 279
Db 622 tattaccttgaccatgatgatgtgtgacgcgtacattgtgtgtgccaccctgtgaag 681
QY 280 TCTTCACCTTGACCATGATGAGCGCTGGAACCGCTACATTGGCGTGTGCCCCCGGTGAAG 339
Db 682 ctltggacttccgaacaccttggaaagcaagatcatcaacatctgcatlttgctccctgg 741
QY 340 CTTTGAAGCTTCCGACACCCCTTGAAGGCAAGATCAICATATCTGCATCTGCTGCTGT 399
Db 742 catcatctgtgtgtatataacagatagtccttggagagcaaccaagtacagagagatgtg 801
QY 400 CGTCACTGTGTGGCACTCTGCAATAGTCCTTGGAGGCCAACCAAGTCAGGGAAGTGTG 459
Db 802 atgtcaatlyaatgtctcccttgcaagttccctgatgatgaatatctctgtgtggatctctca 861
QY 460 ATGTCAATTGAGTGTGCTGTGCAAGTTCCAGATGATGACTACTCCTGTGTGGACTCTTCA 519
Db 862 tgaagatctgtgtctgtgtcttggccttgtgtatcccaagtcctcatcatcatgtctgt 921
QY 520 TGAAGATCTGCGCTCTTCACTTTTGCCCTGATGATCCCTGCTCATCATCATCATGCTGT 579
Db 922 aacacctgatgatccctgcgcctgaagaagtgtccggtctcctgtctgtcccgagagaag 981
QY 580 ACACCCTGATGATCCTTGCGICTCAAGANNNGCCGCTCCTTCTGCTCCCGAGAGAAAG 639
Db 982 accgaatctccgcgcgcatcaaccaagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1041
QY 640 ATNNCAACCTGCGTAGGATCACACAGACTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 699
Db 1042 gttgaccccccatcacatcttattcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1101
QY 700 GCTGACTCCCATTCACATATTATTCATCCCTGATGAGGCTCTGGGAGGACCTCCACAGCA 759
Db 1102 cagctgcctctccagctattatttctgtattgtccttgygttataccaacagcagcctga 1161
QY 760 CAGCTGCTCTCTCCAGCTATTACTTCTGCAATCCCTTAGGCTATACCAACAGTAGCCTGA 819
Db 1162 atcctgttctctatgccccttctgtgatgaaacttcaagcggtgttttagggacttctgt 1221
QY 820 ATCCCATTTCTACGCCCTTCTTGTGATGAAACTTCAAGCGGTGTGTTCCGGGACTTCTGCT 879
Db 1222 tccctattagatgcgaatgagcgccagagcaaccaatagatgagttagaacacagttcag 1281
QY 880 TTCCACTGAAGATGAGNATGAGCGGCGNAGAGCACTAGCAGAGTCCGAATAACAGTTCA 939
Db 1282 atcctgtcttccatgag--agat-gtggagagagatgaataagccagtagtactgtgtg 1338
QY 940 ATCCTGCTTACCTGAGGAGATGATGGGATGATGAATAAACCAAGATAGACTAGTGTG 999
Db 1339 a 1339
QY 1000 A 1000

RESULT 4
ID Q86725 standard; cDNA; 2481 BP.
AC Q86725;

DT	01-DEC-1995	(first entry)	
DE	Mammalian kappa opiod receptor protein cDNA.		
KW	Mammalian kappa opiod receptor; mouse delta opiod receptor; analgesic; amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.		
OS	Rattus rattus.		
FT	Key	Location/Qualifiers	
FT	CDS	111..1253	
FT	/*tag= a		
PN	/product= kappa opiod receptor		
PD	J07070191-A.		
PD	14-MAR-1995.		
PF	30-JUL-1993; 190261.		
PR	09-JUL-1993; JP-170591.		
PA	(TAKE) TAKEDA CHEM IND LTD.		
DR	WPI; 95-144857/19.		
DR	P-PSDB; R72591.		
PT	Kappa opiod receptor protein and cells expressing it - useful for the screening of compounds for analgesic and hypnotic properties		
PS	Claim 2; Page 9-10; 15pp; Japanese.		
CC	The nucleotide sequence of the novel mammalian kappa opiod receptor cDNA. The gene was isolated by amplifying a fragment from rat brain mRNA by reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from the mouse delta-opiod receptor gene. This fragment was cloned into the plasmid pCRII to produce pRII. The plasmid pRII was used to probe a rat brain DNA library in lambda ZAPII to obtain a clone of the rat kappa opiod receptor gene, designatd pKOPR2. This clone was introduced into E.coli JM109 for production of the receptor protein. The receptor protein is useful for screening of analgesic and hypnotic compounds including peptides and proteins.		
CC	Sequence 2481 BP; 629 A; 588 C; 544 G; 720 T; Sequence		

Query Match	66.48;	Score 660;	DB 15;	Length 2481;
Best local Similarity	87.18;	Pred. No. 0.00e+00;		
Matches	785;	Conservative	0;	Mismatches 113;
			Indels	3;
			Gaps	1;

Db	367	gatacacaagaagatgaagaccgcaaccaacatctacatatlttaacctggtcttggcagatg	426
QY	100	gatacacaagaagatgaagacagcaaccaacatttacaatatTTAACTGGCTTTGGCAGATG	159
Db	427	cttggttactaccaciatgcccctccagagtgtgtctactgtatgaaltcttggccct	486
QY	160	CTTAGTtACTACaACCATGccCTTCAgAGTAcGGTCTCTACTGATGAATTCCTGGccCTT	219
Db	487	ttggagatgttctgttgcgaagattgtcatcttccattgactactacaacatgtttaccagca	546
QY	220	TTGGGGATGTGCTGTGCATAGATAGTAATTTCCATTGATTACTACAAcATGTTCAccAGCA	279
Db	547	tattcaacctgacacatgatgatgttggaccgctacattgcccgtgtgccaacctgttgaag	606
QY	280	TCTTCACCTTGACCATGATGAGCGGTGGACCGCTACATTGCCGTGTGCGCCACCCCGTGAAG	339
Db	607	cttggattccggaacacctttgaaagcaaaagatcatcaacatctgtcatlttggctactgg	666
QY	340	CTTTGGACTTCCGCACACCCCTTGAAGGCCAAAGATCATCAATATCTGCATCTGGCTGTGT	399
Db	667	catcatctgttgtatatacagcagatagtccttggaggcaaccaagtcagggaagatgttg	726
QY	400	CGTCATCTGTGGCATCTCTGCAATAGTTCCTTGGAGGCACCAAGTCAGGGGAAGGTGTGG	459
Db	727	atgtcattgatatgtcctcttgcaagtttccctgatatgatgaatatctcctgtgtggaaaccttca	786
QY	460	ATGTCAATTGAGTGTGCTGCTTGCAgTTCCAGATGATGACTACTCCTGTGTGGGAACCTCTTCA	519
Db	787	tgaagatctgtgtctctcgtctcttggcccttgttatccctgtctctaatacatcatgtctgct	846
QY	520	TGAAGATCTGCGTCTTCATCTTTGGCCTTGTGATGCCCTGTCCCTCATCATCATGCTGTGCT	579
Db	847	acaacctgatgatccctgcgcttgaagagtgtccggtccctcctcgcggtctcggagagaag	906
QY	580	ACACCTGATGATCCTCTGCGTCTCAAGANNGTCCGGCTCCTTTCTGTGGCTCCCGAGAGAAAG	639
Db	907	accgaaatctccgcgcgatatccaacgaagtgtgtgtgtgtagtgtgtgcagctcttcatcatct	966

Dy	640	ATNNCAACCTGCGTAGGATCACACCAGACTGGTCCTGGTGGTGTTGGCAGTCTTCGTGCT	699
Dd	967	gttggaccaccatccacatcttatcctggtcgaggctctlaggcagcaccttcacagca	1026
Dy	700	GCTGGACTCCCATTCACATAATTCATCTCGTGGTGAGGCCTCTGGGGAGCACCTCCACAGCA	759
Dd	1027	cagctgtcctctcttagctattactctctgcatgaccttggtatataccacagcagcttga	1086
Dy	760	CAGTGTCTCTCCACAGCTATTACTTCTGCACATGCCCTTAGGCTATACCAACAGTAAGCCTGA	819
Dd	1087	atcctgttctctatgaccttctcttgatgnaaaactccaagcgytgtltagggacutctgct	1146
Dy	820	ATCCCATTTCTTACGCCCTTTCTTGATGAALAACTTCAAAGCGGTGTTCCGGGACTTCGT	879
Dd	1147	tcccocatgaagtgcgaatgagcgccagagcacacaacagagltagaaacacagtttcagg	1206
Dy	880	TTCACATGAAGATGAGNATGAGAGCGCNAGAGCACCTAACAGAGTCCGAAATACAGTTTCAGG	939
Dd	1207	atcctgtcttccatgagsgatgtggtgagatga--ataagccaglatgactagtcatgg	1263
Dy	940	ATCCTGCTTACCCTGAGGGAGATCGATGGATGATGAATAAACCAAGTATGACTAGTCTGTG	999
Dd	1264	a 1264	
Dy	1000	A 1000	

RESULT	5	
ID	Q89226	standard; cDNA; 1610 BP.
AC	Q89226;	
DT	20-OCT-1995	(first entry)
DE	Human mu opioid receptor cDNA.	
KW	Mu opioid receptor; MOR; gene therapy; diagnostic; ss.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	239..1441
FT	/*tag= a	
PN	W09507983-A.	
PD	23-MAR-1995.	
PE	13-SEP-1994; U10358.	
PR	13-SEP-1993; US-120601.	
PA	(INDV) UNIV INDIANA FOUND.	
PI	Yu L;	
DR	WPI; 95-131351/17.	
DR	P-PSDB; R71966.	
PT	New nucleic acid encoding new human mu opioid receptor - and	
PT	related vectors, transformed cells, antibodies etc., useful in	
PT	diagnosis, treatment and drug screening.	
PS	Claim 5; Page 208-210; 266pp; English.	
CC	A cDNA library constructed from human caudate nucleus mRNA was	
CC	screened with rat mu opioid receptor cDNA under conditions of	
CC	low stringency. One positive clone included the sequence given	
CC	Q89226, encoding a mu opioid receptor MOR (R71964). The cDNA	
CC	is used for prodn. of recombinant MOR, in gene therapy, etc.	
SO	Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T;	

Query Match	28.4%;	Score 282;	DB 14;	Length 1610;
Best Local Similarity	71.2%;	Pred. No. 3.87e-173;		
Matches 560;	Conservative	0;	Mismatches 216;	Indels 11;
				Gaps 10;

Db	527	agatacaccagaatgaagactgccaaccaacatctacatlttcaacctgctctggcagat	586
QY	99	AGATACACAAGATGAAGACAGACCAACACATTTCATAITTTAACCTGGCTTTGGCAGAT	158
Db	587	gccttagccaccagtaacctgcctctccagagtgtgaattaacctaattgggaacatggcca	646
QY	159	GCITTAGTTACTACAAACCATGCCCTTTCAGAGTACGGTCTACTTGAATGAAATTTCCTGGCCT	218
Db	647	tttgggaaccatcccttgcagaatagtgtatctccatagattactatatacaatgttcaccagc	706
QY	219	TTTGGGGAATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAAACATGTTACACAGC	278

D	b		707	aatcaccctctgcacccatgagtgttgatcgatacatattgcagtcctgcacacctgtcaag	765
Q	y	ATCITCACCTTGACCATTGAIGAGCGTGGACGCTACATTGCCGTGTGCCACCCCGTGAAG	338		
D	b		767	gccctagattccgtactccccgaatatgccaaaatltaaatgtctccaactggatccc	826
Q	y	GCTTTGGACTTCGCCACAACCCCTGAAAGGCAAGAATCATATACTGCATCTGGCTGCTG	398		
D	b		827	tcttcaggcaattgttcttccctgtaattttcataggctacaacaaatacaggcaagt-tc	885
Q	y	TCCGTCATCTGTTGGCATCTCTGCAATAGTCTTTGGAGGCACCAAAGTACAGGAAGTGTC	458		
D	b		886	catalg-atgy--taaa-ctaaca-ttctctcacocacacotlytlactgs-gaaaac-ctgc	938
Q	y	GATGTCAATTGAGTGTGCTGTTCAGATTCOCAGATGATGACTACTCTCTGTGGGAACTCTTC	518		
D	b		939	-tgaagaatcttgttttccatcttcgacctcatattatgccaagtgtcatacattaacgtgtgc	997
Q	y	ATGAAGATCTGCGCTCTTCATCTTTGCCCTTGTGATCCCCTGTCTCATCATCATCTGCTGC	578		
D	b		998	tatgtagtatgatccttcgcgcctcaagaagltcoogcatgtctctctggtcccaaagaag	1052
Q	y	579 TACACCCTGATGATCCTCGCTCGTCTAAGANNNGTCCGGCTCTTTCTGCTCCCGAGAAA	638		
D	b		1058	gacaggaatccttogaaagatcaccaagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtc	1117
Q	y	639 GATNNCAACCTGCGTAGGATCACCCAGACTGGTCCCTGGTGTGGTGCACTCTTCGTCGC	698		
D	b		1118	tgtctgactcccatlccacatttacgtcatcatlaaagccttggtttaaatcccaagaact	1177
Q	y	699 TGCTGGACTCCCATTCACATATTAICTTGTTGGTGAAGGCTCTGGGAGCACCTCCACAGC	758		
D	b		1178	ac-gttccagactgttctcctgbcacctctgcattgtctctaggttacacacaacagctgcct	1236
Q	y	759 ACAGCTGCTCTCTCCAGCTAAT-ACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCT	817		
D	b		1237	caaccagctccttlatgtcatlcttgatgtaaactlcaaacgatatctcagagattctc	1296
Q	y	818 GAATCCCATCTCTACGCCCTTTCTTGAATGAACACTTCAAGCGGTGTTCCGGGACTTCTG	877		
D	b		1297	tatecca 1303	
Q	y	878 CTTTCCA 884			
R	E	S	L	T	
I	D	O	93102 standard; cDNA; 2160 BP.		
A	C	O	93102;		
D	E	11-DEC-1995 (first entry)			
H	M	Human mu opiate receptor cDNA.			
K	M	Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;			
W	O	drug abuse; analgesic; ds.			
F	H	Homo sapiens.			
K	E	Key	Location/Qualifiers		
F	T	CDS	213..1415		
P	N	/tag= a			
P	D	WO9520667-Al.			
P	F	03-AUG-1995.			
P	R	30-JAN-1995; U01144.			
P	A	28-JAN-1994; US-188275.			
P	A	(USSH) US DEPT HEALTH & HUMAN SERVICES.			
P	I	(USSH) US SEC DEPT HEALTH.			
D	R	Johnson PS, Persico AM, Uhl G, Wang J;			
D	R	MPJ: 95-275452/36.			
D	R	P-BSDB; R76780.			
P	T	New DNA encoding human mu opiate receptor - used esp. for screening			
P	T	pcds. for activity as opiate agonists or antagonists			
P	S	Claim 4; Page 24-25; 49pp; English.			
C	C	hMOR cDNA was obt'd. from a human cerebral cortical cDNA library			
C	C	screened with fragments of a rat mu opiate receptor. Cloned hMOR			
C	C	DNA can be used as probes to examine the structure and function of			
C	C	hMOR genes or to screen individuals for susceptibility to drug			
C	C	abuse. Expression in e.g. COS cells allows production of			

[illegible]

QY	519	ATGAAGATCTGGGTCCTTCATCTTTGCCCTTCGTGATCCCTGTCCCATCATCATCGTCTGC	578
Db	967	tacggcctgatgatctcttaagactcaagagcgcttcgcattgcctatccgggtcccaagaaag	1026
QY	579	TACACCCCTGATGATTCCTGGCTTCACAGANNGTCCGGCTCCTTTCTGGCTCCCGAGAGAAA	638
Db	1027	gacaggaaatctgcgcagagatcaaccggagatggtgctgtgtcgtcgtgtattatcgtc	1088
QY	639	GATNNCAACCTGGCGTAGGATCACCAAGACTGGTCCGTGGTGGTGGCAGTCTTCGTCTGC	698
Db	1087	tgctggacccccatccacatctacgtcatcatcaagcgtgatcaagattccagaacc	1146
QY	699	TGCTGGACTCCCAATTACATATTTCATCTGTGTGAGGCTCTGGGGAGACACTCCACAGC	758
Db	1147	acatttcagaccgcttccctggcaactctctgcattgtcttgggttacacgaaacagctgcctg	1206
QY	759	ACAGCTGCTCTCTCCAGCCTATTACTTCTGCATCGCCCTTAGGCTATTACCAACAGTAGCCTG	818
Db	1207	aatccagttctttaaagcctcttcctgsgatgaaacctcaagcgatgcttccagagagttctgc	1266
QY	819	AATCCCATTTCTTACGCCCTTTCTTGATGAAAACTCAAGCGGTGTTCCGGGACTTCTGC	878
Db	1267	atcccca 1272	
QY	879	TITCCA 884	

ID	Q89223	standard; cDNA; 1618 BP.
AC	Q89223;	
DT	20-OCT-1995	(first entry)
DE	Transcription regulatory protein cDNA.	
KW	Mu opioid receptor; MOR-1; gene therapy; diagnostic;	
KW	transcription regulatory protein; ss.	
OS	Rattus sp.	
FE	Key	Location/Qualifiers
FT	CDS	339..1235
FT	/*tag= a	
PN	WO9507983-A.	
PD	23-MAR-1995.	
PF	13-SEP-1994; U10358.	
PR	13-SEP-1993; US-120601.	
PA	(INDV) UNIV INDIANA FOUND.	
PI	Yu L;	
DR	WPI; 95-131351/17.	
DR	P-PADB; R71965.	
PT	New nucleic acid encoding new human mu opioid receptor - and	
PT	related vectors, transformed cells, antibodies etc., useful in	
PT	diagnosis, treatment and drug screening.	
PS	Disclosure; Page 199-203; 266pp; English.	
CC	A 365 bp fragment of the mouse delta opioid receptor was used to	
CC	screen a rat brain cDNA library under low stringency conditions.	
CC	One positive clone included the sequence given in Q89222, encoding a	
CC	mu opioid receptor, MOR-1 (R71964). Sequence analysis revealed an	
CC	alternative reading frame (Q89223) encoding a zinc	
CC	finger-containing transcription regulatory protein (R71965).	
SO	Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;	

Query Match	27.98;	Score 277;	DB 14;	Length 1618;
Best Local Similarity	70.28;	Pred. No. 1.28e-169;		
Matches	552;	Conservative	0;	Mismatches 225;
			Indels	9;
			Gaps	7;

Db	496	agatacacccaaaatgaagactgccaccaacatctacatlttcaacctgtctgtgcagac	555
QY	99	AGATACACAAGATGAAGACAGACAACACATTACATATTAACTGGCTTGGCAGAT	158
Db	556	gccttagcgaccaggtacactgccccttcaagagtgtcaactactctgatgggaacatggccc	615
QY	159	GCTTAGTACTACTACAACCATGCCCTTTACAGAGTACGGGTCTACTTGAIGATTTCTGCGCT	218
Db	616	ttcggaaccatctctctgcgaagatcgtgatctcaatagattactacaacatgttccaccagc	675
QY	219	TTTGGGGATGTGCTGTGCGAAGATAGTAATTTCATTTGATTACTACACATGTTCCACAGC	278

[illegible]

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RESULT 10
ID Q56700 standard; cDNA; 1821 BP.
AC Q56700;
DT 15-SEP-1994 (first entry)
DE Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.
KW Opioid receptor; morphine; opiate; ss.
OS Mus musculus.

TH Key
FT CDS Location/Qualifiers
      29..1139
      /*tag= a
PN WO9404552-A.
PD 03-MAR-1994.
PF 13-AUG-1993; U07665.
PR 13-AUG-1992; US-929200.
PA (REGC ) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
DR WPI; 94-083099/10.
DR P-PSDB; R48629.

PT DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpds. for opioid (ant)agonist activity
PS Claim 1; Fig 5; 74pp: English.
CC A cDNA library was constructed using mRNA isolated from the NG109-15
CC cell line. A single clone, named the DOR-1 clone was isolated.
CC Comparisons with known sequences in Genbank showed highest homology
CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
CC features of the DOR-1 clone AA sequence deduced from the cDNA

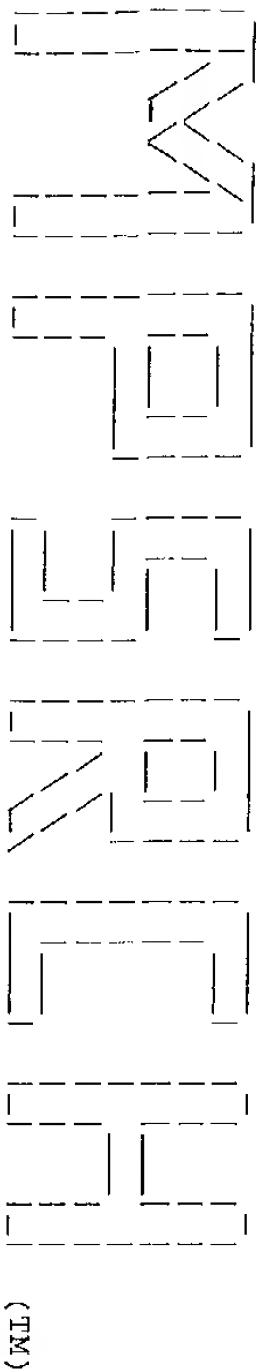
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Db	1249	aaccacgttcttattatgcgttccobgatgaactcaaacgatgtttagagagttctgc	1308
QY	819	AATCCCATTTCTCTACGCCCTTTCTTGATGAAACTTCAAGCGGTGTTTCCGGACTTCTGCG	878
Db	1309	atcccca	1314
QY	879	TTTCCA	884
RESULT	12		
ID	Q75927	standard; DNA; 2272 BP.	
AC	Q75927;		
DT	17-AUG-1995	(first entry)	
DE	Mouse delta opioid receptor MOR1 cDNA.		
KW	Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;		
KW	transmembrane domain; somatostatin; receptor; human; expression vector;		
KW	truncate; chimaeric; assay; probe; ss.		
OS	Mus musculus.		
FH	Key	Location/Qualifiers	
FT	CDS	12..1130	
FT	/*tag= a		
FT	/product= mouse delta opioid receptor		
PN	W09428132-A.		
PD	08-DEC-1994.		
PF	20-MAY-1994; U05747.		
PR	20-MAY-1993; US-066296.		
PR	30-JUL-1993; US-100694.		
PR	05-NOV-1993; US-147592.		
PA	(ARCH-) ARCH DEV CORP.		
PI	Bell GI, Reisine T, Yasuda K;		
DR	WPI: 95-022804/03.		
DR	P-PSDB; R67670.		
PT	Polynucleotides and peptides derived from opioid receptor		
PT	polypeptides - for use in therapeutic compositions and in		
PT	screening assays for useful drug substances.		
PS	Claim 6; Page 215-221; 300pp; English.		
CC	The nucleotide sequence of the novel mouse delta opioid receptor gene		
CC	MOR1. The gene was isolated from a mouse brain cDNA library using a		
CC	fragment (amplified from the cDNA library with primers Q75929-30) as a		
CC	probe. The primers are based on the conserved sequences present in the		
CC	second and third transmembrane domains of somatostatin (SRI) receptor		
CC	subtypes SSRL1, SSRL2 and SSRL3. The 1.3 kb EcoRI-SacI fragment from the		
CC	mouse delta opioid receptor clone, lambda msl-2, was subcloned into the		
CC	CMV promoter-based expression vector PCMV-6c. The resultant construct		
CC	PCMV-msl-2 was transfected into COS-1 cells for protein production. The		
CC	gene encoding the opioid receptor can be used to produce complete,		
CC	truncated or chimaeric opioid receptor proteins. The opioid receptors		
CC	thus produced are useful for the development of novel assays designed to		
CC	select or improve substances, capable of interacting with the opioid		
CC	receptor proteins, for use in diagnosis, drug design and therapeutic		
CC	applications.		
CC	Sequence 2272 BP; 485 A; 665 C; 650 G; 472 T;		
SQ			
Query Match	26.7%;	Score 265;	DB 13; Length 2272;
Best Local Similarity	70.6%;	Pred. No. 3.52e-161;	
Matches	550; Conservative	0; Mismatches 217;	Indels 12; Gaps 10;
Db	240	tacaccaaatgaagacgcgcacacacatctaatcttcaatctgctgtgctgctgacg	299
QY	102	TACACAAAGATGAAGACAGCAGCAACCAACATTTACATATTAACTGGCTTGGCAGATGCT	161
Db	300	ctgagccacagcagcgtgcccctccagagcgccaagtactgtatggaacgtggccgttt	359
QY	162	TTAGTTACTACAACCATGGCCCTTTCAGAGTACGGTCTACTTGATGATATTCCTGGCCTTIT	221
Db	360	ggcagctgctgtgcaagcgtgtgctctccattgactactacacacatgttcaactagcattc	419
QY	222	GGGATGTGCTGTGCAAGATAGTATTTCCATTGATTACTACAACATGTTCCACCAAGCATC	281
Db	420	ttcaccctacacatgatgagcgtggaccgctacatttgtctgtctgcccacctcgttcaagcc	479
QY	282	TTCACTTGACCATGATGAGCGGTGACCGCTACATITGCCGTGTGCCACCCCGTGAAGGCT	341

[illegible]

RESULT	13
ID	Q66656 standard; cDNA; 2216 BP.
AC	Q66656;
DT	19-JAN-1995 (first entry)
DE	Murine delta opioid receptor coding sequence.
KW	delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;
KW	drug addiction; neurological disorder; psychiatric; disorder;
KM	cardiovascular disorder; ds.
OS	Mus musculus.
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	CDs
FT	/tag= a
FT	/product= opioid_receptor
PN	FR2697850-A.
PD	13-MAY-1994.
PF	10-NOV-1992; 013526.
PR	10-NOV-1992; FR-013526.
PA	(UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI	Kieffer B;
DR	WPI; 94-178255/22.
DR	P-PSDB; R66503.
PT	New nucleic acid encoding opioid receptor - and related
PT	polypeptide, antisense nucleic acid, probes, recombinant cells
PT	and ligands, useful in diagnosis and treatment of e.g.
PT	neurological disorders
PS	Claim 3; Page 16-18; 29pp; French.
CC	A cdna bank constructed from hybridoma NG108-15, was used to
CC	transfect COS-1 cells. The cells were tested for ability to bind
CC	tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or
CC	absence of the opioid antagonist naloxone. Clone K56 was isolated
CC	from a positive colony and found to contain a 2216bp insert. This
CC	cDNA encodes a delta opioid (enkephalin) receptor with apparent
CC	dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
SQ	Sequence 2216 BP; 460 A; 647 C; 649 G; 460 T;

Query Match 24.98; Score 248; DB 11; Length 2216;



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MPSrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Mon Apr 20 23:31:55 1998; Maspar time 908.25 Seconds
1301.894 Million cell updates/sec
Tabular output not generated.

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Description: (1-1000) from US08292694A.seq
Perfect Score: 994
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Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 354530 seqs, 591221332 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb153
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7:em_hum1 8:em_hum2 9:em_da 10:em_ro 11:em_un 12:em_v1
13:em_pat
Database: genbank105
14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pl 19:gb_da
20:gb_st 21:gb_v1 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
26:gb_htg

Statistics: Mean 11.021; Variance 5.890; scale 1.871

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	857	86.2	1142	25	A48343	Sequence 1 from Patent	0.00e+00
2	703	70.7	1733	14	CP004092	Cavia porcellus Hartle	0.00e+00
3	670	67.4	1288	14	S81111	kappa-opioid receptor	0.00e+00
4	670	67.4	1410	14	MUSKAPOPRE	Mouse kappa opioid rec	0.00e+00
5	662	66.6	1273	14	RATROD	Rat mRNA for opioid re	0.00e+00
6	662	66.6	1358	14	RATKOR1A	Rat kappa opioid recep	0.00e+00
7	660	66.4	2094	14	RATKOR1B	Rattus norvegicus kapp	0.00e+00
8	660	66.4	2481	14	RATKOR	Rattus norvegicus mRNA	0.00e+00
9	660	66.4	2481	25	E08874	CDNA coding rat kappa-	0.00e+00
10	660	66.4	4742	14	RNT00442	Rattus norvegicus kapp	0.00e+00
11	383	38.5	1186	14	S77858S3	kappa opioið receptor	5.75e-268
12	378	38.0	638	14	MUSMORGDP3	Mouse MORGD gene for k	5.14e-264
13	375	37.7	4048	14	RNKOR3	Rattus norvegicus kapp	1.21e-261
14	316	31.8	1109	14	S77868S2	kappa opioið receptor	3.71e-215

15	315	31.7	488	14	MUSMORGDP2	Mouse MORGD gene for k	2.27e-214
16	314	31.6	658	14	RNKOR2	Rattus norvegicus kapp	1.38e-213
17	294	29.6	432	14	MMU16998	Mus musculus kappa opi	6.82e-198
18	281	28.3	1881	15	PIGMOPR	Sus scrofa mu opioið r	1.03e-187
19	279	28.1	2135	14	RATMOR1A	Rattus norvegicus mu o	3.79e-186
20	279	28.1	2397	14	RATROB	Rat mRNA for rat opioi	3.79e-186
21	277	27.9	1401	14	RATMOPIOID	Rat mu opioið receptor	1.39e-184
22	277	27.9	1448	14	RNU02083	Rattus norvegicus mu-o	1.39e-184
23	277	27.9	1586	14	RATMORA	Rattus norvegicus mu o	1.39e-184
24	275	27.7	1367	14	RNU35424	Rattus norvegicus mu o	5.08e-183
25	273	27.5	1231	16	CCMUOPI	C. communsoni mRNA for	1.86e-181
26	271	27.3	1610	14	MMU26915	Mus musculus mu opioið	6.79e-180
27	269	27.1	2229	14	MMU19380	Mus musculus mu opioið	2.48e-178
28	267	26.9	1415	15	BTU89677	Bos taurus mu opioið r	9.03e-177
29	265	26.7	1366	14	RNU00475	Rattus norvegicus Spra	3.29e-175
30	265	26.7	1418	14	RATROA	Rat mRNA for rat opioi	3.29e-175
31	265	26.7	1834	14	S65335	delta opioið receptor	3.29e-175
32	265	26.7	1835	14	MUSDOPRCP	Mouse delta-opioið rec	3.29e-175
33	265	26.7	2203	14	S66181	delta opiate receptor	3.29e-175
34	265	26.7	2219	14	MUSDELTO	Mus musculus delta-opi	3.29e-175
35	265	26.7	2219	25	A38528	Sequence 1 from Patent	3.29e-175
36	265	26.7	2272	14	MUSDELOPRE	Mouse delta opioið rec	3.29e-175
37	253	25.5	1458	16	DRAJ1596	Danio rerio mRNA for o	7.49e-166
38	238	23.9	720	14	S77863	mu-opioið receptor MOR	3.50e-154
39	237	23.8	686	15	SSU71149	Sus scrofa delta opioi	2.10e-153
40	237	23.8	998	25	A38530	Sequence 3 from Patent	1.10e-153
41	214	21.5	2205	15	SSU72758	Rattus norvegicus opio	1.71e-132
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44	210	21.1	1817	14	RATRORC	Rat mRNA for opioið re	1.71e-132
45	210	21.1	2706	14	RATXOR1A	Rattus norvegicus alte	1.71e-132

ALIGNMENTS

RESULT 1 A48343 1142 bp DNA PAT 07-MAR-1997
LOCUS
DEFINITION Sequence 1 from Patent WO9601898.
ACCESSION A48343
NID g2302133

KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1142)
AUTHORS Kieffer, B. and Simonin, F.
TITLE HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF
JOURNAL Patent: WO 9601898-A 1 25-JAN-1996;
UNITV PASTEUR (FR)
COMMENT Other publication FR 2722209 960112.
FEATURES
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BASE COUNT 236 a 283 g 286 t
ORIGIN

Query Match 86.2%; Score 857; DB 25; Length 1142;
Best Local Similarity 98.7%; Pred. No. 0.00e+00;
Matches 862; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Db 317 CTTAGTTACTACAAACCATGGCCCTTTCAGAGTACGGTCTACTTGATGAATTCCTGGCCCT 376
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QY 880 TTCCACTGAAGATGAGGAGGAGCGGCGAGACACTAGCAGAGTCCGAAATACAGTTTCAGG 939
Db 1097 ATCCTGCTTACCTGAGGAGGAGCATCGATGGGATGA 1129
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QY 940 ATCCTGCTTACCTGAGGAGGAGATCGATGGGATGA 972

RESULT 2
LOCUS CP004092 1733 bp mRNA ROD 24-MAY-1995
DEFINITION Cavia porcellus Hartley kappa opioid receptor mRNA, complete cds.
ACCESSION U04092
NID 9476106
KEYWORDS guinea pig.
SOURCE
ORGANISM Cavia porcellus
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
REFERENCE 1 (bases 1 to 1733)
AUTHORS Xie,G.X., Meng,F., Mansour,A., Thompson,R.C., Hoversten,M.T.,

TITLE Goldstein,A., Watson,S.J. and Akil,H.
JOURNAL Primary structure and functional expression of a guinea pig kappa
MEDLINE opioid (dynorphin) receptor
REFERENCE Proc. Natl. Acad. Sci. U.S.A. 91 (9), 3779-3783 (1994)
AUTHORS 2 (bases 1 to 1733)
Xie,G.
TITLE Direct Submission
JOURNAL Submitted (07-DEC-1993) Guo-xi Xie, Mental Health Research
Institute, The University of Michigan, 205 Zina Pitcher Place, Ann
Arbor, MI 48109-0720, USA
FEATURES
source location/Qualifiers
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/organism="Cavia porcellus"
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BASE COUNT 409 a 416 c 505 g 403 t
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Query Match 70.7%; Score 703; DB 14; Length 1733;
Best local Similarity 89.5%; Pred.No. 0.00e+00;
Matches 807; Conservative 0; Mismatches 92; Indels 3; Gaps 2;
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QY 99 AGATACACAAGATGAAAGACAGCAACCAACATTTACATATTTAACCTGGCTTTGGCAGAT 158
Db 555 GCITTTGCACTACCAACCATGGCTTTCCAGAGCACCCTCTACCTGATGAATTCCCTGGCCC 614
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QY 159 GCITTTAGTTACTACAACCATGGCCCTTTCCAGAGTACGGCTCTACTTGATGAATTCCCTGGCCT 218
Db 615 TTGGGGATGTGCTGTGCAAGATAGTCAATTTCCATTGATTTACTACAAACATGTTCCACCAGC 674
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QY 219 TTGGGGATGTGCTGTGCAAGATAGTCAATTTCCATTGATTTACTACAAACATGTTCCACCAGC 278
Db 675 ATATTCAACCTTGACCATGATGAGTGTGGACCGCTACATTTGCTGTGCCACCCCTGTGAAG 734
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QY 279 ATCTTCACCTTGACCATGATGAGCGGTGGACCGCTACATTTGCCGTGTGCCACCCCGTGAAG 338
Db 735 GCACCTGACCTCCGGACACACCCCTTGAAGGCAAGATCATCATATATCTGATTGGCTCTTG 794
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Db 795 TCATCATCTGTGGCAATTTCTGCCATATCCCTTGAGGCGACCAAAATCAGGGAAGATGTG 854
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QY 399 TCGTCATCTGTGGCAATCTCTGCAATAGTCTTTGAGGCGACCAAAATCAGGGAAGGTGTG 458
Db 855 GATATCATGAGTGTCTCTTGACGTTCCCGGATGATGACTACTCTCGTGGGACCTCTTC 914
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QY 459 GATGTCATGAGTGTCTCTTGACGTTCCCGGATGATGACTACTCTCGTGGGACCTCTTC 518
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QY	519	ATGAAGATCGCGTCTTCATCTTTGCCCTCGTGATCCCTGCTCCTCATCATCATCGCTGC	578
Dp	975	TATACTGTGATGATCCTGCGCTGTGAAGAGTGTACAGCTCCTTTCTGGCTCCGAGAGAA	1034
QY	579	TACACCCGTGATGATTCCTGCGCTCTCAAGANNGCCGCTCCTTCTTGCTCCCGAGAGAA	638
Dp	1035	GATCGAACCCTGCGCAGGATCACCAGGCTGGTCTGTGTGTGTGGCAGTGTTCATTATC	1094
QY	639	GATNNCAACCTGCGGTAGGATCACCAGACTGGTCTGTGTGTGTGGCAGTCTTGTGCTC	698
Dp	1095	TGCTGGACCCCGATTTCATTTTCATCCTTTGTGAAGCGCTGGGGAGCAGCTTCCACAGC	1154
QY	699	TGCTGGACTCCCATTCACATATTTCATCCTGTGTGAAGCTCTGGGGAGCACCTCCACAGC	758
Dp	1155	ACCGCGCTCTCTCCAGCTACTACTTCTGTATCGCCTTGGGCTACACCAACAGACGCTG	1214
QY	759	ACAGCTGCTCTCTCCAGCTATTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCTG	818
Dp	1215	AACCCCATCTCTATGCTTCTCTTGATGAAAACTTCAAGCGGTGTTTTCGGGACTTTTGC	1274
QY	819	AATCCCATTTCTTACGCTTTCTTGTATGAAAACTTCAAGCGGTGTTTTCGGGACTTCTGC	878
Dp	1275	TTTCCCATTAAGATGAGGATGGAGAGACAGACAGCACTAGCAGAGTCAGAAAACACAGTCCAG	1334
QY	879	TTTCCACTGAAGATGAGNATGGAGCGCAGAGACAGCAGAGTCCGAATATACAGTTACAG	938
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QY	939	GATCCTGCTTACCTGAGGAGATCGATGGGATGATGATATAAACCAAGTATGACTAGTGTG	998
Dp	1392	GA 1393	
QY	999	GA 1000	

RESULT	3
LOCUS	81111 1288 bp mRNA ROD 02-AUG-1996
DEFINITION	kappa-opioid receptor [alternatively spliced] [mice, C58/J, R1.1 thymoma cells, mRNA Partial, 1288 nt].
ACCESSION	S81111
NID	G1478285
KEYWORDS	.
SOURCE	Mus sp. C58/J R1.1 thymoma cells.
ORGANISM	Mus sp. Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE	1 (bases 1 to 1288) Belkowski, S.M., Zhu, J., Liu-Chen, L.Y., Eisenstein, T.K., Adler, M.W. and Rogers, T.J. Sequence of Kappa-opioid receptor cDNA in the R1.1 thymoma cell line
TITLE	J. Neuroimmunol. 62 (1), 113-117 (1995)
JOURNAL	96084989
MEDLINE	GenBank staff at the National Library of Medicine created this entry [NCBI gidsq 175931] from the original journal article.
REMARK	This sequence comes from Fig. 3. longer of two transcripts.
COMMENT	Location/Qualifiers
FEATURES	1. 1288
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Query Match	67.48;	Score 670;	DB 14;	Length 1288;
Best Local Similarity 87.7%;				Pred. No. 0.00e+00;
Matches 790;	Conservative 0;	Mismatches 108;	Indels 3;	Gaps 2;
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Db	353	GATACACGAAGATGAAGACCGCAACCAACATCTACATATTTAACCTGGCTTGGCAGATG	412	
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QY	220	TTGGGGATGTGCTGTGCAGAGATAGTAAATTTTCCATTGATTAACACATGTTTACCAGCA	279	
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QY	280	TCTTCACCTTGACCATGATGAGCGGTGGACCGCTACATTTGCCGTGTGCCACCCGTGGAAG	339	
Db	593	CTTTGGACTTCGGAACACCTTTGAAAGCAAGATCATCAACATCTGCCATTTGGCTCCTGG	652	
QY	340	CTTTGGACTTCGGAACACCCCTGGAAGCAAGATCATCAATATCTGCCATCTGGCTCCTGT	399	
Db	653	CATCATCTGTGTATATACGCGATAGTCTCTTGGAGGACACCAAGTCAAGGAAGATGTGG	712	
QY	400	CGTCATCTGTGTGCATCTCTGCAATAGTCTCTTGGAGGACACCAAGTCAAGGAAGTGTGG	459	
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QY	460	ATGTCATTGAATGCTCCTTGACGTTTCCAGATGATGACTACTCTGCTGGGACCTCTTCA	519	
Db	773	TGAAGATCTGTGTCTTCGTCCTTTGGCCTTTGTGATCCGACGTCCTCATCATCTATGTCTGT	832	
QY	520	TGAAGATCTGTGTCTTCATCTTTGGCCTTGTGATCCGTCCTCATCATCTATGTCTGTGT	579	
Db	833	ACACCCCTGATGATCCTGCGCCTGAAGAGTGTCCGCGCTCTGTGCGCTCCCGAGAAGAAG	892	
QY	580	ACACCCCTGATGATCCTGCGCTGAAGANNGTCCGCGCTCTGTGCGCTCCCGAGAAGAAG	639	
Db	893	ACCGAATCTCCGCGCATCACCAAGCTGTGTGTGTAGTATGACGTTCTTCATCATCT	952	
QY	640	ATNNCAACCTGCGTAGGATCACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	699	
Db	953	GTTTGAACCCCATTCACATCTTTATCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	1012	
QY	700	GCTGGACTCCCATTCACATATTCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	759	
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QY	880	TTCCTACTGAAGATGAGNATGAGCGGCNAGACACTAGCAGAGTCCGAAATACAGTTCAGG	939	
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QY	940	ATCCTGCTTACCTGAGGAGATGATGGATGATGAATAAACAAGTATGACTAGTGTGTGTGTGT	999	
Db	1250	A 1250		
QY	1000	A 1000		

RESULT	4				
LOCUS	MUSKAPOPRE	1410 bp	MRNA	ROD	13-DEC-1993
DEFINITION	Mouse kappa opioid receptor mRNA, complete cds.				
ACCESSION	L11065				
NID	g348248				
KEYWORDS	kappa opioid receptor.				
SOURCE	Mus musculus (library: Clontech #ML1036a) brain cDNA to mRNA.				
ORGANISM	Mus musculus				
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 1410)				
AUTHORS	Yasuda,K., Raynor,K., Kong,H., Breder,C.D., Takeda,J., Reisine,T. and Bell,G.I.				
TITLE	Cloning and functional comparison of kappa and delta opioid receptors from mouse brain				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740 (1993)				
MEDLINE	93342064				
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BASE COUNT	322 a	360 c	337 g	391 t	
ORIGIN					
Query Match	67.4%;	Score 670;	DB 14;	Length 1410;	
Best Local Similarity	87.7%;	Pred. No. 0.00e+00;			
Matches	790;	Conservative 0;	Mismatches 108;	Indels 3;	Gaps 2;
Db	442	GATACACGAAGTGAAGACCGCAACCAACATCTACATATTTAACCTGGCTTTGGCAGATG	501		
QY	100	GATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACTGGCTTTGGCAGATG	159		
Db	502	CTTTGGTACTACCACTATGCGCTTTACAGAGTGTCTGCTACTTGATGAATCTTGCGCTT	561		
QY	160	CTTAGTTACTACAACCAATGCGCTTTACAGAGTACGCTGCTACTTGATGAATCTTGCGCTT	219		
Db	562	TTGGAGATGTGCTATGCAAGATGTGCTATTTCCATTGACTACACACATGTTACACACA	621		
QY	220	TTGGGATGTGCTGTGCAAGATAGTAATTTCCATTGATTACTACAACATGTTACACACACA	279		
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QY	280	TCTTCACCTTGACCATGATGAGCGGTGACCGCTACATTTGCCGTGTGCCACCCGTGAAG	339		
Db	682	CTTTGGACTTCGGAACACCTTTGAAAGCAAAAGATCATACATCTGCATTTGGCTCTGG	741		
QY	340	CTTTGGACTTCGCGACACCTTTGAAAGGCAAAAGATCATCATATCTGCATCTGGCTGCT	399		
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QY	400	CGTCATCTGTTGGCATCTCTGCAATAGTCTCTGGAGGACCAAAAGTCAGGGAAGGTGCG	459		
Db	802	ATGTCATTGAATGCTCCCTTGAGCTTCTGATGATGATGATATTCCTGTTGGATCTCTCA	861		
QY	460	ATGTCATTGAGTCTGCTGCTGACGTTCCACAGATGATGATCTCTGTTGGACCTCTTCA	519		
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Db	982	ACCGAAATCTCCGCCGATCACCAAGCTGGTGTCTGTAGTAGTTCAGTCTTCATCATCT	1041		
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Db	1042	GTGGACCCCATTCACATCTTATCTCTGTTGAGGAGGCTCTGGGAAGCACCTCCACAGCA	1101		
QY	700	GCTGACTCCCATTCACATATTCATCTCTGTTGAGGAGGCTCTGGGAAGCACCTCCACAGCA	759		
Db	1102	CAGTGCCTCTCCAGCTATTTATTTCTGTTATTTGCCCTTGGTTATACCAACAGACGCTGA	1161		
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QY	880	TTCCTACTGAAGATGAGNATGGAGCGCCNAGACACTAGCAGATCCGAAATACAGTTGAG	939		
Db	1282	ATCCTGTTCTCATGAG--AGAT-GTGGGAGGATGAATAAGCCATGATGACTAGTCTGG	1338		
QY	940	ATCCTGTTCTCATGAGGAGATGATGATGATGAATAAGCCATGATGACTAGTCTGG	999		
Db	1339	A 1339			
QY	1000	A 1000			
RESULT	5				
LOCUS	RATROD	1273 bp	MRNA	ROD	21-DEC-1993
DEFINITION	Rat mRNA for opioid receptor, complete cds.				
ACCESSION	D16534				
NID	9409390				
KEYWORDS	G-protein coupled receptor; opioid receptor; transmembrane protein.				
SOURCE	Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone pROR2.				
ORGANISM	Rattus norvegicus				
	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
REFERENCE	1 (bases 1 to 1273)				
AUTHORS	Nishi,M., Takeshima,H., Fukuda,K., Kato,S. and Mori,K.				
TITLE	cDNA cloning and pharmacological characterization of an opioid receptor with high affinities for kappa-subtype-selective ligands				
JOURNAL	FEBS Lett. 330 (1), 77-80 (1993)				
MEDLINE	93380575				
REFERENCE	2 (bases 1 to 1273)				
AUTHORS	Takeshima,H.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-JUN-1993) to the DDBJ/EMBL/GenBank databases. Hiroshi Takeshima, International Institute for Advanced Studies; c/o Shimadzu Corporation N-80, 1 Nishinokyo-Kuawahara-cho, Kyoto 604, Japan (Tel:075-823-1208, Fax:075-811-8186)				
COMMENT	Submitted (19-JUN-1993) to DDBJ by: Hiroshi Takeshima				
	International Institute for Advanced Studies				
	c/o Shimadzu Corporation				
	N-80				
	1 Nishinokyo-Kuawahara-cho				
	Kyoto 604				
	Japan				
	Phone: 075-823-1208				
	Fax: 075-811-8186.				
FEATURES	Location/Qualifiers				
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Query Match		66.6%; Score 662; DB 14; Length 1273;	
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QY	160	CTTTAGTTACTACACCACTGCCCTTTCAGAGTAGCGGTCTACTTGATGAATTCCTGGCCTT	219
Db	425	TTGGAGATGTTCTGTGCAAGATGTTCATTTCCATTGACTACTACAACATGTTTACCAGA	484
QY	220	TTGGGAGTGTGCTGTGCAAGATGTAATTTCCATTGATTACTACAACAIGTTTACCAGCA	279
Db	485	TATTCACTTGACCATGATGAGTGTGGAACCGCTACATTGCCGTGTGCCACCCGTGAAAG	544
QY	280	TCTTCACCTTGACCATGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCGTGAAG	339
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QY	400	CGTCATCTGTTGGCATCTCTGCATAGTCCCTTGAGGCGACCAAGTCAAGGAAGGTGTGG	459
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Db	845	ACCGAAATCTCCGCGGATCAACCAAGCTGTGCTGTAGTGTGAGTCTTCATCATCT	904
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Db	965	CAGCTGTCCCTCTCTAGCTATTAATCTTGCAATGGCTTGGGTTATACCAACAGCAGCTTGA	1024

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QY	820	ATCCCATTTCTCTACGCGCTTCTTGATGAACAACTTCAAGCGGTGTTTCCGGACTTCTGCT	879
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QY	1000	A 1000	
RESULT 6			
LOCUS RATTOR1A 1358 bp mRNA ROD 21-OCT-1993			
DEFINITION Rat kappa opioid receptor mRNA, complete cds.			
ACCESSION U22001			
NID g409236			
KEYWORDS kappa opioid receptor; opioid receptor.			
SOURCE Rattus norvegicus whole brain cDNA to mRNA.			
ORGANISM Rattus norvegicus			
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;			
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;			
Murinae; Rattus.			
REFERENCE 1 (bases 1 to 1358)			
AUTHORS Chen,Y., Westek,A., Liu,J. and Yu,L.			
TITLE Molecular cloning of a rat kappa opioid receptor reveals sequence			
JOURNAL similarities to the mu and delta opioid receptors			
MEDLINE Biochem. J. 295, 625-628 (1993)			
FEATURES			
source			
CDS			
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BASE COUNT 304 a 353 c 320 g 381 t			
ORIGIN			
Query Match 66.6%; Score 662; DB 14; Length 1358;			
Best Local Similarity 87.2%; Pred. No. 0.00e+00;			
Matches 786; Conservative 0; Mismatches 112; Indels 3; Gaps 1;			
Db	327	GATACACAAGATGAAGACCGCAACCAACATCTACATATTTAACCTGGCTTTGGCAGATG	386
QY	100	GATACACAAGATGAAGACGACGACCAACATTTACATATTTAACCTGGCTTTGGCAGATG	159
Db	387	CTTTGGTTACTACCACTATGCCCTTCCAGAGTGCTGTCTACTTGATGAATTCCTGGCCTT	446
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QY	220	TTGGGAGATGTGCTGTGCAAGATGTAATTTCCATTGATTACTACAACATGTTTACCAGCA	279
Db	507	TATTCACTTGACCATGATGAGTGTGGAACCGCTACATTGCCGTGTGCCACCCGTGTGAAAG	566

ACCESSION	E08874
NID	G2176978
KEYWORDS	JP 1995070191-A/1.
SOURCE	Rattus sp.
ORGANISM	Rattus sp.
REFERENCE	1 (bases 1 to 2481)
AUTHORS	Kimimichi, S.
TITLE	RECEPTOR PROTEIN, ITS PRODUCTION AND USE THEREOF
JOURNAL	Patent: JP 1995070191-A 1 14-MAR-1995;
COMMENT	TAKEDA CHEM IND LTD
OS	Rattus sp. (rat)
PN	JP 1995070191-A/1
PD	14-MAR-1995
PF	30-JUL-1993 JP 1993190261
PR	09-JUL-1993 JP 93P 170591
PI	SATO KIMIMICHI
PC	C07K14/47, C12N1/21, C12N15/09, C12P21/02//A61K38/00, A61K38/00,
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CC	strandedness: Double;
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FH	Location/Qualifiers
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Best Local Similarity	87.18; Pred. No. 0.00e+00;
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QY	220 TTGGGATGTGCTGTGCAAGATAGTAATTTCATTGATTACTACAACATGTTACACCAGCA 279
Db	547 TATTCACCTTGACCAATGATGAGTGTGACCGCTACATTGCCGTGTGCCACCCGTGAAG 606
QY	280 TCTTCACCTTGACCAATGATGAGCGTGGACCGCTACATTGCCGTGTGCCACCCGTGAAG 339
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Db	727 ATGTCAATGAATGCTCCTTGCAAGTTTCCCTGATGATGATGATATTCCTGGTGGACCTCTCA 786
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Db	787 TGAAGATCTGTCTCTGCTTTGGCTTTGTTATCCCTGTCTTAATCATCATTTGCTGT 846
QY	520 TGAAGATCTGTCTCTGCTTTGGCTTTGTTATCCCTGTCTTAATCATCATTTGCTGT 579

Db	847	ACACCCGTATGATCTCTCGCCCTTGAAGAGTGTCCGGCTCTCTCGGGCTCTCGAGAGAAG	906
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Db	907	ACCGAAATCTCCGCCGGATTCACCAAGCTGTGTCTGTAGTGTGTTGCAGTCTTCATCT	966
QY	640	ATNNCAACCTGCGTAGGATTCACCAGACTGGTCTGTGTGTGTGTGGCAGTCTTCGTGCT	699
Db	967	GTTGGACCCCATCCACATCTTTATCCTGTGTGAGGCTTAGCCAGCACCTCTCACAGCA	1026
QY	700	GCTGGACTCCCATTCACATATTCATCTGTGTGTGTGTGGGAGCACCTCCACAGCA	759
Db	1027	CAGCTGTCTCTCTAGCTATTACTTCTGTGATTCGCTTGGGTTATACCAACAGACGTTGA	1086
QY	760	CAGCTGTCTCTCTCAGCTATTACTTCTGTGATTCGCTTAGGCTATACCAACAGTAGCTGA	819
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QY	820	ATCCCATCTCTCTACGCTTCTTGATGAAAACTTCAGCGGTGTTTCCGGACTTCTGCT	879
Db	1147	TCCCATTAAGATGCGAATGAGCGCCAGAGCAACAACAGAGTTAGAAACACAGTTTCAGG	1206
QY	880	TTCACACTGAAGATGAGNNATGGAGCGCMAGAGCACTACAGAGTCCGAATACAGTTTCAGG	939
Db	1207	ATCCTGTCTTCATGAGGGATGTGGTGGGATGA---ATAAGCCAGTATGACTAGTCATGG	1263
QY	940	ATCCTGTCTTACCTGAGGGAGATCGATGGGATGATGAATAAACCAAGTATGACTAGTCGTGG	999
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QY	1000	A 1000	

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RESULT      10      RNU00442      4742 bp      mRNA      ROD      25-MAY-1994
LOCUS
DEFINITION  Rattus norvegicus kappa opioid receptor mRNA, complete cds.
ACCESSION  U00442
NID        9403486
KEYWORDS
SOURCE     Norway rat.
ORGANISM   Rattus norvegicus
            Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
            Murinae; Rattus.
REFERENCE   1 (bases 1 to 4742)
            Meng, F., Xie, G.-X., Thompson, R.C., Mansour, A., Goldstein, A.,
            Watson, S.J. and Akil, H.
            Cloning and pharmacological characterization of a rat kappa opioid
            receptor
            Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958 (1993)
JOURNAL
MEDLINE    94052210
REFERENCE   2 (bases 1 to 4742)
            Meng, F.
            Direct Submission
            Submitted (05-AUG-1993) Fan Meng, Mental Health Research Institute,
            University of Michigan, 205 Zina Pitcher Place, Ann Arbor, Michigan
            48109, USA
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Matches 785; Conservative 0; Mismatches 113; Indels 3; Gaps 1;

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RESULT 11
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DEFINITION kappa opiod receptor [mice, genomic, 1186 nt, segment 3 of 3].
ACCESSION S77872
NID g998531
KEYWORDS
SEGMENT 3 of 3
SOURCE Mus sp.
ORGANISM Mus sp.
Mus sp.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.

REFERENCE 1 (bases 1 to 1186)
AUTHORS Liu,H.C., Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Loh,H.H.
and Wei,L.N.
TITLE Cloning and promoter mapping of mouse kappa opiod receptor gene
JOURNAL Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
MEDLINE 95251663
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 166539] from the original journal article.
This sequence comes from Fig. 2.
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BASE COUNT 310 a 272 c 254 g 350 t
ORIGIN

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Best Local Similarity 85.5%; Pred. No. 5.75e-268;
Matches 472; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

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QY 449 GGAAGGTGTGATGATGATGATGCTGCTGCTGAGTTTCCAGATGATGACTACTCTGCTG 508
344 GGATCTCTICATGAAGATCTGTGCTCTGCTCTTGGCCTTTGTGATCCAGTCCATCATCAT 403
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QY 509 GGACCTCTTCATGAAGATCTGCGCTCTTCATCTTTGCCCTTGATTCCTGCTCATCAT 568
404 CATGTCTGTCTACACCTGATGATCTGCGCCTGAAGAGTGTCCGGCTCCTGTCTGGCTC 463
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QY 569 CATGCTGTCTACACCTGATGATCTGCGCTCTGAAGANNGTCCGGCTCCTTTCTGGCTC 628
464 CCGAGAGAAGACCGAAATCTCCGCCGATCACCAAGCTGTGTGTGATGATGATGATGAT 523
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QY 989 ACTAGTCGTGA 1000

RESULT 12 MUSMORGD3 638 bp DNA ROD 12-APR-1996
LOCUS Mouse MORGD gene for kappa-opioid receptor, exon 3.
DEFINITION D31665
ACCESSION 9643595
NID
KEYWORDS G-protein associated; kappa opioid receptor; opioid drugs and peptides-binding; transmembrane protein.
SEGMENT 3 of 3
SOURCE Mus musculus DNA, clone_lib:phage lambda fixII.
ORGANISM Mus musculus
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 638)
AUTHORS Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,T.
TITLE Structure and chromosomal mapping of genes for the mouse +kappa-opioid receptor and an opioid receptor homolog (MOR-C)
JOURNAL Biochemical and Biophysical Research Communication 205, 1353-1357 (1994)
REFERENCE 2 (bases 1 to 638)
AUTHORS Takeshima,H.
TITLE Direct Submission
JOURNAL Submitted (28-May-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi Takeshima, Tokyo Institute of Psychiatry, Department of Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan (Tel:03-3304-5701(ex.312), Fax:03-3329-8035)
COMMENT Submitted (28-May-1994) to DDBJ by: Hiroshi Takeshima
Department of Neurochemistry
Tokyo Institute of Psychiatry
2-1-8 Kamikitazawa, Setagaya-ku
Tokyo 156
Japan
Phone: 03-3304-5701 x312
Fax: 03-3329-8035.

FEATURES
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/clone_lib="phage lambda fixII"
join(D31663:111..367,D31664:89..441,28..560)
/codon_start=1
/product="Kappa-opioid receptor"
/db_xref="PID:d1007079"
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/translation="MESPIQIRGDDPPTCSPSACLIPNSSSWFPMWAESDSNGSVGS"

EDQLESASHISPAIPVITIAVSVVYVGLVGNLSLMFVIRYTKMTAINTIENLA
LADALVTTTTPQSAVILMNSWPEGLVCKIVISIDYINMTSIFILMNSVDRIAY
CHPVKALDFRPLKAKIINICIMWLASVGISAIVLGTVKREDVDYIHCLLQFPDE
YSWMDLFMKICVVEAFVILPVLIVGYIMILRLKSVRLSGSREKDRNLRIITKLIV
LVVAVFTICWTPIHIFILVEALGSTSHSTAALSSYFICIALGYTNSLNPVLYAFID
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28..560
/note="third protein coding sequence (P3)"
/number=3

BASE COUNT 141 a 154 c 151 g 192 t
ORIGIN Chromosome 1 A2-3.

Query Match 38.0%; Score 378; DB 14; Length 638;
Best Local Similarity 84.9%; Pred. No. 5.14e-264;
Matches 471; Conservative 0; Mismatches 81; Indels 3; Gaps 2;

Db 20 CAGGACAGATGTGATGTCATGAATGCTTGTGACGTTTCCGTGATGATATTCCTG 79
QY 446 CAGGAGAGGTGTGATGTCATGAGTGTGCTTGCAGTTCACAGATGATGACTACTCTG 505
Db 80 GTGGATCTCTTCATGAAGATCTGTGCTGCTCTTGGCTTTGTGATCCAGTCTCAT 139
QY 506 GTGGACCTCTTCATGAAGATCTGCTCTTCATCTTTGGCTTGTGATCCGTCGTCAT 565
Db 140 CATCATTTCTGCTACACCTGATGATCTCGCGCTGAAGAGTGTCCGGCTGCTGTGG 199
QY 566 CATCATCTGCTGTACACCTGATGATCTCGCTGCTGAAGANNNGTCCGCTCTCTGTGG 625
Db 200 CTCCGAGAGAGGACCGAATCTCCGCCGACACCAAGCTGTGCTGTAGTAGTTGC 259
QY 626 CTCCGAGAGAGAGATNNCAACCTGCGTAGATCACAGACTGTCTGTTGGTGGC 685
Db 260 AGTCTTCATCATCTGTTGGAACCCCATTCACATCTTATCTGTGAGGCTCTGGAG 319
QY 686 AGTCTTCTGCTGCTGTGACCTCCCATTCACATATTCATCTGTTGAGGCTCTGGAG 745
Db 320 CACCTCCACAGACAGCTGCCCTCTCCAGCTATTTCTGTATTCCTTGGTTATAC 379
QY 746 CACCTCCACAGACAGCTGCTCTCTCCAGCTATTTCTGTCATCGCCTTAAAGCTATAC 805
Db 380 CACAGACAGCTGAATCTGTTCTTAATGCTTCTGTGATGAAGAACTTCAAGCGGTGT 439
QY 806 CACAGTAGCCTGAATCCATTTCTTACGCCCTTCTGTGATGAAGAACTTCAAGCGGTGT 865
Db 440 TAGGACTTCTGCTTCCCTATTAGATGCGAATGAGCGCCAGAGCACCAATAGAGTTAG 499
QY 866 CCGGACTTCTGCTTCCACTGAAGATGAGNATGAGCGCAGAGACTAGCAGAGTCCG 925
Db 500 AAACACAGTTCAGATCCTGCTTCCATGAG--AGAT-GTGGAGGAGTGAATAGCCAGT 556
QY 926 AAATACAGTTCAGATCCTGCTTACCTGAGGAGATGATGGATGATGAATAACCAAGT 985
Db 557 ATGACTAGTCGTGA 571
QY 986 ATGACTAGTCGTGA 1000

RESULT 13 RNKOR3 4048 bp DNA ROD 25-MAR-1995
LOCUS Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.
DEFINITION Rattus norvegicus
ACCESSION U17995
NID 9727258
KEYWORDS 3 of 3
SEGMENT Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorphna; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 4048)
AUTHORS Yakovlev,A.G., Krueger,K.E. and Faden,A.I.
TITLE Structure and expression of a rat kappa opioid receptor gene

JOURNAL	U. Biol. Chem. 270 (12), 6421-6424 (1995)
MEDLINE	95204422
REFERENCE	2 (bases 1 to 4048)
AUTHORS	Yakovlev/A.G.
TITLE	Direct Submission
JOURNAL	Submitted (02-DEC-1994) Alexander G. Yakovlev, Georgetown University School of Medicine, Neurology, 3900 Reservoir Rd., Washington, DC 20007, USA
FEATURES	Location/Qualifiers
source	1. 4048
	/organism="Rattus norvegicus"
	/strain="Sprague-Dawley"
	/db_xref="taxon:10116"
	/sex="male"
mRNA	join(UI7993:519..1044,UI7993:1405..1705,UI7994:226..578,89..3951)
	/note="first of two alternate transcripts; uses exons 1, 2, 3, and 4"
mRNA	join(UI7993:1083..1707,UI7994:226..578,89..3951)
	/note="second of two alternate transcripts; does not use exon 1, and the 5' end of exon 2 is extended into intron 1"
CDS	join(UI7993:1451..1707,UI7994:226..578,89..621)
	/codon_start=1
	/product="kappa opiate receptor"
	/db_xref="PID:g727260"
	/translation="MESPQIFRGEPTCAPSACLLPNSSWEPNWAESDSNGSVGS EDQQLPAHISPAIPVITAVSVFVGLVGNLSMVFIRYRKKTATNIYFNLA LADALVTMTMPEQSAVYIMNSWPEGVLCIKVISIDYNNMETSIFLLMSVDYIAV CHPYKALDFRTPLEKAKIINICWILASSVGISAVLGGTKVEDYIECSLQPPDE YSWMDLFMKICVEFAFVILPALLIYCYTIMLRKSVRLSGSREKDRNLRLITKLV LVVAVFILICWPIHIHIFILVEALGSTSHSTAVLSYFICIALGYTNSLNPVLYAFLD ENFKRGRDFCFPIKRMERQSTNRVNTVQDPASMRDVGKMKPV"
intron	<1..88
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	/evidence=experimental
exon	89..3951
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	/evidence=experimental
	/product="kappa opiod receptor"
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Query Match	37.7%; Score 375; DB 14; Length 4048;
Best Local Similarity	84.8%; Pred. No. 1.21e-261;
Matches	468; Conservative 0; Mismatches 81; Indels 3; Gaps 1;
Db	84 GGCAGATGTGGATGATGATGATGCTCCTTGACAGTTTCCTGATGATGATATATTCCTGGT 143
QY	449 GGAAGGTGTCGATGATGATGATGCTGCTTGACAGTTCCAGATGATGATGATGATGATGATG 508
Db	144 GGAACCTCTTCATGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
QY	509 GGAACCTCTTCATGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568
Db	204 CATGTCTGCTACACCCCTGATGATCCTGCGCTTGAAGAGTGTCCGGCTCTCTCGGGCTC 263
QY	569 CATGCTCTGCTACACCCCTGATGATCCTGCGCTTCAAGANNGTCCGGCTCTTCTGGCTC 628
Db	264 TCGAGAGAGAGACCGGAATTCGCCCGGATCACCACCAAGCTGGTGTGCTAGTGTGCACT 323
QY	629 CCGAGAGAGAAAGATNCAACCTGCGGTAGGATCACCACAGACTGCTCCTGGTGTGCGCAGT 688
Db	324 CTTCATCATCTGTTGGACCCCATCCACATCTTATCCTGGTGAAGGCTCTAGGCAGCAC 383
QY	689 CTTCGTCGCTGCTGGACTCCCAATTCACATATTCATCCTGGTGAAGGCTCIGGGAGCAC 748
Db	384 CTCACACAGACAGCTGTCTCTCTAGCTATTACTTCTGCATGACCTTGGGTTATACCAA 443
QY	749 CTCACACAGACAGCTGTCTCTCTAGCTATTACTTCTGCATGACCTTGGGTTATACCAA 808
Db	444 CAGCAGCTTGAATCCTGTTCTATGCCCTTCTTGATGAAGAACTTCAAGCGGTGTTTAA 503

QY	809	CAGIAGCCGTAATCCCATCTCTACGGCCTTCTTGATGAAACTTCAAGCGGTGTTCCG	868
Db	504	GGACTTCTGCTTCCCATTTAAGATGCGAATGGAGCCGACAGCAACAGAGTTAGAAA	563
QY	869	GGACTTCTGCTTCCACTGAAGATGAGNATGGAGCGGNAGAGCACTAGCAGAGTCCGAAA	928
Db	564	CACAGTTCAAGATCCTGCTTCCAGAGGAGTGTGGTGGGATGA---ATAAGCCAGTATG	620
QY	929	TACAGTTCAAGATCCTGCTTACCCTGAGGAGATCGATGGATGATGAATAAACAGATATG	988
Db	621	ACTAGTCATGGA	632
QY	989	ACTAGTCGTGGA	1000
RESULT	14		
LOCUS	S77868S2	1109 bp	DNA
DEFINITION	kappa oploid receptor [mice, Genomic, 1109 nt, segment 2 of 3].		
ACCESSION	S77869		
NID	g998530		
KEYWORDS	.		
SEGMENT	2 of 3		
SOURCE	Mus sp.		
ORGANISM	Mus sp.		
REFERENCE	1 (bases 1 to 1109)		
AUTHORS	Liu,H.C., Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Loh,H.H. and Wei,L.N.		
TITLE	Cloning and promoter mapping of mouse kappa oploid receptor gene		
JOURNAL	Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)		
MEDLINE	95251663		
REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI g1bbsq 166534] from the original journal article. This sequence comes from Fig. 2.		
FEATURES	Location/Qualifiers		
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ORIGIN			361 t
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Best Local Similarity	86.5%;	Pred. No. 3,71e-215;	
Matches	392;	Conservative	0; Mismatches 58; Indels 3; Gaps 2;
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QY	4	AAGCAAAATCAGTAATCCAAAGGCTATCACAAACACATTCACCTATGGGGTTGACTTG	63
Db	333	AGACATGGAAGGAATGTACTGTTTCTTATTTTATGATACACGAAGATGAAGACCGCA	392
QY	64	AAA-ATGAGGGAAGTGTATTGTTCTTCTTTCTTTAGATACACAAAGATGAAGACGCA	122
Db	393	ACCAACATCTACATATTTAACTGGCTTTGGCAGATGCTTTGGTACTACCACTATGCC	452
QY	123	ACCAACATTTACATATTTAACTGGCTTTGGCAGATGCTTTAGTTACTACAACCATGCC	182
Db	453	TTTCAGAGTGTCTGTCTACTTGATGAATCTTGGCCCTTTGGAGATGTGCTATGCAAGATT	512
QY	183	TTTCAGAGTACGGTCTACTTGATGAATTCCTGCGCTTTGGGGATGTGCTGTGCAAGATA	242
Db	513	GTCATTTCCATTTGACTACTACAACATGTTTACCAGCATATTCACCTTGACCATGATGAGT	572
QY	243	GTAATTTCCATTTGATTACTACAACATGTTTACCAGCATCTTCACCTTGACCATGATGAGC	302
Db	573	GTGAGCCGCTACATTTGCTGTGTGCCACCCCTGTGAAGCTTTGGACTTCGGAACACCTTTG	632
QY	303	GTGAGCCGCTACATTTGCCGTGTGCCACCCCGTGAAGGCTTTGGACTTCGGAACACCTTTG	362
Db	633	AAAGCAAGATCATCAACATCTGCATTTGGCTCCTGCATCATCTGTTGTATATCAGCG	692

QY 363 AAGGCAAGATCATCATATCTGCATCTGGCTGCTGCTGTCATCTGTTGGCAICTCTGCA 422

Db 693 ATAGTCCTTGGAGGCACCAAAAGTCAGGGAAGT 725

QY 423 ATAGTCCTTGGAGGCACCAAAAGTCAGGGAAGT 455

RESULT 15

LOCUS MUSMORGP2 488 bp DNA ROD 12-APR-1996

DEFINITION Mouse MORGD gene for kappa-opioid receptor, exon 2.

ACCESSION D31664

NID 9643594

KEYWORDS G-protein associated; kappa opioid receptor; opioid drugs and peptides-binding; transmembrane protein.

SEGMENT 2 of 3

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 488)

AUTHORS Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,T.

TITLE Structure and chromosomal mapping of genes for the mouse +kappa-opioid receptor and an opioid receptor homolog (MOR-C)

JOURNAL Biochemical and Biophysical Research Communication 205, 1353-1357 (1994)

REFERENCE 2 (bases 1 to 488)

AUTHORS Takeshima,H.

TITLE Direct Submission

JOURNAL Submitted (28-MAY-1994) to the DDBJ/EMBL/Genbank databases. Hiroshi Takeshima, Tokyo Institute of Psychiatry, Department of Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan (Tel:03-3304-5701(ex.312), Fax:03-3329-8035)

COMMENT Submitted (28-May-1994) to DDBJ by: Hiroshi Takeshima Department of Neurochemistry Tokyo Institute of Psychiatry 2-1-8 Kamikitazawa, Setagaya-ku Tokyo 156 Japan Phone: 03-3304-5701 x312 Fax: 03-3329-8035.

FEATURES

source location/Qualifiers

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/organism="Mus musculus"

/db_xref="taxon:10090"

/clone_lib="phage lambda fixit"

89..441

/note="second protein coding sequence (P2)"

exon /number=2

BASE COUNT 129 a 103 c 97 g 159 t

ORIGIN Chromosome 1 A2-3.

Query Match 31.7%; Score 315; DB 14; Length 488;

Best Local Similarity 90.5%; Pred. No. 2.27e-214;

Matches 352; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Db 55 ATGGAAGGAATGTACTGTTTCTTATTTTATAGATACAGAGATGAAGACCGCAACCA 114

QY 67 ATGAGGGGAATGCTATGTGTTCTTTCTTTAGATACAGAGATGAAGACAGCAACCA 126

Db 115 ACATCTACATATTTAACCCTGGCTTTGGCAGATGCTTGGTTACTACCACTATGCCCTTTC 174

QY 127 ACATTTACATATTTAACCTGGCTTTGGCAGATGCTTAGTTACTACAACCATGCCCTTTC 186

Db 175 AGAGTGTCTCTACTTGATGAATTCCTTGCCCTTTGGAGATGTGCTATGCAAGATTGTCA 234

QY 187 AGAGTACGGTCTACTTGATGAATTCCTTGCCCTTTGGGAGATGTGCTGTGCAAGATTAGTAA 246

Db 235 TTTCATTGACTACTACACATGTTTACACAGCATATTCACCTTGACCATGATGAGTGTGG 294

QY 247 TTTCATTGATTACTACACATGTTTACACAGCATTTCACTTGACCATGATGAGCGTGG 306

Db 295 ACCGCTACATTGCTGTGTGCCAACCCCTGTGAAGCCTTTGGACCTCCGAACACCTTTGAAAG 354

QY 307 ACCGCTACATTGCGCGTGTGCCAACCCCGTGAAGCCTTTGGACCTCCGACACACCTTTGAAAG 366

Db 355 CAAAGATCATCAACATCTGCATTTGGCTCCTGGCATCATCTGTGTATATCAGCATAG 414

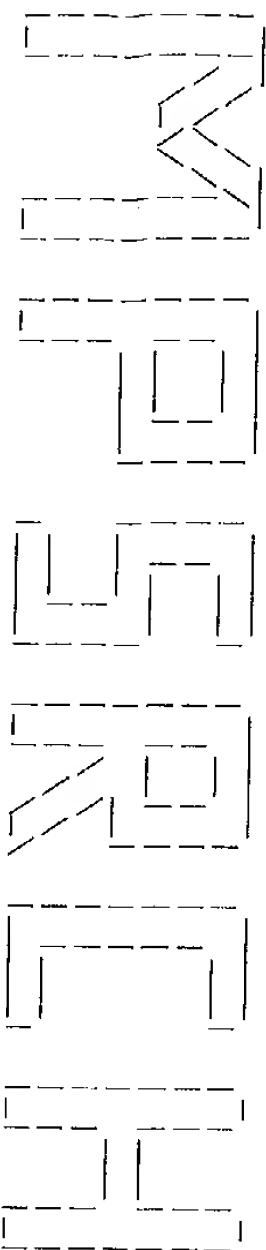
QY 367 CAAAGATCATCAATATCTGCATCTGGCTGCTGCTGTCATCTGTGTGGCACTCTGCAATAG 426

Db 415 TCCTTGGAGGCACCAAAAGTCAGGGAAGT 443

QY 427 TCCTTGGAGGCACCAAAAGTCAGGGAAGT 455

Search completed: Mon Apr 20 23:47:15 1998

Job time : 920 secs.



Release 3.0.4A John F. Collins, Biocomputing Research Unit.
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Msrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Mon Apr 20 23:10:34 1998; MasPar time 1013.06 Seconds
Tabular output not generated. 1172.160 Million cell updates/sec

Title: >US-08-292-694A-1
Description: (1-1410) from US08292694A.seq
Perfect Score: 1410
N.A. Sequence: 1 GCGCAGCTTGCTGATCCCAA.....AACCCAGATTACACTGCAG 1410
Comp: CGCGTGGAGACGACTAGGGTT.....TTGGGTCTAATGTTGACGCTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1126798 seqs, 421087984 bases x 2

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: emb1-est
1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
6:em_est6 7:em_est8 8:em_gss
Database: genbank-est
9:gb_est1 10:gb_est2 11:gb_est3 12:gb_est4 13:gb_est5
14:gb_est6 15:gb_est7 16:gb_est8 17:gb_est9 18:gb_est10
19:gb_est11 20:gb_sts 21:gb_gss 22:gb_est12 23:gb_est13

Statistics: Mean 11.354; Variance 1.916; scale 5.926

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	123	8.7	183	10	R81583	Yj04b04.r1	Homo sapien	2.22e-214	
2	103	7.3	153	10	R31984	Yh62c10.r1	Homo sapien	5.21e-168	
3	78	5.5	433	10	R81332	Yj04b04.s1	Homo sapien	1.17e-111	
4	42	3.0	373	9	T08926	EST06818	Homo sapiens	9.14e-37	
5	41	2.9	450	13	W04836	za81f05.r1	Soares feta	6.99e-35	
6	32	2.3	324	9	T77094	yc93b07.r1	Homo sapien	8.30e-19	
7	30	2.1	435	10	R31938	Yh62c10.s1	Homo sapien	1.67e-15	
8	29	2.1	3055	20	G28604	human STR SHGC-35403.		6.76e-14	
9	27	1.9	249	11	H29103	Ym31f07.r1	Homo sapien	8.71e-11	
10	27	1.9	319	13	HSC27C021	H. sapiens partial cDN		8.71e-11	
11	27	1.9	386	11	H14301	Ym63c04.r1	Homo sapien	8.71e-11	
12	27	1.9	416	16	AA182250	mt83h08.r1	Soares feta	8.71e-11	
13	27	1.9	478	17	AA189997	mt98e07.r1	Soares feta	8.71e-11	
14	27	1.9	492	21	B50064	CIT978SK-2206.TV	CIT97	8.71e-11	
15	27	1.9	602	23	AA511931	vg17f07.r1	Soares feta	8.71e-11	

16	27	1.9	1664	20	G28514	human STR SHGC-31461.	8.71e-11
17	25	1.8	217	22	C10515	C.elegans cDNA clone Y	7.87e-08
18	24	1.7	249	11	T29782	EST94762	Homo sapiens
19	24	1.7	391	22	AA436714	z666d05.s1	Soares test
20	24	1.7	391	13	N93987	z666d05.r1	Soares para
21	24	1.7	442	15	W56386	z675a06.r1	Soares para
22	24	1.7	442	15	W79255	z675c02.r1	Soares feta
23	24	1.7	453	15	W63664	z657g11.r1	Soares para
24	24	1.7	514	22	HUM421E11B	Human fetal brain cDNA	2.04e-06
25	24	1.7	598	15	W37328	zcl1h02.r1	Soares para
26	24	1.7	2856	20	G28560	human STR SHGC-35278.	2.04e-06
27	22	1.6	255	10	R15444	Y46a09.s2	Homo sapien
28	23	1.6	261	18	AA331167	EST35211	Embryo, 8 wee
29	23	1.6	300	22	C11312	C.elegans cDNA clone Y	4.71e-05
30	23	1.6	316	19	AA386021	EST99944	Pancreas tumo
31	23	1.6	327	10	R27256	Yh53d01.r1	Homo sapien
32	23	1.6	339	13	HSB18A052	H. sapiens partial cDN	4.71e-05
33	23	1.6	370	23	R1CS16541A	Rice cDNA, partial seq	4.71e-05
34	23	1.6	385	11	R91585	Yq10a01.r1	Homo sapien
35	23	1.6	404	11	H14901	Y126a04.r1	Homo sapien
36	23	1.6	416	11	H44713	Yp24d06.r1	Homo sapien
37	23	1.6	420	11	H26756	Y15b08.s1	Homo sapien
38	22	1.6	431	23	AA467444	Vf05g04.r1	Knowles Sol
39	22	1.6	443	20	G09917	human STR CH1C.GGAA20B	9.66e-04
40	23	1.6	462	10	R43005	Yg09a07.s1	Homo sapien
41	23	1.6	501	11	H43475	Y064e04.r1	Homo sapien
42	23	1.6	559	17	AA239704	my15c07.r1	Bartstead mo
43	23	1.6	580	19	AA054783	zk68d04.r1	Soares preg
44	23	1.6	598	21	FR0027571	F.rubripes GSS sequenc	4.71e-05
45	23	1.6	791	13	W28236	44a1 Human retina cDNA	4.71e-05

ALIGNMENTS

RESULT 1
LOCUS R81583 183 bp mRNA EST 12-JUN-1995
DEFINITION Yj04b04.r1 Homo sapiens cDNA clone 147727 5' similar to gb:L25119
MU-TYPE OPIOID RECEPTOR (HUMAN);.
ACCESSION R81583
NID g858186
KEYWORDS EST.
SOURCE human clone=147727 library=Soares placenta Nb2HP vector=pT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13R1 Rs1tel=Not I Rs1tel2=Eco RI female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dt) primer (5',
AACTGAGAGAAATTCGGCGGCGGAGGAAATTTTCTTTTCTTTTCTTTT 3'), double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
Homo sapiens

ORGANISM

Eukaryota; Metazoa; Eumetazoa; Bilateria; Chordata; Osteichthyes;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chordata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 183)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Irevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1

High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.

FEATURES
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1. 183
/organism="Homo sapiens"
/clone="147727"

BASE COUNT
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ORIGIN

Query Match 8.7%; Score 123; DB 10; Length 183;
Best Local Similarity 81.2%; Pred. No. 2.22e-214;
Matches 147; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Db 3 TCTTTGCTTCGAGCCCTGTCTCATCATCATGCTGCTACACCCCTNATGATCCTGC 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 880 TCTTGCCTTTGTGATCCAGTCCATCATCATGCTGTGCTACACCCCTGATGATCCTGC 939
Db 63 GTCTCAAGAGCNTCNGNTCTTCTTCTGCTCCGAGAGANGATCGCAACCTGGCTAGGA 122
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 940 GCCTGAAGAGTGTCCGCTCTGTCTGCTCCGAGAGAGACCGAATCTCCGCCGCA 999
Db 123 TCACCAAGACTGTCTGTAGTNGTGGCAGANATCTGCTGTGACTCCCATTCACA 182
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1000 TCACCAAGCTGTGTGTAGTAGTTGCAGTCTTCATCATCTGTGTGGACCCCATTCACA 1059
Db 183 T 183
QY 1060 T 1060

RESULT 2 R31984 153 bp mRNA EST 28-APR-1995
LOCUS yh62c10.r1 Homo sapiens cDNA clone 134322 5' similar to gb:L25119
DEFINITION NO-TYPE OPIOID RECEPTOR (HUMAN);.
ACCESSION R31984
NID 9787827
KEYWORDS EST.
SOURCE human clone=134322 library=Soares placenta Nb2HP vector=PT7T3D

(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13Rp1 Rsite1=Not I Rsite2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dt) primer [5',
AACTGGAAGAATTCGGCGCCGACGAGAAATTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified PT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 153)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 120
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source
1. 153
/organism="Homo sapiens"
/clone="134322"

BASE COUNT
25 a 49 c 37 g 42 t
ORIGIN

Query Match 7.3%; Score 103; DB 10; Length 153;
Best Local Similarity 87.1%; Pred. No. 5.21e-168;
Matches 121; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 3 GTCTCATCTTTGCTTCGTGATCCCTGTCTCATCATGCTGTGCTACACCCGTGATG 62
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QY 873 GTCTTCGCTTTTGCTTTGTGATCCAGTCCATCATCATGCTGTGCTACACCCGTGATG 932
Db 63 ATCTGCGCTCTCAGAGCGCTCCGGCTCTTCTGCTCCCGAGAGAAAGATCGCAACTG 122
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 933 ATCTGCGCTCTCAGAGAGTGTCCGGCTCTTCTGCTCCCGAGAGAGAACCGAAATCTC 992
Db 123 CGTAGCATCACCAGACTGG 141
QY 993 CGCCGATCACCAGCTGG 1011

RESULT 3 R81332 433 bp mRNA EST 12-JUN-1995
LOCUS yj04b04.s1 Homo sapiens cDNA clone 147727 3'.
DEFINITION R81332
ACCESSION R81332
NID 9857935
KEYWORDS EST.
SOURCE human clone=147727 library=Soares placenta Nb2HP vector=PT7T3D

(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=Promega -21m13 Rsite1=Not I Rsite2=Eco RI Female
placenta obtained at birth (full term). 1st strand cDNA was primed
with a Not I - oligo(dt) primer [5',
AACTGGAAGAATTCGGCGCCGACGAGAAATTTTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified PT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 433)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 241
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES
source
1. 433
/organism="Homo sapiens"
/clone="147727"

BASE COUNT 102 a 97 c 100 g 114 t 20 others
ORIGIN

Query Match 5.5%; Score 78; DB 10; Length 433;


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/sex="male"
/dev_stage="4 weeks"
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Query Match      1.9%; Score 27; DB 16; Length 416;
Best Local Similarity 71.4%; Pred. No. 8.71e-11;
Matches 45; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
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Db 286 TCA 288
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QY 1195 TCA 1197
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RESULT 13
LOCUS      AA189997      478 bp      mRNA      EST      17-FEB-1997
DEFINITION mt98e07.r1 Soares mouse 3NbMS Mus musculus cDNA clone 637956 5'
ACCESSION  AA189997
NID         g1776584
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
REFERENCE  1 (bases 1 to 478)
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
          Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
          Scheilenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
          Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
          Waterston,R.
          The WashU-HHMI Mouse EST Project
          Unpublished (1996)
TITLE     The WashU-HHMI Mouse EST Project
JOURNAL
COMMENT
```

Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:389948
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 467.
Location/Qualifiers
1..478
/organism="Mus musculus"
/strain="C57BL/6J"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAGTGGAGCGGCCGCGCTTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."

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/tissue_type="Spleen"
/dev_stage="4 weeks"
/lab_host="DH10B"
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Query Match      1.9%; Score 27; DB 17; Length 478;
Best Local Similarity 71.4%; Pred. No. 8.71e-11;
Matches 45; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
Db 118 CCTGGCTTCTTCACACAGCTGCCTCAATCCATGCTTTATGTTTATGGCCAGACT 177
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QY 1135 CCTGGCTTATACCAACAGCAGCCTGAATCCTGTTCTCTATGCCCTTCTGATGAAACT 1194
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Db 178 TCA 180
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QY 1195 TCA 1197
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RESULT 14
LOCUS      B50064      492 bp      DNA      GSS      10-NOV-1997
DEFINITION CIT978SK-2206.TV CIT978SK Homo sapiens genomic clone 2206.
ACCESSION  B50064
NID        g2602301
KEYWORDS   GSS.
SOURCE     human.
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 492)
AUTHORS   Kim,U.-J., Adams,M.D. and Simon,M.I.
TITLE     Determination of clone end sequences of human Bacterial Artificial
          Chromosomes
JOURNAL   Unpublished (1997)
COMMENT   other_GSSs: CIT978SK-2206.TP
          Contact: Ung-Jin Kim
          Caltech Genome Research Lab
          California Institute of Technology
          Division of Biology, MS 147-75, Pasadena, CA 91125, USA
          Tel: 626 796 7066
          Fax: 626 395 4901
          Email: ung@ash.tree.caltech.edu
          For clone availability, please contact Ung-Jin Kim
          (ung@ash.tree.caltech.edu)
          Seq primer: T7
          Class: BAC ends.
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Location/Qualifiers
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Caltech Human BAC Library A"
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/clone="2206"
/clone_lib="CIT978SK"
/sex="Female"
/cell_type="Fibroblast"
BASE COUNT 130 a 102 c 160 g 98 t 2 others
ORIGIN

Query Match 1.9%; Score 27; DB 21; Length 492;
Best Local Similarity 77.6%; Pred. No. 8.71e-11;
Matches 38; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Db 340 GTAGCAAGCTGTGATGATGAGGACTGGAGCAAGCAAGCAAGCAAGCAAG 388
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Cp 923 GTAGCAGACAATGATGATGAGGACTGGATCACAAGGCAAGCAAGCAAG 875

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LOCUS      AA511931      602 bp      mRNA      EST      08-JUL-1997
DEFINITION vg17f07.r1 Soares mouse NbMH Mus musculus cDNA clone 861637 5'
          similar to gb:LI9315 CHOLECYSTOKININ TYPE A RECEPTOR (HUMAN);.
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ACCESSION AA511931
NTID g2249785
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 602)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

TITLE The WashU-HM1 Mouse EST Project
JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
WashU-HM1 Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
MGI:505725
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 388.
Location/Qualifiers

FEATURES
source
1..602
/organism="Mus musculus"
/strain="O57BL/6J"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer 15'
TGTTACCAATCTGAAGTGGAGCGCGCGCAAGTTTCTTTTCTTTTCTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT7T3 vector. RNA
provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
/db_xref="taxon:10090"
/clone_lib="Soares mouse NbMH"
/sex="male"
/tissue_type="heart"
/dev_stage="4 weeks"
/lab_host="DH10B"
<1..>602

BASE COUNT 142 a 164 c 144 g 152 t
ORIGIN

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Best Local Similarity 66.3%; Pred.No. 8.71e-11;
Matches 55; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
Db 355 TGGGGAACGCTGGTTATCAGCGTGTGCTGATTCGAACAAGAGATCGGACTGTACCA 414
QY 409 TGGGCAATTCCTGTCATGTTGTGATCATCCGATACACGAAGATGAAGACCGCAACCA 468
Db 415 ACATCTTCCTGCTGTCCCTGGCT 437
QY 469 ACATCTACATAATTAACTGGCT 491

Search completed: Mon Apr 20 23:27:43 1998
Job time : 1029 secs.

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Best Local Similarity 100.0%;		Pred. No. 0.00e+00;			
Matches 1410;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Db	1	GCGCACCTTGCTGATCCCAAAACAGCAGAGCTCTCTCCAGTCTTGGAGGACAAATTGA	60		
QY	1	GCGCACCTTGCTGATCCCAAAACAGCAGAGCTCTCTCCAGTCTTGGAGGACAAATTGA	60		
Db	61	GCATCAGGAACGTGGACCCATCAGGGCTGAACAGCTACTCAGGATCTAAAGTGTGACTT	120		
QY	61	GCATCAGGAACGTGGACCCATCAGGGCTGAACAGCTACTCAGGATCTAAAGTGTGACTT	120		
Db	121	GGAAGCTGACGCTGACTTGGGAAGGAGGTGCGCAATCAGCGATCTGAGCTGCACGCG	180		
QY	121	GGAAGCTGACGCTGACTTGGGAAGGAGGTGCGCAATCAGCGATCTGAGCTGCACGCG	180		
Db	181	TCACCATGGAGTCCCCCATTCAGATCTTCCGAGAGATCCAGGCCCTACCTGCTCTCCA	240		
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QY	421	TGGTCATGTTTGTTCATCATCCGATACACGAAGATGAAGACCGCAACACATCTACATAT	480		
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QY	481	TTAACCTGGCTTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTTCAGAGTGTGCT	540		
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Db	601	ACTACAACATGTTTACCAGCATATTCACCTTGACCATGATGATGTGGACCGCTACATTG	660		
QY	601	ACTACAACATGTTTACCAGCATATTCACCTTGACCATGATGATGTGGACCGCTACATTG	660		
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QY	721	ACATCTGCATTTGGCTCCTGGCATCACTGTGTGATATCAGCGATAGTCCCTTGAGGCA	780		
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QY	781	CCAAAGTCAGGGAAGATGTGATGTCAATGAATGCTCCTTGACATTTCCATGATGAAT	840		
Db	841	ATTCCGTGTGGGATCTCTTCATGAAGATCTGTCTCTGCTTTGCCCTTTGTGATCCAG	900		
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Db	901	TCCTCATCATCAATGTCTGTCTACACCCCTGATCCTCGCCCTGAAGAGTGTCCGGCTCC	960		
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QY	1201	GGTGTTTAGGGACTTCTGCTTCCCTATTAGATGCGAATGGAGCGCCAGACCAATA	1260	
Db	1261	GAGTTAGAACACAGTTCAAGATCCTGCTTCCATGAGAGATGTGGAGGATGAATPAAGC	1320	
QY	1261	GAGTTAGAACACAGTTCAAGATCCTGCTTCCATGAGAGATGTGGAGGATGAATPAAGC	1320	
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QY	1321	CAGTATGACTAGTCTGTGAATGCTCTTATTTCTCTCCAGGTAGAGAAAGTTCAATG	1380	
Db	1381	ATCTTGTTTAACCCAGATTACAACCTGCAG	1410	
QY	1381	ATCTTGTTTAACCCAGATTACAACCTGCAG	1410	
RESULT	2			
LOCUS	S81111	1288 bp	mrna	ROD 02-AUG-1996
DEFINITION	kappa-opioid receptor [alternatively spliced] [mice, C58/J, R1.1 thymoma cells, mRNA Partial, 1288 nt].			
ACCESSION	S81111			
NID	91478285			
KEYWORDS	Mus sp. C58/J R1.1 thymoma cells.			
SOURCE	Mus sp.			
ORGANISM	Mus sp.			
REFERENCE	1 (bases 1 to 1288) Belkowski,S.M., Zhu,J., Liu-Chen,L.Y., Eisenstein,T.K., Adler,M.W. and Rogers,T.J. Sequence of kappa-opioid receptor cDNA in the R1.1 thymoma cell line J. Neuroimmunol. 62 (1), 113-117 (1995) MEDLINE 96084989 REMARK Genbank staff at the National Library of Medicine created this entry [NCBI g1bbsq 175931] from the original journal article. This sequence comes from Fig. 3. longer of two transcripts. location/Qualifiers source 1..1288 /organism="Mus sp." /db_xref="taxon:10095" 97..1239 /gene="kappa-opioid receptor" 97..1239 /gene="kappa-opioid receptor" /codon_start=1 /translation="MESPIQIFRGDPPTCSACLLPNSSSWFPPNWAESDSNGSVGS EDQLESASHPAIVITAVYVVFVGLVGNLSLMEVIRITKMKLATNIIYFNLA LADALVTITMPEQSAAYLMSWPEFDVICKIVISIDYNNMFTSIFTLMSVDRYTAV CHPVKALDFRTPLEKAIINICWLLASSVGISATVLGGTKVREDVDVIECSLQFPDDE XSWWDLFMKICVEVFAVIVPVLIIIVCYTLMILRLKSVRLLSGSREKDRNLRITKLV LVVAVFIIICWPIHIFILVEALGSTSHIAAISYFICIALGYTNSLNPVLYAFLD ENFKRCFRDFCFPIKMRERQSTNRVNTVQDPASMRDVGGMKPV"			
COMMENT				
FEATURES				
source				
gene				
CDS				
BASE COUNT	283 a	336 c	305 g	364 t
ORIGIN				
Query Match	85.7%; Score 1208; DB 14; Length 1288;			
Best Local Similarity 100.0%;	Pred. No. 0.00e+00;			
Matches 1208; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			


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Db 141 CTGCTCTCCAGTGTGGCTTCTCCCAACAGCAGCTCTTGGTTCCCACTGGGCGAGA 200
QY 230 CTGCTCTCCAGTGTGGCTTCTCCCAACAGCAGCTCTTGGTTCCCACTGGGCGAGA 289
Db 201 ATCCGACAGTATGGCAGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGCGACATCTC 260
QY 290 ATCCGACAGTATGGCAGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGCGACATCTC 349
Db 261 TCCGCGCATCCCTGTATTCATCACCGCTGTCTACTCTGTGTATTTGTGGGCTTAGT 320
QY 350 TCCGCGCATCCCTGTATTCATCACCGCTGTCTACTCTGTGTATTTGTGGGCTTAGT 409
Db 321 GGGCAATCTCTGGTTCATGTTTGTTCATCATCCGATACACGAGATGAAGCCGCAACCA 380
QY 410 GGGCAATCTCTGGTTCATGTTTGTTCATCATCCGATACACGAGATGAAGCCGCAACCA 469
Db 381 CATCTACATATTTAACTGGCTTTGGCAGATGCTTTGGTTACTTACCACATATGCCCTTCA 440
QY 470 CATCTACATATTTAACTGGCTTTGGCAGATGCTTTGGTTACTTACCACATATGCCCTTCA 529
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Db 501 TTCCATTGACTACTACACATGTTTACACGATATTCACCTTGACCATGATGAGTGTGA 560
QY 590 TTCCATTGACTACTACACATGTTTACACGATATTCACCTTGACCATGATGAGTGTGA 649
Db 561 CCGCTACATGCTGTGTGCCACCCCTGTGAAGCTTTGACCTCCGACACCTTTGAAGC 620
QY 650 CCGCTACATGCTGTGTGCCACCCCTGTGAAGCTTTGACCTCCGACACCTTTGAAGC 709
Db 621 AAAGATCAATCAATCTGCAATTTGGCTCTGGCATCATCTGTGTATATCAGCGATAGT 680
QY 710 AAAGATCAATCAATCTGCAATTTGGCTCTGGCATCATCTGTGTATATCAGCGATAGT 769
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Db 861 TGTCCGGCTCTCTGTGGCTCCCGAGAGAGAGACCGAATCTCCGCCCATCACCAAGCT 920
QY 950 TGTCCGGCTCTCTGTGGCTCCCGAGAGAGAGACCGAATCTCCGCCCATCACCAAGCT 1009
Db 921 GGTGCTGGTAGTAGTTCAGTCTTCATCATCTGTGGACCCCATTCACATCTTTATCT 980
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Db 981 GGTGAGAGGCTCTGGAGACACCTCCACACAGCAGCAGCTGCCCTCTCCAGCTATTATTTCTG 1040
QY 1070 GGTGAGAGGCTCTGGAGAGCAGCTCCACACAGCAGCAGCTGCCCTCTCCAGCTATTATTTCTG 1129
Db 1041 TATTCCTTGGGTTATACCAACAGCAGCTGAATCTCTCTATGCTTCTTGATGA 1100
QY 1130 TATTCCTTGGGTTATACCAACAGCAGCTGAATCTCTCTATGCTTCTTGATGA 1189
Db 1101 AAACCTCAAGCGGTGTTTGAAGGACTTCTGCTTCCCTATTTAGATGCGAATGAGCGCCA 1160
QY 1190 AAACCTCAAGCGGTGTTTGAAGGACTTCTGCTTCCCTATTTAGATGCGAATGAGCGCCA 1249
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Db 1161 GAGCACCAATAGAGTTAGAAACACACAGTTCAGGATCTGCTTCCATGAGAGATGGGAGG 1220
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Db 1221 GATGAATAGCCAGATAGACTAGTGTGGAATGTCTTCTTATTTGTCTCCAGGTAGAGA 1280
QY 1310 GATGAATAGCCAGATAGACTAGTGTGGAATGTCTTCTTATTTGTCTCCAGGTAGAGA 1369
Db 1281 AGAGTTCA 1288
QY 1370 AGAGTTCA 1377
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RESULT 3
LOCUS RATRORD 1273 bp mRNA ROD 21-DEC-1993
DEFINITION Rat mRNA for opioid receptor, complete cds.
ACCESSION D16534
NID 9409390
KEYWORDS G-protein coupled receptor; opioid receptor; transmembrane protein.
SOURCE Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone PROR2.
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ORGANISM

Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Rattus.

REFERENCE

1 (bases 1 to 1273)
Nishi, M., Takeshima, H., Fukuda, K., Kato, S. and Mori, K.
cDNA cloning and pharmacological characterization of an opioid
receptor with high affinities for kappa-subtype-selective ligands
FEBS Lett. 330 (1), 77-80 (1993)

JOURNAL

MEDLINE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (19-JUN-1993) to the DDBJ/EMBL/GenBank databases. Hiroshi
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FEATURES

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ORIGIN

278 a 340 c 294 g 361 t

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LOCUS		RATKORLA	1358 bp	mRNA
DEFINITION		Rat kappa opiod receptor mRNA, complete cds.		ROD
ACCESSION		L22001		21-OCT-1993
NID		9409236		
KEYWORDS		kappa opiod receptor; opiod receptor.		
SOURCE		Rattus norvegicus whole brain cDNA to mRNA.		
ORGANISM		Rattus norvegicus		
REFERENCE		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.		
AUTHORS		1 (bases 1 to 1358)		
TITLE		Chen, Y., Mestek, A., Liu, J. and Yu, L.		
JOURNAL		Molecular cloning of a rat kappa opiod receptor reveals sequence similarities to the mu and delta opiod receptors		
MEDLINE		Biochem. J. 295, 625-628 (1993)		
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RESULT 5
LOCUS RAXOR1B 2094 bp mRNA
DEFINITION Rattus norvegicus kappa opioid receptor (KOR-1) mRNA, complete cds.

ACCESSION L22536
NID G425188
KEYWORDS G-protein coupled receptor; kappa opioid receptor; transmembrane protein.
SOURCE Rattus norvegicus (strain Sprague-Dawley) (Library: lambda gt10) adult brain (striatum) cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryotes; mitochondria eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 2094)
Li, S., Zhu, J., Chen, C., Chen, Y.-W., de Riel, J.K., Ashby, B. and Liu-Chen, L.-Y.
Molecular cloning and expression of a rat kappa opioid receptor
Biochem. J. 295, 629-633 (1993)
94059009
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RESULT 6
LOCUS RNU00442 4742 bp mRNA
DEFINITION Rattus norvegicus kappal opioid receptor mRNA, complete cds.
ACCESSION U00442
NID 5403486

KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus

REFERENCE
AUTHORS 1 (bases 1 to 4742)
Meng, F., Xie, G.-X., Thompson, R.C., Mansour, A., Goldstein, A.,
Watson, S.J. and Akil, H.

TITLE	Cloning and pharmacological characterization of a rat kappa opioid receptor			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958 (1993)			
MEDLINE	94052210			
REFERENCE	2 (bases 1 to 4742)			
AUTHORS	Meng, F.			
TITLE	Direct Submission			
JOURNAL	Submitted (05-AUG-1993) Fan Meng, Mental Health Research Institute, University of Michigan, 205 Zina Pitcher Place, Ann Arbor, Michigan 48109, USA			
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Db 1175 GAGCACAACAGAGTTAGAAACACAGTTTCAAGATCCTGCTTCCATGAGGATGTTGGTGG 1234
QY 1250 GAGCACAACAGAGTTAGAAACACAGTTTCAAGATCCTGCTTCCATGAGGATGTTGGTGG 1309
Db 1235 GATGAATAGCCAGTATGACTAGTATGATGAATGCTTCTCTATGTTCTCCGGGTAGAGA 1294
QY 1310 GATGAATAGCCAGTATGACTAGTATGATGAATGCTTCTCTATGTTCTCCAGGTAGAGA 1369
Db 1295 AGAGTTCAATGATCTTGGTTTAAACCAGATTACCACTGCAG 1335
QY 1370 AGAGTTCAATGATCTTGGTTTAAACCAGATTACCACTGCAG 1410

RESULT 9
LOCUS CPT04092 1733 bp mRNA ROD 24-MAY-1995
DEFINITION Cavia porcellus Hartley kappa opioid receptor mRNA, complete cds.
ACCESSION U04092
KEYWORDS 9475106
SOURCE guinea pig.
ORGANISM Cavia porcellus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
REFERENCE 1 (bases 1 to 1733)
AUTHORS Xie,G.X., Meng,F., Mansour,A., Thompson,R.C., Hoversten,M.T.,
Goldstein,A., Watson,S.J. and Akil,H.
TITLE Primary structure and functional expression of a guinea pig kappa
opioid (dynorphin) receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (9), 3779-3783 (1994)
MEDLINE 94224825
REFERENCE 2 (bases 1 to 1733)
AUTHORS Xie,G.
TITLE Direct Submission
JOURNAL Submitted (07-DEC-1993) Guo-xi Xie, Mental Health Research
Institute, The University of Michigan, 205 Zina Pitcher Place, Ann
Arbor, MI 48109-0720, USA
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Query Match 60.8%; Score 857; DB 14; Length 1733;
Best Local Similarity 86.7%; Pred. No. 0.00e+00;
Matches 1013; Conservative 0; Mismatches 156; Indels 0; Gaps 0;
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QY 242 TGCCTGCTGCTCCCAACGAGCAGCGCTTGCTCCCGGCTGGGCCGACCGGACGCA 301
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QY 302 TGGCAGTGTGGGCTCAGAGATCAGCAGCTGGAGTCCGGCACATCTCTCCGGCCATCCC 361
Db 416 GGTATCATACAGGCGCTCTACTCCGTGCTGCTGCTGGTGGGCTGGTGGGCACTGCT 475
QY 362 TGTATCATACAGCGCTGCTACTCTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 421
Db 476 GGTATGTTGTTGTTATCATCATGATATACAAAGATGAAAACAGCAACATCTATATAT 535
QY 422 GGTATGTTGTTGTTATCATCATCGATACAGAAAGATGAAAGACCGCAACATCTATAT 481
Db 536 TAACCTGCTTGGCGGATGCTTGGTCACTACCAACCATGCTTTCCAGAGCAACGCTCA 595
QY 482 TAACCTGCTTGGCGGATGCTTGGTCACTACCAACCATGCTTTCCAGAGTGTGCTCA 541
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Db 716 TGTGTGCCAACCTGTGAAGGACGTGACCTCCGGACACCCCTTGAAGGCAAGATCATCAA 775
QY 662 TGTGTGCCAACCTGTGAAGGACGTGACCTCCGGACACCCCTTGAAGGCAAGATCATCAA 721
Db 776 TATCTGATTTGGCTCTGTCATCATCTGTTGGCATTTCTGCCATCATCTTGGAGGAC 835
QY 722 CATCTGATTTGGCTCTGTCATCATCTGTTGGCATTTCTGCCATCATCTTGGAGGAC 781
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QY 782 CAAAGTCAGGGAAGATGGAATATCATTTGAGTGTGCTTGCAGTTCGCCGATGATGATA 841
Db 896 CTCTGCTGGGACCTCTTCATGAAGATCTGCGCTTTGTTGCTTTGCCCTTGTGATCCCGGT 955
QY 842 TTCTGCTGGGATCTCTTCATGAAGATCTGTTGCTTTGCTTTGCCCTTGTGATCCCGGT 901
Db 956 CCTCATCATTTATGTTGCTATACTCTGATGATGCTGCTGTAAGAGTGTGAGGCTCCT 1015
QY 902 CCTCATCATTTATGTTGCTATACTCTGATGATGCTGCTGTAAGAGTGTGAGGCTCCT 961
Db 1016 TTCTGCTCCCGAGAGAAAGATGAAACCTTGGCAGGATCACCAGGCTGTCTGTGTGT 1075
QY 962 GTCTGCTCCCGAGAGAAAGATGAAACCTTGGCAGGATCACCAGGCTGTGTGTGTGT 1021
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QY 1022 AGTTGCAAGTGTATATCTGCTGACCCCGATTCACATTTTCATCTCTGTGAGGCGCT 1081
Db 1136 GGTGCAAGTGTATATCTGCTGACCCCGATTCACATTTTCATCTCTGTGAGGCGCT 1195

QY	1082	GGGAAGCACCTCCACAGACAGCTGCCCTCTCCAGCTATTATTCTGTATTGCCCTTGGG	1141
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QY	1142	TTATACCAACAGCAGCGCTGAATCCTGTCTCTATGCTTTCGATGAAAACTTCAAGCG	1201
Db	1256	GTGTTTCGGGACTTTTGTCTTCCATTAAAGATGAGATGAGAGACAGACGACTAGCAG	1315
QY	1202	GTGTTTAAAGGACTTCTGCTTCCCTATTAAAGATGCGAATGAGCGCCAGACCAATAG	1261
Db	1316	AGTCAGAAACACAGTCCAGATCCTGCTTACATGAGGAATGTGATGGGTTGAATAAGCC	1375
QY	1262	AGTTAGAAACACAGTCCAGATCCTGCTTCCATGAGAGATGTGGAGGGATGAATAAGCC	1321
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QY	1322	AGTATGACTAGTCTGTGGAATGTCTTCTTATGTCTTCTCCAGGTAGAGAAGAGTTCAATGA	1381
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QY	1382	TCTTGGTTTAAACCCAGATTTCAACTGCAG	1410

RESULT 10
LOCUS A48343 1142 bp DNA PAT 07-MAR-1997
DEFINITION Sequence 1 from Patent WO9601898.
ACCESSION A48343
NID 92302133
KEYWORDS
SOURCE .
ORGANISM unidentified.
unclassified.
unidentified.
unclassified.
1 (bases 1 to 1142)
REFERENCE Kieffer, B. and Simonin, F.
AUTHORS HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF
TITLE Patent: WO 9601898-A 1 25-JAN-1996;
JOURNAL UNITV PASTEUR (FR)
COMMENT Other publication FR 2722209 960112.
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CDS

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ORIGIN
Query Match 59.4%; Score 838; DB 25; Length 1142;
Best Local Similarity 86.7%; Pred. No. 0.00e+00;
Matches 990; Conservative 0; Mismatches 152; Indels 0; Gaps 0;
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QY 186 ATGGAAGTCCCCCATTCAGATCTTCCGAGGAGATCCAGGCCCTACCTGCTCTCCAGTGT 245
Db 61 TGCTGCCCCCAACAGCAGCGCTGTTTCCCGGCTGGCGCCGAGCCCGACAGCAACGCG 120
QY 246 TGCTTCTCCCAACAGCAGCTTCTTGTTCCTCCCACTGGCGAGAAATCCGACAGTAATGCG 305
Db 121 AGCGCGGCTCGGAGGAGCGGAGCTGAGCGCCGCGACATCTCCCGGCATCCCGGTC 180
QY 306 AGTGTGGGCTCAGAGGATCAGAGCTGAGAGTCCGCGCACATCTCTCCGCCATCCCTGTT 365

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QY	366	ATCATCAGCGGGCTCTACTCCGTAAGTGTTCGTCGTGGGCTTGGTGGCAACTGCGTGGTC	425
Db	241	ATGTCGTGATCATCCGATACCAAGATGAAGACAGCAACCAATTTACATATTAAAC	300
QY	426	ATGTTTTCATCATCCGATACCAAGATGAAGACCGCAACCAATCTACATATTAAAC	485
Db	301	CTGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCCCTTTCAGAGTACGGTCTACTTG	360
QY	486	CTGCTTTGGCAGATGCTTTAGTTACTACAACCATGCCCCCTTTCAGAGTACGGTCTACTTG	545
Db	361	ATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCATTTGATTTACTAC	420
QY	546	ATGAATTCCTGGCCTTTTGGGATGTGCTGTGCAAGATAGTAATTTCATTTGATTTACTAC	605
Db	421	AACATGTTACCAAGCATCTTACCTTGACCATGATGAGCGTGAGCCGCTACATTTGCCGTG	480
QY	606	AACATGTTACCAAGCATCTTACCTTGACCATGATGAGCGTGAGCCGCTACATTTGCCGTG	665
Db	481	TGCCACCCGTTGAAGGCTTTGAGCTTCCGACACCCCTTGAAGCAAGATCATCAATATC	540
QY	666	TGCCACCCGTTGAAGGCTTTGAGCTTCCGACACCCCTTGAAGCAAGATCATCAATATC	725
Db	541	TGCATCTGGCTGCTGCTGCTCATCTGTGTCATCTCTGCAATAGTCTTGAGGACACCAA	600
QY	726	TGCATCTGGCTGCTGCTGCTCATCTGTGTCATCTCTGCAATAGTCTTGAGGACACCAA	785
Db	601	GTGAGGGAAGAGCTCGATGTCATTTGAGTGTGCTCTGCAAGTTCGACATGATGACTACTCC	660
QY	786	GTGAGGGAAGAGCTCGATGTCATTTGAGTGTGCTCTGCAAGTTCGACATGATGATATTTCC	845
Db	661	TGTTGGGACCTCTTCATGAAGATCTGCTTTCATCTTTGCTTGCCTGCTGCTGCTGCTC	720
QY	846	TGTTGGGACCTCTTCATGAAGATCTGCTTTCATCTTTGCTTGCCTGCTGCTGCTGCTC	905
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QY	906	ATCATCATGCTGCTTACACCCCTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	965
Db	781	GGCTCCGAGAGAAAGATCGCAACCTGCGTAGAGATCACAGACTGCTGCTGCTGCTGCTG	840
QY	966	GGCTCCGAGAGAGAAAGATCGCAACCTGCGTAGAGATCACAGACTGCTGCTGCTGCTGCTG	1025
Db	841	GCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	900
QY	1026	GCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1085
Db	901	AGCACTCCGACAGCAGAGCTGCTCTCTCCAGCTATTACTTCTGCATGCGCTTAGGCTAT	960
QY	1086	AGCACTCCGACAGCAGAGCTGCTCTCTCCAGCTATTACTTCTGCATGCGCTTAGGCTAT	1145
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QY	1206	TTTAAAGGACTTCTGCTTCCCTATTAAAGATGCGAATGAGCGCGCAGAGCAACCAATAGATT	1265
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QY	1266	AGAACAACAGTTCAGAGATCCTGCTTCCATGAGAGATGTGGAGAGGATGAATAAGCACTA	1325
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QY	1326	TG 1327	

RESULT 11
LOCUS S77868S3 1186 bp DNA ROD 26-SEP-1995
DEFINITION kappa opioid receptor [mice, genomic, 1186 nt, segment 3 of 3].
ACCESSION S77872

NID	KEYWORDS	3 of 3	Mus sp.	Mus sp.	Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
9998531	SEGMENT	Mus sp.	Mus sp.		
	SOURCE	Mus sp.	Mus sp.		
	ORGANISM	Mus sp.	Mus sp.		
	REFERENCE	1 (bases 1 to 1186)			
	AUTHORS	Liu,H.C., Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Loh,H.H. and Wei,L.N.			
	TITLE	Cloning and promoter mapping of mouse kappa opioid receptor gene			
	JOURNAL	Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)			
	MEDLINE	95251663			
	REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 166539] from the original journal article. This sequence comes from Fig. 2.			
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	mrna	join(S77868:919..1894,S77869:371..723,289..>821)			
	gene	order(S77868:1638..2074,S77869:1..1109,1..821)			
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Best Local Similarity	99.8%;	Pred. No. 0.00e+00;			
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				Indels	0;
				Gaps	0;
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	11				
Db	344	GGATCTCTTCATGAGATCTGTGCTCTGCTGCTTGCCTTTGTGATCCACAGTCCATCAT	403		
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QY	851	GGATCTCTTCATGAGATCTGTGCTCTGCTGCTTGCCTTTGTGATCCACAGTCCATCAT	910		
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QY	911	CATTGCTGCTACACCCCTGATGATCCTGCGCCTGAAGAGTGTCCGGCTCCTGTGGCTC	970		
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Db	464	CCGAGAGAAGACCGAAATCTCCGCCGATCACCAGCTGGTGGTAGTAGTTCAGT	523		
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QY	971	CCGAGAGAAGACCGAAATCTCCGCCGATCACCAGCTGGTGGTAGTAGTTCAGT	1030		
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Db	524	CTTCATCATCTGTGGACCCCATTCACACCTTATCCTGGTGGAGGCTGGGAAGCAC	583		
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QY	1031	CTTCATCATCTGTGGACCCCATTCACACCTTATCCTGGTGGAGGCTGGGAAGCAC	1090		
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Db	644	CAGCAGCCTGAATCCTGTTCTCTATGCCCTTCTGATGAAGAACTTCACGCGTGTITAG	703		

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QY      1151 CAGCAGCCTGATTCCTGTCTTCTCIATGCGCTTCTTGATGAAGAACTTCAAGCGGTGTTTAG 1210
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QY      1391 AACCCAGATTACAACTGCAG 1410

RESULT 12
LOCUS   MUSMORBDP3 638 bp DNA ROD 12-APR-1996
DEFINITION Mouse MORGD gene for kappa-opioid receptor, exon 3.
ACCESSION D31665
NID      9643595
KEYWORDS G-protein associated; kappa opioid receptor; opioid drugs and
SOURCE   Mus musculus DNA, clone_lib:phage lambda fixit.
ORGANISM Mus musculus
          Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
          Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
          Murinae; Mus.
REFERENCE 1 (bases 1 to 638)
AUTHORS  Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,T.
TITLE    Structure and chromosomal mapping of genes for the mouse
          +kappa-opioid receptor and an opioid receptor homolog (MOR-C)
JOURNAL  Biochemical and Biophysical Research Communication 205, 1353-1357
          (1994)
REFERENCE 2 (bases 1 to 638)
AUTHORS  Takeshima,H.
TITLE    Direct Submission
JOURNAL  Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi
          Takeshima, Tokyo Institute of Psychiatry, Department of
          Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-Ku, Tokyo 156, Japan
          (Tel:03-3304-5701(ex.312), Fax:03-3329-8035)
          Submitted (28-May-1994) to DDBJ by:
          Hiroshi Takeshima
          Department of Neurochemistry
          Tokyo Institute of Psychiatry
          2-1-8 Kamikitazawa, Setagaya-Ku
          Tokyo 156
          Japan
          Phone: 03-3304-5701 x312
          Fax: 03-3329-8035.

FEATURES
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exon

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|||||
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QY 1331 AGTCGTGGAATGTCTTCIATTTGTTCTCCAGGTAGAGAAGTTCATGATCTTGTTT 1390
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QY 1391 AACCAGATTACCACTGCAG 1410
RESULT 14
LOCUS MUSMORGP2 488 bp DNA ROD 12-APR-1996
DEFINITION Mouse MORGD gene for kappa-opioid receptor, exon 2.
ACCESSION D31664
NID g643594
KEYWORDS G-protein associated; kappa opioid receptor; opioid drugs and peptides-binding; transmembrane protein.
SEGMENT 2 of 3
SOURCE Mus musculus DNA, clone_lib:phage lambda fixII.
ORGANISM Mus musculus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 488)
AUTHORS Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,T.
TITLE Structure and chromosomal mapping of genes for the mouse +kappa-opioid receptor and an opioid receptor homolog (MOR-C) Biochemical and Biophysical Research Communication 205, 1353-1357 (1994)
JOURNAL 2 (bases 1 to 488)
REFERENCE Takeshima,H.
AUTHORS Direct Submission
TITLE Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi Takeshima, Tokyo Institute of Psychiatry, Department of Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan (Tel:03-3304-5701(ex.312), Fax:03-3329-8035)
JOURNAL Submitted (28-May-1994) to DDBJ by: Hiroshi Takeshima
Department of Neurochemistry
Tokyo Institute of Psychiatry
2-1-8 Kamikitazawa, Setagaya-ku
Tokyo 156
Japan
Phone: 03-3304-5701 x312
Fax: 03-3329-8035.
FEATURES
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Query Match 25.1%; Score 354; DB 14; Length 488;
Best Local Similarity 100.0%; Pred. No. 1.77e-275;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 148 CTTTGGTTACTACCACTATGCCCCCTTTCAGAGTGTCTGCTACTGTGATGAATTCCTGGCCTT 207
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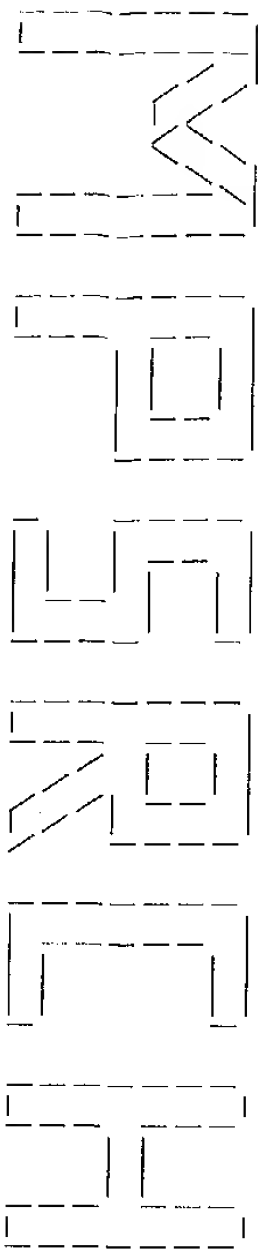
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QY 622 TATTCACCTTGACCATGATGAGTGTGGACCGCTACATTTGCTGTGTGCCACCGCTGAAAG 681
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QY 682 CTTTGGACTTCGGAACACCTTTGAAAGCAAGATCATCAACATCTGCATTTGGCTCTGG 741
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QY 742 CATCATCTGTGTGTATATCAGCGATAGTCTTGGAGGCAACCAAGTCAGGGAAG 795
RESULT 15
LOCUS S77868S2 1109 bp DNA ROD 26-SEP-1995
DEFINITION kappa opioid receptor [mice, genomic, 1109 nt, segment 2 of 3].
ACCESSION S77869
NID g998530
KEYWORDS 2 of 3
SEGMENT 2 of 3
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1109)
AUTHORS Liu,H.C., Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Loh,H.H. and Wei,L.N.
TITLE Cloning and promoter mapping of mouse kappa opioid receptor gene Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
JOURNAL 95251663
MEDLINE
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibs9 166534] from the original journal article. This sequence comes from Fig. 2.
FEATURES
source location/Qualifiers
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/organism="Mus sp."
/db_xref="taxon:10095"
BASE COUNT 331 a 213 c 204 g 361 t
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Best Local Similarity 100.0%; Pred. No. 1.77e-275;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 370 GATACACGAAGATGAAGACCGCAACCAACATCTACATATTAACTGGCTTTGGCAGATG 429
QY 442 GATACACGAAGATGAAGACCGCAACCAACATCTACATATTAACTGGCTTTGGCAGATG 501
Db 430 CTTTGGTTACTACCACTATGCCCTTTCAGAGTGTCTGCTACTGTGATGAATTCCTGGCCTT 489
QY 502 CTTTGGTTACTACCACTATGCCCTTTCAGAGTGTCTGCTACTGTGATGAATTCCTGGCCTT 561
Db 490 TTGGAGATGTGCTATGCAAGATGTGATTTCCATTTGACTAGTACTACAACATGTTTACAGCA 549
QY 562 TTGGAGATGTGCTATGCAAGATGTGATTTCCATTTGACTAGTACTACAACATGTTTACAGCA 621
Db 550 TATTCACCTTGACCATGATGAGTGTGGACCGCTACATTTGCTGTGTGCCACCGCTGTGAAG 609
QY 622 TATTCACCTTGACCATGATGAGTGTGGACCGCTACATTTGCTGTGTGCCACCGCTGTGAAG 681
Db 610 CTTTGGACTTCGGAACACCTTTGAAAGCAAGATCATCAACATCTGCATTTGGCTCTGG 669
QY 682 CTTTGGACTTCGGAACACCTTTGAAAGCAAGATCATCAACATCTGCATTTGGCTCTGG 741
Db 670 CATCATCTGTGTGTATATCAGCGATAGTCTTGGAGGCAACCAAGTCAGGGAAG 723
QY 742 CATCATCTGTGTGTATATCAGCGATAGTCTTGGAGGCAACCAAGTCAGGGAAG 795

Tue Apr 21 08:03:54 1998

US-08-292-694A-1.rge

Page 14

Search completed: Mon Apr 20 23:10:13 1998
Job time : 1368 secs.



(TM)

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Mpsrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Mon Apr 20 23:28:06 1998; MasPar time 199.87 Seconds

Tabular output not generated. 814.103 Million cell updates/sec

Title: >US-08-292-694A-1
(1-1410) from US08292694A.seq

Perfect Score: 1410
N.A. Sequence: 1 GCGCACCTTGTGTCGATGCCAA.....AACCCAGATTACACTGCAG 1410
CGCGTGGAGACGACTAGGGT.....TTGGGTCTAATGTGACGTC

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 159651 seqs, 57698962 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq30
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8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 9.344; Variance 5.218; scale 1.791

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1410	100.0	1410 13	Q75926	Mouse kappa opioid re	0.00e+00
2	1129	80.1	2481 15	Q86725	Mammalian kappa opioi	0.00e+00
3	838	59.4	1142 20	T12550	Human kappa opioid re	0.00e+00
4	668	47.4	1000 13	Q75931	Human kappa opioid re	0.00e+00
5	311	22.1	2070 12	Q79199	Rat mu-subtype opioid	6.98e-207
6	309	21.9	1618 14	Q89222	Rat mu opioid recepto	2.27e-205
7	309	21.9	1618 14	Q89223	Transcription regulat	2.27e-205
8	309	21.9	1981 10	Q56705	Partial sequence of t	2.27e-205
9	291	20.6	1821 10	Q56700	Sequence of murine de	8.82e-192
10	291	20.6	2272 13	Q75927	Mouse delta opioid re	8.82e-192
11	289	20.5	1610 14	Q89226	Human mu opioid recep	2.84e-190
12	289	20.5	2160 15	Q93102	Human mu opiate recep	2.84e-190
13	276	19.6	2216 11	Q66656	Murine delta opioid r	1.78e-180
14	230	16.3	829 10	Q56703	Partial sequence of t	6.07e-146
15	220	15.6	1567 14	Q89233	Rat opioid receptor c	1.81e-138

16	218	15.5	1330 13	Q75928	Mouse opioid receptor	5.64e-137
17	218	15.5	2706 15	Q92972	Rat opiorph receptor	5.64e-137
18	207	14.7	2600 14	Q90096	Mouse kappa-3 opioid	8.98e-129
19	195	13.8	2447 10	Q56702	Partial sequence of t	7.58e-120
20	97	6.9	1265 7	Q45654	Murine somatostatin r	2.23e-48
21	91	6.5	1047 2	Q10572	Human Natriuretic Pep	3.80e-44
22	78	5.5	1047 2	Q10572	Human Natriuretic Pep	4.42e-35
23	77	5.5	1518 14	Q83682	Epsilon opioid recept	4.17e-34
24	78	5.5	1634 7	Q45653	Human somatostatin re	4.42e-35
25	75	5.3	1110 5	Q29155	Pituitary somatostati	5.16e-33
26	73	5.2	1244 7	Q45656	Murine somatostatin r	1.22e-31
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29	67	4.8	1296 7	Q45657	Human somatostatin re	1.48e-27
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31	68	4.8	1796 7	Q45658	Murine somatostatin r	3.11e-28
32	56	4.0	1054 14	Q83681	Epsilon opioid recept	3.26e-20
33	52	3.7	726 31	T77788	G-protein coupled rec	1.33e-17
34	46	3.3	1162 11	Q66170	Seven transmembrane r	9.20e-14
35	46	3.3	2254 11	Q66167	Seven transmembrane r	9.20e-14
36	45	3.2	1200 16	Q95036	Rat hippocampal neuro	3.92e-13
37	45	3.2	1556 16	Q95035	Rat hippocampal neuro	3.92e-13
38	44	3.1	1065 33	T86154	Human MIP-1alpha/RANF	1.66e-12
39	44	3.1	1495 11	Q62695	C-C chemokine recepto	1.66e-12
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41	39	2.8	91 9	Q51746	Oligonucleotide probe	1.20e-10
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43	40	2.8	204 1	N81164	Base substituted E.co	4.90e-10
44	39	2.8	1900 11	Q66162	Partial coding sequen	1.99e-09
45	39	2.8	2154 11	Q64125	Epstein Barr virus in	1.99e-09

ALIGNMENTS

RESULT 1
ID Q75926 standard; DNA: 1410 BP.
AC Q75926;
DT 17-AUG-1995 (first entry)
DE Mouse kappa opioid receptor MORK1 cDNA.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 186..1328
FT /tag= a
FT /product= mouse kappa opioid receptor
PN W09428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR P-PSDB; R67669.
PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 10; Page 207-211; 300pp; English.
CC The nucleotide sequence of the novel mouse kappa opioid receptor gene
CC MORK1. The gene was isolated from a mouse kappa opioid receptor gene
CC fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRI) receptor
CC subtypes SSTRL, SSIR2 and SSTR3. The 1.2 kb psti fragment from the mouse
CC kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV
CC promoter-based expression vector pCMV-6b. The resultant construct
CC pCMV-msl-1 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete,
CC truncated or chimaeric opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to

CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.

Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T;

Query Match	100.08;	Score 1410;	DB 13;	Length 1410;
Best Local Similarity	100.08;	Pred. No. 0.00e+00;		

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RESULT      2
ID          086725 standard; cDNA; 2481 BP.
AC          Q86725;
DE          01-DEC-1995 (first entry)
DE          Mammalian kappa opioid receptor protein cDNA.
KW          Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;
KW          amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
OS          Rattus rattus.
FH          Key
FH          CDS          Location/Qualifiers
FT          /*tag= a
FT          /product= kappa opioid receptor
PN          J07070191-A.
PD          14-MAR-1995.
PF          30-JUL-1993; 190261.
PR          09-JUL-1993; JP-170591.
PA          (TAKE ) TAKEDA CHEM IND LTD.
DR          WPI; 95-144857/19.
DR          P-PSDB; R72591.
PT          Kappa opioid receptor protein and cells expressing it - useful
PT          for the screening of compounds for analgesic and hypnotic
PT          properties
PS          Claim 2; Page 9-10; 15pp; Japanese.
CC          The nucleotide sequence of the novel mammalian kappa opioid receptor
CC          cDNA. The gene was isolated by amplifying a fragment from rat brain mRNA
CC          by reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
CC          the mouse delta-opioid receptor gene. This fragment was cloned into the
CC          plasmid pCRIT to produce pR11. The plasmid pR11 was used to probe a rat
CC          brain DNA library in lambda ZAPII to obtain a clone of the rat kappa
CC          opioid receptor gene, designatd pKOPR2. This clone was introduced into
CC          E.coli JM109 for production of the receptor protein. The receptor protein
CC          is useful for screening of analgesic and hypnotic compounds including
CC          peptides and proteins.
SQ          Sequence      2481 BP;      629 A;      588 C;      544 G;      720 T;

Query Match      80.1%; Score 1129; DB 15; Length 2481;
Best Local Similarity 95.5%; Pred. No. 0.00e+00;
Matches 1185; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
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Db	575	ccgctacattgcctgtgtgccaccctgtgaaagcctlttgattccgaacaccttgaagc	634
QY	650	CCGCTACATTCCTGTGTGCCACCCTGTGAAGCTTTGACCTTCGAAACACCTTTGAAGC	709
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QY	710	AAAGATCATCAACATCTGCATTTGGCTCTCCGGCATCATCTGTGGTATATCAGCGATAGT	769
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QY 1370 AGAGTTCAATGATCTTGGTTTAACCCAGATTACAACACTGCAG 1410

RESULT 3
ID T12550 standard; cDNA; 1142 BP.
AC T12550;
DT 03-SEP-1996 (first entry)
DE Human kappa opioid receptor cDNA.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1142
FT /*tag= a
FT /product= kappa_opioid_receptor
FT /note= "incomplete termination codon"
PN WO9601898-A1.
PD 25-JAN-1996.
PE 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B, Simonin F;
PI WPI; 96-097628/10.
DR P-PSDB; R88722.
PT New nucleic acid encoding the human Kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 3; Page 13-15; 30pp; French.
CC This sequence codes for the human kappa opioid receptor and was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

Query Match 59.4%; Score 838; DB 20; Length 1142;
Best local Similarity 86.7%; Pred. No. 0.00e+00;
Matches 990; Conservative 0; Mismatches 152; Indels 0; Gaps 0;

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QY 306 AGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGGCACATCTCTCCGCCATCCCTGTT 365
Db 181 atcatcacggyggtctactccgtagtgcgtgcgtggtggtggtggtggtggtggtggtg 240
QY 366 ATCATCACCGGCTGTCTACTCTGTGTGTAATTTGTGGTGGGCTTAGTGGGCAATTCCTG 425
Db 241 atgttcgtgatcatccgatatcacaaagatgaagacagcaaccaattacattac 300
QY 426 ATGTTTGTATCATCCGATACACGAGATGAAGACCGCAACCAACATCTACATATTTAAC 485
Db 301 ctggtcttgagcagatgccttagtactacaacatgccccttaagagtaogtctacttg 360

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QY 486 CTGGCTTTGGCAGATGCTTTGGTTACTAACCACTATGCCCTTTTCAGAGTGCCTCTACTTTG 545

Db 361 atgaatccctggcccttltggggatgctgtgtgcaagataagtaattccattgtactac 420

QY 546 ATGAATCTTGGCCCTTTTGGAGATGTCCTATGCAAGATTGTCAITTTCCATTGACTACTAC 605

Db 421 aacatgttcaccagcaatcttcacacctgaacatgatgagcgtggaaccgtacaattgcgctg 480

QY 606 AACATGTTTACCAGCATATTACACCTTCACCATGATGAGTGTGACCGCTACATTGCTGTG 665

Db 481 tggcacccttgaaagccttggacctccgacacaccttgaaagcaagatacatcatatc 540

QY 666 TGGCACCCCTGTAAGACTTTGGACCTTCGAAACACCTTTGAAAGCAAGATCATCAACATC 725

Db 541 tgcactctgctgtctgtctcatctgttggcatctctgcaatagtcccttggaggacccaaa 600

QY 726 TGCATTTGGCTCCTGGCATCATCTGTGTATATACGCGATAGTCCCTTGGAGGCCACCAA 785

Db 601 gtcaagggaagacgtcgatgtcatatgagtcctccttgcagttcccagatgatgactactcc 660

QY 786 GTCAGGGGAAGATGTGATGTTCATTTGATGCTTCCCTTGAGTGAATATTTCC 845

Db 661 tgggtggaccttcatatgaagatcgtgcgttcttcatccttgccttcgtgataccctgtctc 720

QY 846 TGGTGGGATCTCTCATGAAGATCTGTCTTCTTCTTTCCTTTGCTTGTGATCCCACTCCTC 905

Db 721 atcatcatcgtctgtctacacccctgatgatcctgctcgtctcaagagcgtccgctccttct 780

QY 906 ATCATCATTTGTGCTTACACCCCTGATGATCCTGCGCCTGAAGAGTGTCCGCTCCTGTCT 965

Db 781 ggtcccgagagaagaatcgcaacctgctgtagagatcacacagactggtcctggtggtg 840

QY 966 GGCTCCCGAGAGAAAGACCGAAATCTCCGCCGATCACCAAGCTGTGCTGTAGTAGTT 1025

Db 841 gcagtctctgctgtctgtgactcccatcaacatatcatcctgtgtgaggctctg 900

QY 1026 GCAGTCTTTCATCTCTGTGTGAGCCCCCATTCACATCTTATCTCGTGGAGGCTCTGGGA 1085

Db 901 agcacctcccaagacaagctgtctctcctcagctattacttctgcatcgcccttaagctat 960

QY 1086 AGCACTCTCCACAGACAGACTGCCCTCTCCAGCTATTATTCTGTATTGCCCTTGGGTTAT 1145

Db 961 accaacaagtacgttaatcccatctctacagccttcttcatatgaataaactcaagcgtgt 1020

QY 1146 ACCAACAGCAGCCTGAATCTCTTCTATGCTTCTTGATGAAAACTTCAACCGGTGT 1205

Db 1021 ttcgggacctctgtcttccactgaagatgagatgagcgagcgagagcaactgacagctc 1080

QY 1206 TTTAGGACTTCTGCTTCCCTATTAAAGATGCGAATGAGCGCCAGAGCACCATAAGAGTT 1265

Db 1081 cgaatacagttcagagatcgtcttaccctgagggagacatgagtgatgaataaaccagta 1140

QY 1266 AGAAACACAGTTCAGATCTCTGCTTCCATGAGAGATGGGAGGGATGAATAAGCCAGTA 1325

Db 1141 tg 1142

QY 1326 TG 1327

RESULT 4

ID Q75931 standard; DNA; 1000 BP.

AC Q75931;

DT 18-ADG-1995 (first entry)

DE Human kappa opioid receptor partial cDNA fragment.

KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify; transmembrane domain; somatostatin; receptor; human; expression vector; truncate; chimeraic; assay; probe; ss.

OS Homo sapiens.

OS Key Location/Qualifiers

FT CDS 102..989

FT /tag= a

FT /product= partial human kappa opioid receptor

PN WO9428132-A.

PD 08-DEC-1994.

PF 20-MAY-1994; U05747.

PR 20-MAY-1993; US-066296.

PR 30-JUL-1993; US-100694.

PR 05-NOV-1993; US-147592.

PA (ARCH-) ARCH DEV CORP.

PI Bell GI, Reisine T, Yasuda K;

DR WPI; 95-022804/03.

DR P-PSDB; R67672.

PT Polynucleotides and peptides derived from opioid receptor

PT polypeptides - for use in therapeutic compositions and in

PT screening assays for useful drug substances.

PS Claim 10; Page 236-239; 300pp; English.

CC The partial nucleotide sequence of the novel human kappa opioid receptor

CC gene. The gene was isolated from a human brain hippocampus cDNA library

CC using a probe from the mouse kappa opioid receptor gene (Q75926). The

CC gene is missing the N-terminal sequence. The C-terminal sequence is

CC very similar to the mouse kappa opioid receptor sequence. Of the

CC C-terminal 293 amino acids, 281 residues are identical and 6 residues

CC have conservative substitutions. The gene encoding the human opioid

CC receptor can be placed in a suitable expression vector for production of

CC the protein in a cell. The opioid receptors thus produced are useful for

CC the development of novel assays designed to select or improve substances,

CC capable of interacting with the opioid receptor proteins, for use in

CC diagnosis, drug design and therapeutic applications.

SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T;

Query Match 47.4%; Score 668; DB 13; Length 1000;

Best Local Similarity 87.6%; Pred. No. 0.00e+00;

Matches 789; Conservative 0; Mismatches 109; Indels 3; Gaps 2;

Db 100 gatacacaagaatgaagacaagcaaccaacattacatatattaacctgcttggcagatg 159

QY 442 GATACACGAAGATGAAGAACCGCAACCAACACTACATATTTAACCTGCGCTTGGCAGATG 501

Db 160 ctttaagttactacaaccatgccccttccagatgtaacggttacttattgatattccctg 219

QY 502 CTTGGTTACTTACCACTATGCCCCCTTTCAGAGTGTGCTACTTGTGATGATTTCTGGCCTT 561

Db 220 ttggggatgtgctgtgcaagatagtaattccattgattactacaacatggttcaaccaga 279

QY 562 TTGAGATGTGCTATGCAAGATTGTTCATTTCATTGACTACTACACATGTTTACCAGCA 621

Db 280 tctcaccttgacaatgatgagcgttgagccgctacattgcccgtgtgccaccccgtgaag 339

QY 622 TATTCACTTGACCATGATGAGTGTGAGCCGCTTACATTTGCTGTGTGCCACCTGTGAAG 681

Db 340 ctttgacctccgacaccccttgaaggcaagaatcalcatatctgcatctgctgctgt 399

QY 682 CTTTGGACTTCCGACACCTTTGAAAGCAAAGATCATCAACATCTGCATTGTGCTCCTGG 741

Db 400 cgtcatctgttgcatctctgcaatagtccttggagggacaccaaagtcaaggaggtgtcg 459

QY 742 CATCATCTGTGTGATATACAGCGATAGTCTCTTGAGGGCACCAAGTCAAGGGAAGTGG 801

Db 460 atgtcattgagtgtctgttgcagttcccatgatgactactcctggttgggacctttca 519

QY 802 ATGTCAATTGAATGCTCCTTGCAGTTTCCCTGATGATGAATATTCTGCTGGGATCTCTTCA 861

Db 520 tgaagatcgtcgtcttaactcttgccttcgtcatccctgtcctcatcatcatcgtctgt 579

QY 862 TGAAGATCTGTGTCTTCTTGTGCTTGTGATCCAGTCTCATCATCATTTGCTGCT 921

Db 580 acaacctgatgatcctgctctcaagangtccgctccttctgtgtcccgagagaag 639

QY 922 ACACCTGATGATCTGCGCTGAAGAGTGTCCGCTCCTGTGTGCTCCGAGAGAAGG 981

Db 640 atncaacctgctgtagatcaccagactggtcctgtgtgtgtgtgtgtgtgtgtgtgtgt 699

QY 982 ACCGAATCTCCGCCGATCACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1041

Db 700 gctggactcccatcacaatatcatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 759


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QY 1042 GTTGAGCCCCCATTCACATCTTTATCCTGTGGAGGCTCTGGGAAGCACCTCCACAGCA 1101
Db 760 cagctgtctctccagctattactctgcacgccttaggctataaccaagtagcctga 819
QY 1102 CAGCTGCCCTCTCCAGCTATTATTTCTGTATTGCTTGGCTTATACCAACAGACGCTGA 1161
Db 820 atcccatctctacagcctttcttgatgaanaactcaagcgytggttccggactctgct 879
QY 1162 ATCCTGTCTCTATGCTTCTTCTTGATGAAACTTCACAGCGGTGTTTAGGACTTCTGCT 1221
Db 880 ttccactgaagatgagnatggagcgcnagagcaactagcagagtccgaataacagttcagg 939
QY 1222 TCCCTATTAGATGCGAATGGAGCGCCAGACGACCAATAGAGTTAGAACAACAGTTGAGG 1281
Db 940 atcctgtcttacctgagggagatcgatggatgaataaaccagtatgactagtcgtg 999
QY 1282 ATCCTGCTTCCATGAG--AGAT-GTGGAGGGATGAATPAGCCAGTATGACTAGTCGTGG 1338
Db 1000 a 1000
QY 1339 A 1339
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RESULT 5
ID Q79199 standard; cDNA; 2070 BP.
AC Q79199;
DT 19-APR-1995 (first entry)
DE Rat mu-subtype opioid receptor cDNA.
KW Mu-subtype opioid receptor; MSOR; drug addiction; ds.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 83..1154
FT /*tag= a
FT /product= Mu-subtype_opioid_receptor
PN EP-612845-A.
PD 31-AUG-1994.
PF 09-FEB-1994; 101968.
PR 26-FEB-1993; US-026140.
PA (AMCY ) AMERICAN CYANAMID CO.
PI Corbett MJ, Eppler CM, Shieh H, Zysk JR;
DR WPI; 94-265963/33.
DR P-PSDB; R65188.
PT Pure mu-type opioid receptor protein - and nucleic acid coding
PT for it
PS Claim 1; Fig 11; 39pp; English.
CC R65188 is the rat mu-subtype opioid receptor protein purified
CC from rat brain membranes, with biotinyl-b-endorphin (R56666)
CC as its ligand. It is encoded by the nucleotide sequence Q79199
CC which was synthesised using Q71022 and Q71023 as PCR primers.
CC R65188 is useful for identifying other receptor subtypes, for
CC screening new opioid ligands, and for studying mechanisms of
CC opioid action, e.g. drug addiction.
SQ Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T;
```

Query Match 22.1%; Score 311; DB 12; Length 2070;
Best Local Similarity 70.6%; Pred. No. 6.98e-207;
Matches 609; Conservative 0; Mismatches 244; Indels 9; Gaps 8;

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Db 171 ttaccatcatgcccctactctatcgctgtgtgtagtgcccttcggaactcctg 230
QY 364 TTATCATACACCGCTGTCTACTCTGTGTATTGTGTGGGCTTAGTGGCAATTCTCTGG 423
Db 231 tcatgtatgtgattgtaatatacaaaaatgaagactgccacaacatctacatttca 290
QY 424 TCATGTTTGICATCATCCGATACGAAAGATGAAGACCGCAACCAACATCTACATATTTA 483
Db 291 acctgtctctgcagagccttcgcagccagctacactgcccttcagagtgtcaactacc 350
QY 484 ACCGTGCTTTGGCAGATGCTTGTGTTACTACCACTATGCCCTTTCAGAGTGTCTACT 543
Db 351 tgatgggaaacatggcccttcggaacacatcctctgcaagatcgatctcaatagattact 410
QY 544 TGATGAATTCCTTGCCCTTTGGAGATGTGCTATGCAAGATTGCAATTTCATTGACTACT 603
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Db 411 acaacatgttcaccagcatatcacccctcgcacacatgagcgtgagccgtacattgctg 470
QY 604 ACAACATGTTTACAGCATATTCACCTTGACCATGATGAGTGTGGACCGCTACATTGCTG 663
Db 471 tctgccaccacagtcnaagcccttgatcttcgtaacccccccgaataatgccaaaaatcgtaacg 530
QY 664 TGTGCCACCCCTGTAAAGCTTTGGACTTCCGACACACCTTTGAAAGCAAGATCATCAACA 723
Db 531 tctgcaactggaatcctctctctgcacatcgctgcctgtaatgttcatgccaacaca 590
QY 724 TCTGCAATTGGCTCTCTGGCATCATCTGTGTTATATCAGCGATAGTCTCTTGGAGGACCA 783
Db 591 aatacagga-g--g-gg-tc-catagattgcaocctcaagttctccacccaacctggt 644
QY 784 AAGTCAGGGAAGATGTGATGTGATGATGATGCTCCTTGACGTTTCCGTGATGATATAT 843
Db 645 actgg-gagaac-ctgc-tcaaatctgtgtcttattcttgcgttccatcatgcccgtcc 701
QY 844 CCTGTGGGATCTCTTCATGAGATCTGTGCTTCTGCTTTCCTTGGCTTGTGATCCACAGTCC 903
Db 702 tcatacatcactgtgtgttacggcctgatatcttaagactcaagagcgttcgcatgtat 761
QY 904 TCATCATCATATGCTGTCTACACCCGTGATGATGCTGCGCTGAAGAGTGTCCGGCTCCTGT 963
Db 762 cggctcccaagaaaaggacaggaatctgcgcagagatcaccccgatggtgtgtgtcg 821
QY 964 CTGGCTCCCGAGAGAAGGACCGAATCTCCGCCGATCACCAAGCTGTGTGTAGTAG 1023
Db 822 tggctgtattatctgtctgtgcgaccccatccacatctacgtcatcatcaagaagcgtga 881
QY 1024 TTGCACTCTTCATCATCTGTGTGACCCCATTCACATCTTATCCGTGATGAGGCTCTGG 1083
Db 882 tcagatccagaacaacacatttcagacggtttcctgacattctgcatgttctgtgt 941
QY 1084 GAAGCACCTCCACACAGACAGCTGCCCTCCATCCAGCTATTATTCTGTAATTGCCCTGGGT 1143
Db 942 acacgaacagctgcctgaatccagttctttaagccttccctgagatgaanaactcaagcgt 1001
QY 1144 ATACCAACAGCAGCCTGAATCTGTCTCTATGCTTCTTGATGAAGAAACTCAAGCGGT 1203
Db 1002 gcttcagagagttctgcatccc 1023
QY 1204 GTTTAGGCACTTCTGCTTCCC 1225
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RESULT 6
ID Q89222 standard; cDNA; 1618 BP.
AC Q89222;
DT 20-OCT-1995 (first entry)
DE Rat mu opioid receptor cDNA.
KW Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.
OS Rattus sp.
FH Key Location/Qualifiers
FT CDS 214..1410
FT /*tag= a
FT /product= a
PN WO9507983-A.
PD 23-MAR-1995.
PF 13-SEP-1994; U10358.
PR 13-SEP-1993; US-120601.
PA (INDV ) UNITV INDIANA FOUND.
PI Yu L;
DR WPI; 95-131351/17.
DR P-PSDB; R71964.
PT New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.
PS Disclosure; Page 190-194; 266pp; English.
CC A 365 bp fragment of the mouse delta opioid receptor was used to
CC screen a rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in Q89222, encoding a
CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in
CC transfected CHO cells.
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[illegible]

KW	transcription regulatory protein; ss.
OS	Rattus sp.
FH	Key
FT	CDS
	Location/Qualifiers
	339..1235
	/*tag= a
PN	w09507983-A.
PD	23-MAR-1995.
PF	13-SEP-1994; U10358.
PR	13-SEP-1993; US-120601.
PA	(INDV) UNIV INDIANA FOUND.
PI	Yu L;
DR	WP1; 95-131351/17.
PT	P-PSDB; R71965.
PT	New nucleic acid encoding new human mu opioid receptor - and
PT	related vectors, transformed cells, antibodies etc., useful in
PT	diagnosis, treatment and drug screening.
PS	Disclosure; Page 199-203; 266pp; English.
CC	A 365 bp fragment of the mouse delta opioid receptor was used to
CC	screen a rat brain cDNA library under low stringency conditions.
CC	One positive clone included the sequence given in Q89222, encoding a
CC	mu opioid receptor, MOR-1 (R71964). Sequence analysis revealed an
CC	alternative reading frame (Q89223) encoding a zinc
CC	finger-containing transcription regulatory protein (R71965).
SQ	Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;

Db	Query Match	21.9%;	Score 309;	DB 14;	Length 1618;
Db	Best Local Similarity	70.5%;	Pred. No. 2,27e-205;		
QY	Matches 608;	Conservative 0;	Mismatches 245;	Indels 9;	Gaps 8;
Db	419 ttaccatcatgccccttactctatcgtgtgtgtagtggcccttcggaacctcctg	478			
QY	364 TTATCATACCGCTGTCTACTCTGTGTTTGGTGCGCTTAGTGGCAATTCTCTGG	423			
Db	479 tcatgtatgtattgtaagatacaccaaatgaagactgcaccaacatctacatttca	538			
QY	424 TCATGTTTGTTCATCACCAGATACAGAAAGATGAAGACCGCAACAACATCTACATATT	483			
Db	539 acccttgctcgtgcagaacyccttagcgaccagttacactgcccttcagagtgtcaactacc	598			
QY	484 ACCTGGCTTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTTACAGAGTGCTGTCTACT	543			
Db	599 tgatgggaacatggcccttcggaaccatcctctgcaagatcgttatctcaatagattact	658			
QY	544 TGATGAATTTTGCCCTTTTGAGAGATGTGTATGCAGAATTGTTCATTGCACTACT	603			
Db	659 acaacatgttcaaccagcatatlcaccctctgcaccatgagcgtgacccgtacattgctg	718			
QY	604 ACAACATGTTTACCAGCATATTCAACCTTGACCATGATGAGTGTGGACCGCTCACATTGCTG	663			
Db	719 tctgccaccagtcacaaggccctgatttccgttacccccgaalgcacaaatcgtcaacy	778			
QY	664 TGTGCCACCCTGTGAAGCTTTGGACTTCCGAACACCTTTGAAGCAAGATCATCAACA	723			
Db	779 tctgcaactggtatcctctcttctctgccaatcggtctgcctgtaatttcattgcaaccacaa	838			
QY	724 TCTGCATTTGGCTCTTGCCATCATCTGTTGGTATATCAGCGATAGTCTTGAGGACACA	783			
Db	839 aatacagqca-g--g-gg-tc-catagattgcaccctcaagcttctcccaaccaacctggt	892			
QY	784 AAGTCAGGGAAGATGTGATGTCAATTGAATGCTCCTTGCAGTTTCTGATGATGAATAIT	843			
Db	893 actgg-gagaac-ctgc-tcaaaaatcgttgtcttatctlgcttcatcatgcgatcc	949			
QY	844 CCTGTGGGATCTCTTCATGAAGATCTGTCTTCTGCTTTGGCTTTGTGATCCCACTCC	903			
Db	950 tcatcatcactgtgtgttaagcgcctgatgatcttaagactcaagagcgttcgatctat	1009			
QY	904 TCATCATCATTTGTCTGCTACACCCCTGATGATCTCGCCCTGAAGAGTGTCCGGCTCCTGT	963			
Db	1010 cgggctccaagaaaaaggaaggaatctgcgcaggaatcaccccgatggtgtgtgtcg	1069			
QY	964 CTGGCTCCCAGAGAGAACCGAATAATCTCCGCCGCATCACCAAGCTGGTGTGGTAG	1023			

Db 1070 tggctgtattatcgtctgtcgtggaccccatccacatctacgtcatcatcaagcgtga 1129
QY 1024 TTGCAGTCTTCATCATCTCTGTTGGACCCCACTTCACATCTTTATCCTGGTGAGGCTCTGG 1083
Db 1130 tcaagattccaagaaccacatttcaagacgtttccctcgtgcaattctgcattgttgggtt 1189
QY 1084 GAAGCACTCTCCACAGACAGCTGCCCTCTCCAGCTATTTCTGTATTCGCTTGGGT 1143
Db 1190 aacggaacagctgcccgaatccagttcttctacgccttcctcgtgatgaaacttcaagcat 1249
QY 1144 ATACCAACAGACAGCCTGAATCCCTGTCTCTATGCTTCTTGATGAATACTTCAACGGGT 1203
Db 1250 gcttcaagagattctgcattccc 1271
QY 1204 GTTTAGGACTTCTGCTTCCC 1225

RESULT 8
ID Q56705 standard; cDNA; 1981 BP.
AC Q56705;
DT 15-SEP-1994 (first entry)
DE Partial sequence of the murine mu-receptor clone DOR-2
KW (MOR-1, MOR-1alpha)
OS Opioid receptor; morphine; opiate; ss.
PN Mus musculus.
PD WO9404552-A.
PF 03-MAR-1994.
PR 13-AUG-1993; U07665.
PA 13-AUG-1992; US-929200.
PI (REGC) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
DR WPI; 94-083099/10.
PT DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpds. for opioid (ant)agonist activity
PS Example; Fig 9; 74pp; English.
CC A cDNA library prepd. from mouse brain was probed using DOR-1 (see
CC Q56704) as a probe. One clone was recovered and sequenced. This
CC clone, designated DOR-2, represented a new gene. DOR-2 hybridised
CC to a different pattern of heurns than did DOR-1 and showed greater
CC labeling of the striatum. The identity of DOR-2 (mMOR-1) as that of
CC a mu receptor was confirmed.
SQ Sequence 1981 BP; 499 A; 549 C; 436 G; 496 T;

Query Match 21.9%; Score 309; DB 10; Length 1981;
Best Local Similarity 70.6%; Pred. No. 2.27e-205;
Matches 606; Conservative 0; Mismatches 243; Indels 9; Gaps 8;

Db 465 catcatggccctctatctctatcgtgtgtgtgagtgggcctcttggaaacttctgtcat 524
QY 368 CATCACCGCTGTCTACTCTGTGTATTTGTGTGGCTTAGTGGCCAAITTCCTGTGCAT 427
Db 525 gtatgtgatcgttaagatatataccaaaatgaagactgcaccaacatctaacatttcaacct 584
QY 428 GTTGTTCATCATCCGATACACGAAGATGAGAGACCGCAACCAACATCTACATTTAACCT 487
Db 585 tgcctcgtcagatggccttagccactagacgctgccccttccagagtgttaactatgat 644
QY 488 GGCTTTGGCAGATGCTTTGGTTACTTACCACTATGCCCCCTTTCAGAGTGTCTACTTGAT 547
Db 645 gggaacgtggcccttggaaacatcctctcgaagatcgtgatctcaatagactactacaa 704
QY 548 GAATTCCTTGGCCTTTTGGAGATGTGCTATGCAAGATGTGCATTTCCATTGACTACTACAA 607
Db 705 catgtcaaccagtatcttccacctctgcaccatgatgtgtagaccgctacattggcgtctg 764
QY 608 CATGTTTACCAAGCATATTCACCTTGACCATGATGAGTGTGAGCGGCTTACATTTGCTGTG 657
Db 765 ccaccgcgtcaagggcctgattccgtacccccggaatgcgaataatgtcaatgtctg 824
QY 668 CCACCCCTGTGAAGCTTTGGACTTCGGAACACCTTTGAAGCAAGAATCATCAACATCTG 727
Db 825 caactggatcctctcttctgcacattggtctgcocgtaatgttcatgtgcaaccacaaata 884

QY 728 CATTTGGCTCCGCAATCATCTGTTGGTATATACCGATAGTCCCTTGAGAGCAACCAAGT 787
Db 885 cagga-g--g-gg--tc-catagattgcacccctcaagcttctctcatccacatggtactg 938
QY 788 CAGGGAAGATGTGCAATGTCATTTGAATGCTCCCTTGACAGTTTCCGTGATGATGAATTCCTG 847
Db 939 g-gagaac-ctgc--tcaaaatctgtgtcttcatcttcgccttccatcatgcgggcctcat 995
QY 848 GTGGGATCTCTTCATGAAGATCTGTGTCTTCTTTGCTTGTGATCCAGTCTCAT 907
Db 996 catcactgtgttatgacctgatgatccttcaagctcaagagtgtccgcatgtctcgg 1055
QY 908 CATCATGTCTGTACACCCCTGATGATCCTGGCCTGAAGAGTGTCCGGCTCCTGTCTG 967
Db 1056 ctccaagaagaagcaggaacctgagcagatcaccocgagatgtgtcgtgtcgtgc 1115
QY 968 CTCCCGAGAGAAGACCGAAATCTCCCGCGCATCACCAGAGCTGTGCTGTAGTATGCTGC 1027
Db 1116 tgtattatgtctcgtcgtgaccccccatccatctatgtcatcatcaagcactgatcac 1175
QY 1028 AGTCTTCATCATCTGTGTGAGACCCCATTCACATCTTTATCCTGTGTGAGGCTCTGGGAAG 1087
Db 1176 gattccagaaccacttccagactgtttccctggcacttctgcattgccttgggttacac 1235
QY 1088 CACCTCCACAGACACAGCTGCCCTCTCCAGCTATTATTTCTGTATTCCTTGGCTTATAC 1147
Db 1236 aaacagctgtctgaacccagttcttlatggttccctgtagtgaactcaaaagatgtt 1295
QY 1148 CAACAGCAGCCTGAAATCCTGTCTCTATGCTTCTTGATGAAAACTTCAAGCGGTGTT 1207
Db 1296 tagagagttcgtcatccc 1313
QY 1208 TAGGACTTCTGCTTCCC 1225

RESULT 9
ID Q56700 standard; cDNA; 1821 BP.
AC Q56700;
DT 15-SEP-1994 (first entry)
DE Sequence of murine delta opioid receptor in the DOR-1 cDNA clone.
KW Opioid receptor; morphine; opiate; ss.
OS Mus musculus.
PN Key Location/Qualifiers
FT CDS 29..1139
FN /*tag= a
PD WO9404552-A.
PF 03-MAR-1994.
PR 13-AUG-1993; U07665.
PR 13-AUG-1992; US-929200.
PI (REGC) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
DR WPI; 94-083099/10.
DR P-PSDB; R48629.
PT DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpds. for opioid (ant)agonist activity
PS Claim 1; Fig 5; 74pp; English.
CC A cDNA library was constructed using mRNA isolated from the NG109-15
CC cell line. A single clone, named the DOR-1 clone was isolated.
CC Comparisons with known sequences in GenBank showed highest homology
CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other
CC features of the DOR-1 clone AA sequence deduced from the cDNA
CC sequence include 3 consensus glycosylation sites at residues 18 and
CC 33 (predicted to be in the extracellular N-terminal domain), and at
CC residue 310 (close to the C-terminus and predicted to be
CC intracellular). Phosphokinase C consensus sites are present within
CC predicted intracellular domains, at residues 242,255, 344 & 352.
CC Seven putative membrane-spanning regions were identified. The DOR-1
CC clone produces a delta receptor with a predicted mol. wt. of 40,558
CC kaltons prior to post-translational modifications.
SQ Sequence 1821 BP; 339 A; 559 C; 541 G; 382 T;

Query Match		20.6%;	Score 291;	DB 10;	Length 1821;
Best Local Similarity		70.8%;	Pred. No. 8.82e-192;		
Matches		597;	Conservative	0;	Mismatches 234; Indels 12; Gaps 8;
Db	181 catcacccgcgtctactcgcgtgtgtgctggcggtctctctggcaacgtgtctgtcat	240			
QY		368 CATCACCGCTGCTTACTCTGTGTTATTTGTGTGGCTTAGTGGGCAATTTCTGTGTCAT	427		
Db	241 gtttggcatcgtcccggtacacccaattgaagaccgccaaccaatctacatcttcaatct	300			
QY		428 GTTTGTATCATCGATCGATACACGAAGATGAAGCCGCAACCAACATCTACATTTTAACCT	487		
Db	301 ggcttggctgatalgcgtggtccaccagcagctgccttccagagcgccaagtacttgat	360			
QY		488 GGCTTTGGCAGATGCTTTGGTTACTACCACATAGCCCTTTCAGAGTGTGTCTACTTGAT	547		
Db	361 ggaacacgtgcccgtttggcgagctgtgtgcaagctgtgtctccattgactactacaa	420			
QY		548 GAATTCCTTGGCCTTTGGAGATGTGCTATGCAAGATTGTCAATTCATGACTACTACAA	607		
Db	421 catgttcaactagcatcttcaacctcaaccatgatgagcgttgaccgctacattgtctg	480			
QY		608 CATGTTTACCAAGCATATTTCACTTGACCATGATGATGATGTGACCCGCTACATTTGCTGTG	667		
Db	481 ccatacctgtcaaacccctggactccggaacacccaagccaagccaagctgataatatg	540			
QY		668 CCACCCCTGTGAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAAAGATCATCAACATCTG	727		
Db	541 catctgggtccttgcttcaagtggtcgggtgcccatcatggtcatgycagtgacccaacc	600			
QY		728 CATTTGGCTCCTGGCATCATCTGTTGTATATACAGGATAGTCCTTGGAGGACCAAAAGT	787		
Db	601 ccggatggtgcagtggt-at-gcatgctcc---agttcccccagttcccagctgttactg	654			
QY		788 CAGGGAAGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	847		
Db	655 g-gaca-ctgtg-accaagatctgcgtgttccctctttgcttgccttgctgtgtccgattccat	711			
QY		848 GTGGGATCTCTTTCATGAAGATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT	907		
Db	712 catcaacggtgtgtatgtgctctcatgtctactgcgctcgtgcagcgtgtcgtctgtccgg	771			
QY		908 CATCATTTGTCTGTACACCCCTGATGATCTCTGCGCCTGAAGAAGTGTCCGGCTCTCTGTG	967		
Db	772 ttccaaggaagaagaccgagcctgctgcggcatcaacgcgcgcatgtgtgtgtgtgtgg	831			
QY		968 CTCGCCGAGGAAGGACCGAAATCTCCGCCGATCACCAAGCTGTGCTGTGTAGTAGTTGC	1027		
Db	832 cgccttcgt	891			
QY		1028 AGTCTTCATCATCTGTGTGACCCCATTCACATCTTTATCTGTGGT--GGAGGCTCTGGGA	1085		
Db	892 calcaatcggcgagccaccattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	951			
QY		1086 -AGCACCTCCACACAGACAGAGCTGCCCTCTCCAGCTATTATTTCTGTATTTGCCCTTGGTTA	1144		
Db	952 cgcacaacagcagcctcaaccgggttctctacgcttctctgtgagcagagaactcaagcgtg	1011			
QY		1145 TACCAACAGCAGCGCTGAATCTGTCTCTATGCTTTCTGTGATGAAGAACTTCAAGCGGTG	1204		
Db	1012 ctt 1014				
QY	TTT 1207				
RESULT 10					
ID	Q75927 standard; DNA; 2272 BP.				
AC	Q75927;				
DT	17-AUG-1995 (first entry)				
DE	Mouse delta opioid receptor MORD1 cDNA.				
KW	Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify; transmembrane domain; somatostatin; receptor; human; expression vector; truncate; chimeraic; assay; probe; ss.				

RESULT 10
ID Q75927 standard; DNA; 2272 BP.
AC Q75927;
AT 17-ATG-1995 (first entry)
DE Mouse delta opioid receptor MOR1 cDNA.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
transmembrane domain; somatostatin; receptor; human; expression vector;
truncate; chimeraic; assay; probe; ss.

OS	Mus musculus.	Location/Qualifiers
PH	Key	12..1130
FT	CDS	
FT	/*tag= a	
FT	/product= mouse delta opioid receptor	
PN	W09428132-A.	
PD	08-DEC-1994.	
PF	20-MAY-1994; U05747.	
PR	20-MAY-1993; US-066296.	
PR	30-JUL-1993; US-100694.	
PR	05-NOV-1993; US-147592.	
PA	(ARCH-) ARCH DEV CORP.	
PI	Bell GI, Reisine T, Yasuda K;	
DR	WPI; 95-022804/03.	
DR	P-PSDB; R67670.	
PT	Polynucleotides and peptides derived from opioid receptor	
PT	polypeptides - for use in therapeutic compositions and in	
PT	screening assays for useful drug substances.	
PS	Claim 6; Page 215-221; 300pp; English.	
CC	The nucleotide sequence of the novel mouse delta opioid receptor gene	
CC	MOR1. The gene was isolated from a mouse brain cDNA library using a	
CC	fragment (amplified from the cDNA library with primers Q75929-30) as a	
CC	probe. The primers are based on the conserved sequences present in the	
CC	second and third transmembrane domains of somatostatin (SRIF) receptor	
CC	subtypes SSTR1, SSTR2 and SSTR3. The 1.3 kb EcoRI-SacI fragment from the	
CC	mouse delta opioid receptor clone, lambda msl-2, was subcloned into the	
CC	CMV promoter-based expression vector pCMV-6c. The resultant construct	
CC	pCMV-msl-2 was transfected into COS-1 cells for protein production. The	
CC	gene encoding the opioid receptor can be used to produce complete,	
CC	truncated or chimeraic opioid receptor proteins. The opioid receptors	
CC	thus produced are useful for the development of novel assays designed to	
CC	select or improve substances, capable of interacting with the opioid	
CC	receptor proteins, for use in diagnosis, drug design and therapeutic	
CC	applications.	
SQ	Sequence	2272 BP; 485 A; 665 C; 472 T;
Query Match 20.6%; Score 291; DB 13; Length 2272;		
Best Local Similarity 70.8%; Pred. No. 8.82e-192;		
Matches 597; Conservative 0; Mismatches 234; Indels 12; Gaps 8;		
Db	164 catcacgcgcgtctactcgcgtgtgtgcgcagltggygcctcttgycgaacgtgtcgtcat	223
QY	368 CATCACCGCTGTCTACTCTGTGTATTGTGGTGGGCTTAGTGGGCAATTCCTGGTCA	427
Db	224 gtttgcatacgtccggtacacaattgaagacgcgcacacacatctcatcttcaatct	283
QY	428 GTTGTCAATCATCCGATACACGAAGATGAAGACCGCAACCAATCTAATTAACT	487
Db	284 ggccttgctgatgcgtgcgcacacagcagctgcctccagagcgcaagtacttgat	343
QY	488 GGCCTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTTCAGAGTGTCTACTTGA	547
Db	344 ggaacgtgcccgtttgycgagctgtgcaagcgtgtgtctctccatgtaactacaa	403
QY	548 GAATTTCTTGCCCTTTGGAGATGTGCTATGCAAGATTGTCAATTTCCATTGACTAC	607
Db	404 catgttcaactagcatcttcaaccctaacatgatgagcgttgaccgctacattgctctg	463
QY	608 CATGTTTACCAAGCATATTCACTTGACCATGATGAGTGTGGACCGCTACATGCTGTG	667
Db	464 ccatacctgtcaaaagccctggaactccggaacacccagccaagcgcaagctgataata	523
QY	668 CCACCTCTGTGAAGCTTTGGACTTCCGAACACCTTTGAAAGCAAAAGATCATCA	727
Db	524 catctggtgtccttggtcctcaggtgtcggygtccccaatcatgttcatgtgcagtgaa	583
QY	728 CATTTGGCTCCTGGCATCATCTGTTGGTATATCAGCGATAGTCTTGGAGGCA	787
Db	584 ccggagtggtgcagtgt-at-gcatgtccc---agttccccagttcccagctgttactg	637
QY	788 CAGGGAAGATGTGATGTCAATGAATGCTCTCTTGACGTTTCCCTGATGATGAATAT	847
Db	638 g-gaca-ctgtg-accaagatctgcgtgttctctctttgcocttcgtgtgcccgatcc	694

Query Match 20.6%; Score 291; DB 13; Length 2272;
Best Local Similarity 70.8%; Pred. No. 8.82e-192;
Matches 597; Conservative 0; Mismatches 234; Indels 12; Gaps 8;

Db	164	catcacccgcgtctactcgcgt	223
QY	368	CATCACCGCTGTCTACTCTGTGTATTTGTGTGGCTTAGTGGCAATCTCTGTGTCAT	427
Db	224	gtttggcatcgtccggttacaccaaatlgaagaccgccaaccaatctacatcttcaatct	283
QY	428	GTTTGTATCATCTCCGATACACGAAGATGAAGACCGCAACCAACATCTACATATTTAACT	487
Db	284	ggcttggctgtatgcgt	343
QY	488	GGCTTTGGCAGATGCTTTGGTTACTACCACTATGCCCTTTTCAGAGTGTCTGTACTTGAT	547
Db	344	ggaacacgtggccgtttgt	403
QY	548	GAATTCCTTGGCCTTTGGAGATGTGCTATGCAAGATTGTCAATTTCCATTGACTACTACAA	607
Db	404	catgttcaactagcatcttcaacctcaaccatgatgagcgtgtgaacgctacatgtgtctg	463
QY	608	CATGTTTACCAAGCATATTTCACTTGACCATGATGAGTGAACCGCTACATTTGCTGTG	667
Db	464	ccatacctgtcaagccctggaactccggaacaccagccaagccaagctgatcaatatatg	523
QY	668	CCAACCTGTGAAGCTTTGAGCTTCGGAACACCTTTGAAGCAAAAGATCATCAACTCTG	727
Db	524	catctgggtccttgcttcaagtgctcgggttccccatcatggtcatgycagtgacccaacc	583
QY	728	CATTTGGCTCCTGGCATCATCTGTTGTATATACGCGATAGTCTCTTGAGGACCAAGT	787
Db	584	ccggatgtgtgcagtggt-at-gcatgctcc---agttcccccagttcccagctgtgtactg	637
QY	788	CAGGGAAGATGTGATGTCAATGAATGCTCTTGACAGTTTCTGTGATGAATATTTCTCTG	847
Db	638	g-gaca-ctgtg-accaagatcgtgttctcctcttgccttgctgtgtgtgtgtgtgtgtgt	694

Db	739	catcaacggtgtgtctatgctatgacctatcagtactgagcctgagcagcgtgctctgtctgtccgg	798
QY	908		
		CATCATTGTCTGTCTACACCCCTGATGATCCTGCGCCTGAGAGTGTCCGGCTCCTGTCTGG	967
Db	799	ttccaagagagaagagaccgcagccctgcgcgcgcatacagcgcatggtgtgtgtgtgtgg	858
QY	968		
		CTCCCGAGAGAGAGGACCAGCAATCTCCGCCGATCACCAAGCTGGTGGTAGTAGTTCC	1027
Db	859	cgccttcgtgtgtgtgtgtgcgtggcgcccatccacatcttcgtcatcgtctctgagcgtgtgtga	918
QY	1028		
		AGTCTTCATCATCTGTGTGAGACCCCCCATTCACATCTTTATTCCTGGT--GGAGGCCTCTGGGA	1085
Db	919	catcaatcggcgcgcaccacacttgtgtgtgcccgcactgcacctgtgcattgcgctggcta	978
QY	1086		
		-AGCACCTCCACACAGCACAGCTGCCCTCTCCAGCTATTATTCTGTATTTGCTTGGGTTA	1144
Db	979	cgccaacagcagcctcaaccccggttctctctacgcctctctggaagagaacttcaacgcgtg	1038
QY	1145		
		TACCAACAGCAGCGCTGAACTCTGTCTCTATAGCCCTTCTGTGGATGGAATAAAGCTTCAAGCGGTG	1204
Db	1039	ctt 1041	
QY	1205	TTT 1207	

RESULT 14
ID Q56703 standard; DNA; 829 BP.
AC Q56703;
DT 15-SEP-1994 (first entry)
DE Partial sequence of the human mu opioid receptor
DE genomic clone H20 (MORA).
KW Opioid receptor; morphine; opiate; ss.
OS Homo sapiens.
PN M09404552-A.
PD 03-MAR-1994.
PF 13-AUG-1993; U07665.
PR 13-AUG-1992; US-929200.
PA (REGC) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
DR WPI: 94-083099/10.
PT DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpds. for opioid (ant)agonist activity
PS Example; Fig 8c; 74pp; English.
CC To isolate opiate receptor genomic clones, 300,000 human genomic
CC clones and a similar number of mouse genomic clones were probed
CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI
CC fragment. One mouse clone and three human genomic clones were
CC isolated. The 3 human clones had very different EcoRI patterns
CC which indicated that three different genes were represented by the
CC human genomic clones which were designated H3, H14 and H20. H20 maps
CC to chromosome 6. It encodes the human mu receptor. In addition, H20
CC appears to contain a CACACA marker (Q56704) which provides a means
CC to track the inheritance of this gene.
SQ Sequence 829 BP; 182 A; 205 C; 134 G; 214 T;

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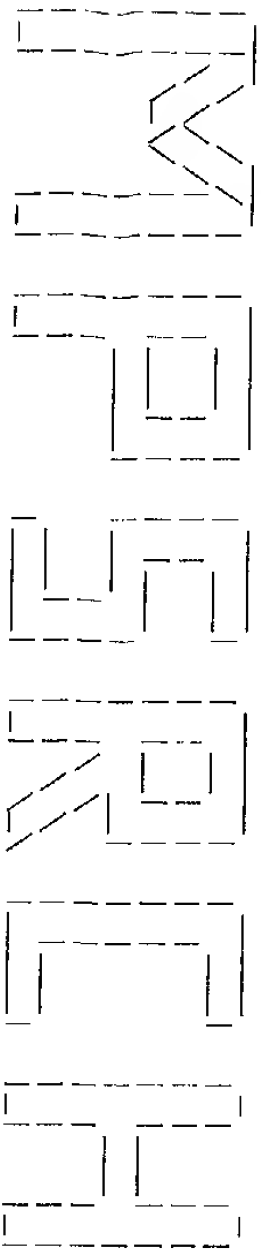
Query Match      16.38; Score 230; DB 10; Length 829;
Best Local Similarity 62.88; Pred. No. 6.07e-146;
Matches 493; Conservative 0; Mismatches 279; Indels 13; Gaps 12;

```

Db	16	gatacaaccaagatgaagactgccaccaacatctacatlltccaacctgctctg-cagatg	74
QY	442	GATACACGAGATGAGAGACCGCAACACATCTACATATTTAAACCTGGCTTTGGCAGATG	501
Db	75	ccttagcaaccagtaaccctgccccttccagagtgltgaattaccctaatyggaacatggccat	134
QY	502	CTTTGGTTACTACCACTATGCCCCCTTTACAGAGTGCGTCTCTACTTGTATGAATTTCTTGCCCTT	561
Db	135	ttggaaccatccttltgcaagatagtgatctccatagatltactataacatgttcaaccagca	194
QY	562	TTGAGAGATTTGCCTATGCAAGATTTGCAATTTCCATTGACTACTACAACAATGTTTACCAGCA	621

Db	195	tattcaccctctgcaccatgagtgltgatcgatcacatgcygtctgccaccctgtcaagg	254
QY	622	TATTCAccCTTGACCATGAGTGAgtGTGACCGCTACATTTGCTGTGTGCGCACCCGTGAAG	681
Db	255	ccttagatttccgtactcccnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn	314
QY	682	CTTTGGACTTCCGAACACCCCTTTGAAGAACAAGATCATCACATCTGCATTTGGCTCTGG	741
Db	315	nnngt-tcc	373
QY	742	CATCACTCTGTTGGTAATACAGCATAGTCTCTGGAGGACACCAAGTCAAGGAAGATGTGG	801
Db	374	atcg-attgta--cac-taacattctc-tcatccaacctgtactgg-gaaaac-ctgc-	425
QY	802	ATGTCATTTGAATGCTCTCCTTGCAGTTTCTCGATGATGAATAATTCTCGTGGATCTCTTCA	861
Db	426	tgaagatctgtgttltcatcttcgccttcattatgccaagtgcatacatcattaccgtgtgt	485
QY	862	TGAAGATCTGTGTCTTCGTCTTGGCTTTGTGATCCACAGTCTCATCATCTGTCTGCT	921
Db	486	atgagctgatgatcttgcgcctcaagagtgtccgcgatctctctgtgtcccaagaaaag	545
QY	922	ACACCCGTGATGATCCTGGCGCTGAAGAGTGTCCGGCTCTGTGCTCCCGAGAGAAGG	981
Db	546	acaggaatcttcgaagatcaccaagatggtgtcgtgtgtgtgtgtgtgtgttcatcgtct	605
QY	982	ACCGAAATCTCCGCCGCATCACCAAGCTGGTGTGCTGGTAGTGTGCAGTCTTCAICATCT	1041
Db	606	gctggaactcccatcacattacgtcatcatcattaaagccttgytlaacaatcccagaacta	665
QY	1042	GTTGGACCCCATTCACATCTTATCTGCTGGTGAGGCTCTGGGAAGCACCTCCACAGCA	1101
Db	666	c-gttccagactgttcttggcaactctctgcattgtctctaggttacacaacacgtgctc	724
QY	1102	CAGCTGCCCTCTCCAGCTATN-ATTTCGTATTGCCCTTGGTTATACCAACACAGCAGCCTG	1160
Db	725	aaccocagtccttlatatgcatlctctgatatgaaacttcca-cgatgcttcagagagtctgt	783
QY	1161	AATTCGTCTCTATGCTTTCTGGATGAATACTTCAAGCGGTGTTTAAAGGACTTCTGC	1220
Db	784	atccc 788	
QY	1221	TTCCT 1225	

RESULT	15	
ID	Q89233	standard; cDNA; 1567 BP.
AC	Q89233;	
DT	20-OCT-1995	(first entry)
DE	Rat opioid receptor cDNA.	
KW	Opioid receptor; MOR-1; gene therapy; diagnostic; ss.	
OS	Rattus sp.	
EH	Key	Location/Qualifiers
FT	CDS	173..1276
FT	/*tag= a	
PN	W09507983-A.	
PD	23-MAR-1995.	
PE	13-SEP-1994; U10358.	
PR	13-SEP-1993; US-120601.	
PA	(INDV) UNITV INDIANA FOUND.	
PI	yu L;	
DR	WPI; 95-131351/17.	
DR	P-PSDB; R71968.	
PT	New nucleic acid encoding new human mu opioid receptor - and	
PT	related vectors, transformed cells, antibodies etc., useful in	
PT	diagnosis, treatment and drug screening.	
PS	Example 9; Page 218-222; 266pp; English.	
CC	The cDNA given in Q89233 was isolated from a rat brain library by	
CC	low stringency hybridization with rat mu opioid receptor cDNA	
CC	(Q89222). The clone encoded a 367-amino acid protein (R71968)	
CC	that showed high homology with mu, kappa and delta opioid receptors	
CC	but lacked affinity for their ligands, suggesting it to be	
CC	a novel member of the opioid receptor family.	



(TM)

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MPsrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Mon Apr 20 23:47:36 1998; MasPar time 728.47 Seconds
1156.083 Million cell updates/sec
Tabular output not generated.

Title: >US-08-292-694A-11
Description: (1-1000) from US08292694A.seq
Perfect Score: 994
N.A. Sequence: 1 AAGAGCAAAATCAGTAATC.....CCAGTATGACTAGTCGTGGA 1000
Comp: TTCTTCGTTTATGATTAG.....GGTCAATCTGATCAGCACCT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 1126798 seqs, 421087984 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-est
1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5
6:em_est6 7:em_est8 8:em_gss
genbank-est
9:gb_est1 10:gb_est2 11:gb_est3 12:gb_est4 13:gb_est5
14:gb_est6 15:gb_est7 16:gb_est8 17:gb_est9 18:gb_est10
19:gb_est11 20:gb_ests 21:gb_gss 22:gb_est12 23:gb_est13

Statistics: Mean 11.137; Variance 2.017; scale 5.520

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
	1	163	16.4		183	10	R81583	yj04b04.r1 Homo sapien	3.10e-289
	2	137	13.8		153	10	R31984	yn62c10.r1 Homo sapien	1.85e-231
	3	40	4.0		433	10	R81332	yj04b04.s1 Homo sapien	3.82e-31
	4	35	3.5		345	13	HSC1ZF101	H. sapiens partial cDN	1.22e-22
	5	35	3.5		386	11	H14301	ym63c04.r1 Homo sapien	1.22e-22
	6	34	3.4		181	19	AA039537	zk39h11.r1 Soares preg	5.34e-21
	7	34	3.4		377	18	AA236709	EST112493 Retina II Ho	5.34e-21
	8	34	3.4		484	10	R77881	yi177h05.r1 Homo sapien	5.34e-21
	9	31	3.1		442	15	W79255	zd75c02.r1 Soares feta	3.26e-16
	10	31	3.1		1664	20	G28514	human STR SHGC-31461.	3.26e-16
	11	30	3.0		304	18	AA327933	EST31339 Embryo, 12 we	1.14e-14
	12	30	3.0		320	10	R81133	yi91h09.r1 Homo sapien	1.14e-14
	13	30	3.0		351	18	AA330028	EST33738 Embryo, 12 we	1.14e-14
	14	30	3.0		363	19	HSPD07459	H.sapiens EST sequence	1.14e-14
	15	30	3.0		370	23	R1CS16541A	Rice cDNA, partial seq	1.14e-14

16	30	3.0	384	9	T90564	y440h01.s1 Homo sapien	1.14e-14
17	30	3.0	390	23	HUMHBC4896	similar to HMG-1.	1.14e-14
18	30	3.0	402	23	HUMGS01731	Human HL60 3'directed	1.14e-14
19	30	3.0	422	15	AA101746	zn80d1.r1 Stratagene	1.14e-14
20	30	3.0	422	10	R34185	yh84c06.r1 Homo sapien	1.14e-14
21	30	3.0	431	23	AA467444	vf05g04.r1 Knowles Sol	1.14e-14
22	30	3.0	431	13	W07682	zb02b02.r1 Soares feta	1.14e-14
23	30	3.0	451	15	AA045606	zl66e12.s1 Stratagene	1.14e-14
24	30	3.0	451	15	AA123213	mn25h03.r1 Beddington	1.14e-14
25	30	3.0	455	12	N26696	yx93h03.s1 Homo sapien	1.14e-14
26	30	3.0	476	12	N38949	yy43h05.s1 Homo sapien	1.14e-14
27	30	3.0	572	14	W97542	mf98g08.r1 Soares mous	1.14e-14
28	30	3.0	580	19	AA054783	zk68d04.r1 Soares preg	1.14e-14
29	30	3.0	588	16	AA196344	zp96h01.r1 Stratagene	1.14e-14
30	30	3.0	628	17	AA120232	mp85b01.r1 Soares 2Nm	1.14e-14
31	29	2.9	339	13	HSB18A052	H. sapiens partial cDN	3.74e-13
32	29	2.9	404	11	H14901	yl26a04.r1 Homo sapien	3.74e-13
33	29	2.9	416	11	H44713	yp24d06.r1 Homo sapien	3.74e-13
34	29	2.9	521	16	AA196802	zq08g11.r1 Stratagene	3.74e-13
35	29	2.9	791	13	W28236	44a1 Human retina cDNA	3.74e-13
36	28	2.8	203	19	AA360842	EST70092 T-cell lympho	1.14e-11
37	28	2.8	249	11	H29103	ym31f07.r1 Homo sapien	1.14e-11
38	28	2.8	261	18	AA331167	EST35211 Embryo, 8 wee	1.14e-11
39	28	2.8	266	17	AA247271	cs90874.seq.F Human fe	1.14e-11
40	28	2.8	274	13	HSC27C022	H. sapiens partial cDN	1.14e-11
41	28	2.8	385	15	AA083771	zn39f12.s1 Stratagene	1.14e-11
42	28	2.8	547	18	AA275567	vc16g04.r1 Barstead MP	1.14e-11
43	27	2.7	200	14	N88386	K3212F Fetal heart, Ia	3.24e-10
44	27	2.7	492	21	B50064	CIT978SK-2206 TV CIT97	3.24e-10
45	27	2.7	614	13	W26028	1994 Human retina cDNA	3.24e-10

ALIGNMENTS

RESULT 1
LOCUS R81583 183 bp mRNA EST 12-JUN-1995
DEFINITION yj04b04.r1 Homo sapiens cDNA clone 147727 5' similar to gb:L25119
MU-TYPE OPIOID RECEPTOR (HUMAN);.
ACCESSION R81583
NID 9858186
KEYWORDS EST.
SOURCE human clone=147727 library=Soares placenta Nb2HP vector=pt7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13Rp1 Rsitel=Not I Rsitel2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5'
AACTGGAAGATTTCGGCGCCGCGAGAAATTTTCTTTTCTTTTCTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified pT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)

TITLE
JOURNAL
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1

High quality sequence stops: 1

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Trace considered overall poor quality.

Location/Qualifiers
1. .183

BASE COUNT ORIGIN	a	c	g	t	others
	31	56	40	46	10

Query Match 16.48; Score 163; DB 10; Length 183;

[illegible]

RESULT	2				
LOCUS	R31984	153 bp	mRNA	EST	28-APR-1995
DEFINITION	yh62c10.r1 Homo sapiens cDNA clone 134322 5' similar to gb:L25119				
	MU-TYPE OPIOID RECEPTOR (HUMAN);.				

ORGANISM Homo sapiens

Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 153)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
High quality sequence stops: 120
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

FEATURES	Location/Qualifiers
source	1. .153

BASE COUNT	25 a	49 c	37 g	42 t
ORIGIN				

Query Match	13.8%;	Score 137;	DB 10;	Length 153;
Best Local Similarity	97.2%;	Pred. No. 1.85e-231;		
Matches 137; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

Db	1	GGCTTCATCTTTGCCCTTCGTATCCCTGTCTCATCATCATCGTCTGCTACACCCCTGA	60
QY	529	GGCTTCATCTTTGCCCTTCGTATCCCTGTCTCATCATCATCGTCTGCTACACCCCTGA	588
Db	61	TGATCCTGGCTCTCAGAGCGTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATCGCAACC	120
QY	589	TGATCCTGGCTCTCAGAGANNGTCCGGCTCCTTTCTGGCTCCCGAGAGAAAGATNNCAACC	648
Db	121	TGCGTAGGATCACCAAGACTGG	141
QY	649	TGCGTAGGATCACCAAGACTGG	669

RESULT	3					
LOCUS	R81332	433 bp	mRNA	EST	12-JUN-1995	
DEFINITION	YJ04b04.s1	Homo sapiens	CDNA	clone 147727 3'.		
ACCESSION	R81332					
NID	9857935					
KEYWORDS	EST.					
SOURCE	human	clone=147727	library=Soares	placenta	Nb2HP	vector=pt773D

ORGANISM Homo sapiens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
AUTHORS
1 (bases 1 to 433)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marras, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and
Wilson, R.

TITLE	Project
JOURNAL	The WashU-Merck EST unpublished (1995)

Contact: Wilson RK
 WashU-Merck EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 High quality sequence stops: 241
 Source: IMAGE Consortium, LLNL
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Location/Qualifiers

FEATURES	Location/Qualifiers
source	1. .433

BASE COUNT	102 a	97 c	100 g	114 t	20 others
ORIGIN					

query Match 4.0%; Score 40; DB 10; Length 433;


```

Best Local Similarity 78.38; Pred. No. 3.82e-31;
Matches 72; Conservative 0; Mismatches 16; Indels 4; Gaps 3;

Db 333 TNCAGNCTAGTCATACCTGGGCGCTAT--TCATCCCATCGCATGTCCCTCAGGTAGNAGGG 390
    | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Cp 1000 TCCACGACTAGTCATACACTGCTTTTATTCATCATCATCCCATCGATCTCCCTCAGGTAAGCAGG- 942
    | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||

Db 391 NTCCGGAACCTGNATTTNGGGAATTNGCTAGNG 422
    ||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Cp 941 ATCCGAACTGTATTTCCG-ACCTCTGCTAGTG 911
    ||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||

```

RESULT	4				
LOCUS	HSC1ZF101	345 bp	RNA	EST	21-SEP-1995
DEFINITION	H.sapiens partial cDNA sequence; clone c-1zf10.				
ACCESSION	F07228				
NID	G672877				
KEYWORDS	EST; partial cDNA sequence; transcribed sequence fragment.				
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	1 (bases 1 to 345)
AUTHORS	Genexpress.
TITLE	Direct Submission
JOURNAL	Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France

REFERENCE 2 (bases 1 to 345)

TITLE	The Genexpress cDNA program
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 345)
AUTHORS	Auffray,C., Behar,G., Bois,

TITLE	IMAGE:
molecular integration of the analysis of the human genome	

JOURNAL C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
MEDLINE 95277534

Cloning_method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lacmid BA vector;

```
SequencingMethod: single read, full automatic;
Primer: M13_reverse
cDNA sequence colinear to mRNA
StretchRemoved: nothing
NormalizationMethod: Bento Soares, P.N.A.S. 91:9228-9232(1994);
GenePress_Library_Idt: C;
GenePress_Sequence_Idt: Y1C-1Z10.
```

Source

T. 345

```
/organism="Homo sapiens"  
/isolate="muscular atrophy patient"
```

/db_xref="taxon:9606"
/clone_lib="normalized infant brain cDNA from B.Soaresh
Psychiatry Dept. Columbia University USA"

BASE COUNT	67	a	118	c	79	g	80	t	1	others
ORIGIN										

Query Match	3.5%;	Score 35;	DB 13;	Length 345;
Best Local Similarity	61.5%;	Pred. No. 1.22e-22;		
Matches	91;	Conservative	0;	Mismatches 57;
				Indels 0;
				Gaps 0;

Db 169 TGGCACCTTTGGGGGAGACCATGTGCACCCCTCATCACGGCCATGGATGCCAATAGTCACTTC 228
 1111 11111111 111111 11111111 11111111
 QY 213 TGGCCCTTTTGGGGATGTGCTGTGCAGATAGTAATTTCCATTCATTACTACAAACATGTTC 2722

[illegible]

RESULT	5
LOCUS	H14301 386 bp mRNA EST 10-JUL-1995
DEFINITION	ym63c04.r1 Homo sapiens CDNA clone 163590 5' similar to gb:U03642_cdsl PROBABLE G PROTEIN-COUPLED RECEPTOR APJ (HUMAN); .
ACCESSION	H14301
NTID	9879121
KEYWORDS	EST.
SOURCE	human clone=163590 library=Soares adult brain N2b4HB55Y

human clone-163590 library=Soares adult brain N2b4HB55Y vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RPI Rsite1=Not I Rsite2=Eco RI 55-year old male. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCAATCTGAAGTGGGAGCGCCGCCGTCTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fátima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla.

ORGANISM

iens

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS

המחיר

Wilson, R., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Holman, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevasakis, E., Waterston, R., Williamson, A., Wohlmann, P. and

TITLE	The WashU-Merck EST Project
JOURNAL	Unpublished (1995)

COMMENT

Contact: Wilson RK
WashU-Merck EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence stops: 212

Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.linl.gov) for further information.

FEATURES	Location/Qualifiers
source	1. .386

2000.11.1

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/organism="Homo sapiens"  
/clone="163590"
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PAGE COUNT

58 a	122 c	104 g	98 t	4 others
------	-------	-------	------	----------

Query Match	3.58;	Score 35;	DB 11;	Length 386;
Best Local Similarity	78.78;	Pred. No. 1.22e-22;		
Matches	48;	Conservative	0;	Mismatches 13;
				Indels 0;
				Gaps 0;

[illegible]

Db	167 G	167
QY	323 G	323

RESULT
LOCUS
DEFINITION
ACCESSION
NID
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

6
AA039537
181 bp mRNA EST
Soares pregnant uterus NbHPV Homo sapiens cDNA clone
485253 5' similar to SW:BLR1_HUMAN P32302 BURKITT'S LYMPHOMA RECEPTOR 1. [1] ;
AA039537
g1515815
EST.
human.
Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.

1 (bases 1 to 181)
Fillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Matra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
WashU-Merck EST Project
Unpublished (1995)

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1023 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 89.

Location/Qualifiers
1..181
/organism="Homo sapiens"
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I -
cligo(dT) primer [5'
AAGTGAGAATTGCGGGCCCTTTTTTTTTTTTTTTT 3'] ,
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by M. Fatima Bonaldo."
/db_xref="taxon:9606"
/clone="485253"
/clone_lib="Soares pregnant uterus NbHPV"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
<1..>181
/db_xref="GDB:3758967"

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 79.3%; Pred. No. 5.34e-21;
Matches 46; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Dd 94 GAGTGGCCGTGATGATGATGATGATGATCCTTCCTTCCTGCCTGGACTCCCATCACATTTT 151
||| | ||||||| |||| | ||||||| |||| | |||| |
QY 664 GACTGCTCCTGATGATGATGATGATGATCCTTCCTTCCTGCCTGGACTCCCATTCACATATT 721

RESULT 7 AA296709 377 bp mRNA EST 18-APR-1997

DEFINITION	EST112493 Retina II Homo sapiens cDNA 5' end similar to guanine nucleotide-binding protein coupled receptor A23B.		
ACCESSION	AA296709		
NID	G1949271		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Homo sapiens; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 377) Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulder,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstein,R.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.		
TITLE	Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence		
JOURNAL MEDLINE	Nature 377 (6547 Suppl), 3-174 (1995) 96026280		
COMMENT	Other_ESTs: THCI77269 Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: arkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.		
FEATURES	Location/Qualifiers 1..377 /organism="Homo sapiens" /note="Organ: retina; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI" /db_xref="ATCC (inhost):118592" /db_xref="taxon:9606" /clone_lib="Retina II" /sex="mixed" /dev_stage="adult" <1..>377		
BASE COUNT	78 a 90 c 89 g 116 t 4 others		
ORIGIN	mRNA		
Query Match	3.4%; Score 34; DB 18; Length 377;		
Best Local Similarity	77.6%; Pred. No. 5.34e-21;		
Matches	45; Conservative 0; Mismatches 13; Indels 0; Gaps 0;		
Db	103 GAGTGGCCGTGTGTGTGTGGTGTGTTTNTTGTCTGTGCTGACATCCATACCATTTT 160		
QY	11 111 1 1111111111 11 11 1 1111111111 1111 11 664 GACTGCTCCTGTGTGTGTGGCAGTCTTCGTCGTCGTGACATCCATTCACATATT 721		
RESULT	8		
LOCUS	R77881 484 bp mRNA EST 07-JUN-1995		
DEFINITION	Y177h05.r1 Homo sapiens cDNA clone 145305 5' similar to SP:BLR1_HUMAN P32302 BURKITT'S LYMPHOMA RECEPTOR ;.		
ACCESSION	R77881		
NID	9852991		

KEYWORDS	EST.
SOURCE	human clone=145305 library=Soares placenta Nb2HP vector-pt7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RPI Rsite1=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGAGAAGATTGCGCGCCGACGAGAAATTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bernaldo.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 484) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE	The Washu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK Washu-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 251 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Location/Qualifiers 1. 484 /organism="Homo sapiens" /clone="145305"
BASE COUNT	107 a 117 c 111 g 147 t 2 others
ORIGIN	
Query Match	3.4%; Score 34; DB 10; Length 484;
Best Local Similarity	79.3%; Pred. No. 5.34e-21;
Matches	46; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Db	250 GAGTGGCCGTGGTGGTGGCTGCTCTTCTTGTGCTGAGACTCCATACACATTT 307 QY 664 GACTGGTCCGTGGTGGTGGCAGTCTTCGTGCTGCTGCTGGACTCCATTCACATATT 721
RESULT	9
LOCUS	W79255 442 bp mRNA EST 17-OCT-1996
DEFINITION	zd75cc02.r1 Soares fetal heart Nb2HP Homo sapiens cDNA clone 346466 5' similar to gb:X12597 HIGH MOBILITY GROUP PROTEIN HMGI (HUMAN); contains element 11 repetitive element ;.
ACCESSION	W79255
NID	g1390386
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS	1 (bases 1 to 442) Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
TITLE	The Washu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	

FEATURES	source	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 580 Std Error: 0.00 Seq primer: mob.REGA-ET.
	Location/Qualifiers	
	1..442	
	/organism="Homo sapiens"	
	/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5 TGTTACCAATCTGAGTGGAGCGCGCCATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."	
	/db_xref="taxon:9606"	
	/clone="346466"	
	/clone_lib="Soares fetal heart NbHL19W"	
	/sex="unknown"	
	/dev_stage="19 weeks"	
	/lab_host="DH10B (ampicillin resistant)"	
	<1..>442	
BASE COUNT	148 a 55 c 111 g 126 t 2 others	
ORIGIN	mrna	
	Query Match 3.1%; Score 31; DB 15; Length 442; Best Local Similarity 68.3%; Pred. No. 3.26e-16; Matches 56; Conservative 0; Mismatches 26; Indels 0; Gaps 0;	
Db	55 AGGAAGATGAGGAAGATGAAGAGATGANGAGAGAGAGATGAAGATGAAGATG 114 Cp 595 AGGATCATCAGGGGTGTAGCAGACAGATGATGATGAGAGACAGGATCAGCAAGCAAGATG 536 Db 115 AAGAAGAAGATGATGATGATGA 136 Cp 535 AAGACGCAGATCTTCATGAAGA 514	
RESULT	10	
LOCUS	G28514 1664 bp DNA STS 01-JUL-1995	
DEFINITION	human STS SHGC-31461.	
ACCESSION	G28514	
NID	g1408329	
KEYWORDS	STS; STS sequence; primer; sequence tagged site.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1664) Myers,R.M. Unpublished (1996)	
AUTHORS	Contact: Richard M. Myers	
JOURNAL	Stanford Human Genome Center (SHGC) Stanford University School of Medicine Department of Genetics, M-344, Stanford, CA 94305, USA Tel: 4157259687 Fax: 4157259689 Email: myers@shgc.stanford.edu	
COMMENT	Primer A: TTGTACAGTTTATTCCTGTGTG Primer B: CGTGATTAACCTACACGCTCTGTG	


```

STS size: 207
PCR Profile:
  Initial incubation: 94 degrees C for 90 seconds
  Denaturation: 94 degrees C for 15 seconds
  Annealing: 62 degrees C for 23 seconds
  Polymerization: 72 degrees C for 30 seconds
  PCR Cycles: 30
  Thermal Cycler: Perkin Elmer 9600

Protocol:
  Template: 25 ng
  Primer: each 1 uM
  dNTPs: each 200 uM
  Taq Polymerase: 0.05 units/uL
  Total Vol: 10 uL

Buffer:
  MgCl2: 2.5 mM
  KCl: 50 mM
  Tris-HCl: 20 mM
  pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from D10924
-- Washington University/Merck EST sequence.
  Location/Qualifiers
    1. .1664
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /map="2"
1220. .1426
1220. .1244
complement(1405. .1426)
414 a 398 c 359 g 493 t

```

Query Match	3.1%;	Score 31;	DB 20;	Length 1664;
Best Local Similarity	62.8%;	Pred. No. 3.26e-16;		
Matches	76;	Conservative	0;	Mismatches 45; Indels 0; Gaps 0;
Db 379	CTGTACTTTGGGAAGCTTCTATGCAAGGACAGTCCATGTCATCTACACAGTCAACCTCTA	438		
QY 212	CTGGCCCTTTGGGAGTGTCTGTGCAAGATAGTAAATTTTCATTGATTACTACACATGTT	271		
Db 439	CAGCAGTGTCCCTCAATCCCTGGCCTTCATCAGTCTGACCGCTAACCTGGCCATCGTCCACGC	498		
QY 272	CACACGATCTTCACTCACCCTTGACCATGATGAGCGGTGACCGCCATACATTGCCGTGTGCCACCC	331		
Db 499	C 499			
QY 332	C 332			

LOCUS	11	AA327933	304 bp	mRNA	EST	20-APR-1997
DEFINITION		EST31339	Embryo, 12 week I	Homo sapiens	cdna 5'	end similar to
ACCESSION		AA327933				similar to high mobility group protein 1, placenta.
NID		g1980177				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				
REFERENCE		1 (bases 1 to 304)				
AUTHORS		Adams,M.D., Kellavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Ene,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,				

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudex, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melsner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

TITLE
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL
Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE
96026280

Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi.html>)
 Seq primer: M13 Reverse.
 Location/Qualifiers
 1..304

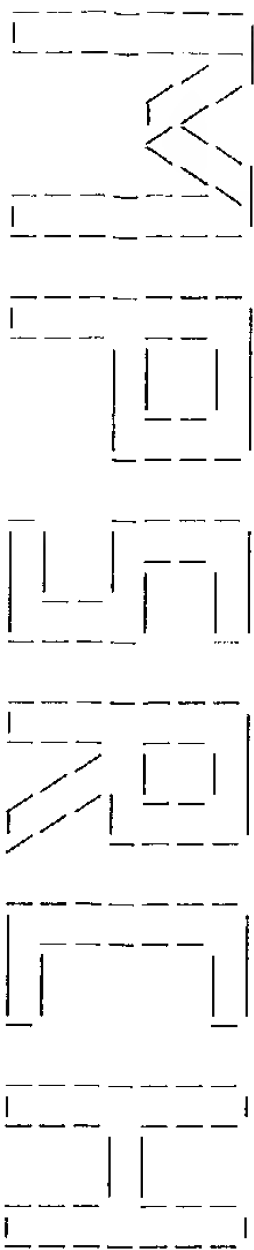
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      |||| | ||| | | ||| |||| | | |||| | ||| |||| | |||| |
Cp     595 AGGATCATCAGGGGTTCACAGACAGCATGATGATGATGAGGACAGGGATCACGAAGCAAAAGATG 536
      |||| | |||| | |||| | |||| | |||| | |||| | |||| |
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Cp      53 AAGACGACAGATCTTCATGAAGA 514
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RESULT	12
LOCUS	R81133 320 bp mRNA EST 12-JUN-1995
DEFINITION	y91h09.r1 Homo sapiens cDNA clone 146657 5' similar to gb:X12597
	HIGH MOBILITY GROUP PROTEIN HMGI (HUMAN); contains THR repetitive
	element ; .
ACCESSION	R81133
NID	g857736
KEYWORDS	EST.
SOURCE	human clone=146657 library=Soares placenta Nb2HP vector=pt7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGGCGCCGACAGAATTTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. .
ORGANISM	Homo sapiens
	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;

REFERENCE 1 (bases 1 to 320)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Woldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
High quality sequence stops: 275
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
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/clone="146657"
BASE COUNT 114 a 44 c 82 g 73 t 7 others
ORIGIN
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Best Local Similarity 68.3%; Pred. No. 1.14e-14;
Matches 56; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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Cp 595 AGGATCATCAGGGGTGTAGCAGACGATGATGATGAGACAGACGATCATCAAGCAAGATG 536
Db 191 AAGAAGAAGATGATGATGATGA 212
Cp 535 AAGACGCAGATCTTCATGAAGA 514
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LOCUS AA330028 351 bp mRNA EST 21-APR-1997
DEFINITION EST33738 Embryo, 12 week II Homo sapiens cDNA 5' end similar to
ACCESSION AA330028
NID g1982303
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 351)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult,C.J., Iee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligri,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)
MEDLINE 96026280
COMMENT Contact: Kerlavage, AR
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavet@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
FEATURES
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ORIGIN
Query Match 3.0%; Score 30; DB 18; Length 351;
Best Local Similarity 68.3%; Pred. No. 1.14e-14;
Matches 56; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
Db 179 AGGAAGATGAGGAAGATGAAGAGATGAGAGAGAGAGAGATGAAGATGAAGATG 238
Cp 595 AGGATCATCAGGGGTGTAGCAGACGATGATGATGAGACAGACGATCATCAAGCAAGATG 536
Db 239 AAGAAGAAGATGATGATGATGA 260
Cp 535 AAGACGCAGATCTTCATGAAGA 514
RESULT 14
LOCUS HSPD07459 363 bp DNA EST 30-APR-1997
DEFINITION H.sapiens EST sequence (095-X1-20) from skeletal muscle.
ACCESSION F22618
NID g2061794
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
REFERENCE 1 (bases 1 to 363)
AUTHORS Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
TITLE Identification of 4,370 expressed sequence tags (ESTs) from a 3'-end specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridisation
REFERENCE 2 (bases 1 to 363)
AUTHORS Valle,G.
JOURNAL Direct Submission
TITLE Submitted (29-APR-1997) CRIBI Biotechnology Centre, University of Padua, Via U. Bassi 58/B, 35121 Padua, Italy
JOURNAL ABI Chromatograms and other information are available on WWW at <http://eos.bio.unipd.it>
COMMENT Vector: pCDNAII (Invitrogen)
V_type: Plasmid
RE_1: BstXI
RE_2: NotI
PRIMER: PC2R
DESCR: The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer



Release 3.0.4A John F. Collins, Biocomputing Research Unit.
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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 16 13:40:06 1998; MasPar time 8.55 seconds
Tabular output not generated. 479.455 Million cell updates/sec

Title: >US-08-292-694A-12
Description: (1-295) from US08292694A.pep
Perfect Score: 2229
Sequence: 1 YTKMKTATNIIYFNALADA.....NTVQDPAYLREIDGMNKPV 295

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseg30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 33.578; Variance 148.821; scale 0.226

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	2223	99.7	295	12	R67672 Human kappa opioid re	4.45e-199
2	2192	98.3	380	17	R88722 Human kappa opioid re	4.42e-196
3	2136	95.8	380	12	R67669 Mouse kappa opioid re	1.15e-190
4	2132	95.6	380	13	R72591 Mammalian kappa opioi	2.79e-190
5	2132	95.6	380	13	R76783 Rat kappa opiate rece	2.79e-190
6	1522	68.3	356	11	R65188 Murine mu-subtype opi	1.81e-131
7	1522	68.3	398	13	R76781 Rat mu opiate recepto	1.81e-131
8	1522	68.3	400	13	R71964 Human mu opioid recep	1.81e-131
9	1520	68.2	398	13	R71964 Rat mu opioid recep	2.82e-131
10	1520	68.2	400	13	R76780 Human mu opiate recep	2.82e-131
11	1452	65.1	372	13	R76782 Rat delta opiate rece	9.62e-125
12	1448	65.0	372	9	R48629 Sequence of murine de	2.33e-124
13	1448	65.0	372	12	R67670 Mouse delta opioid re	2.33e-124
14	1348	60.5	371	10	R66503 Murine delta opioid r	9.17e-115
15	1345	60.3	367	13	R71968 Rat opioid receptor.	1.78e-114
16	1343	59.9	367	12	R67671 Mouse opioid receptor	2.77e-114
17	1336	47.8	367	13	R76638 Rat opiorh receptor	1.30e-113
18	1066	47.8	367	13	R74298 Mouse kappa-3 opioid	8.46e-88
19	830	37.2	391	7	R39259 Human somatostatin re	2.19e-65
20	830	37.2	391	7	R39260 Murine somatostatin r	2.19e-65

21	785	35.2	369	7	R39262 Murine somatostatin r	3.91e-61
22	780	35.0	369	7	R39261 Human somatostatin re	1.16e-60
23	780	35.0	369	18	R97269 Human somatostati	1.16e-60
24	767	34.4	369	5	R27504 Pituitary somatostati	1.95e-59
25	736	33.0	333	13	R72985 Epsilon opioid recept	1.62e-56
26	727	32.6	322	15	R48754 Rat RGH G-protein cou	1.14e-55
27	727	32.6	322	19	W02726 Rat RGH G-protein c	1.14e-55
28	683	30.6	418	7	R39263 Human somatostatin re	1.56e-51
29	661	29.7	328	13	R72984 Epsilon opioid recept	1.80e-49
30	658	29.5	242	22	W10017 G-protein coupled rec	3.43e-49
31	599	26.9	428	7	R39264 Murine somatostatin r	1.12e-43
32	586	26.3	241	22	W10016 G-protein coupled rec	1.83e-42
33	545	24.5	349	14	R79443 Galanin receptor.	1.19e-38
34	545	24.5	349	17	R95070 Human galanin recepto	1.19e-38
35	518	23.2	348	17	R91229 Mouse pancreas G-prot	3.77e-36
36	518	23.2	348	17	R95069 Mouse pancreas beta-c	3.77e-36
37	510	22.9	402	17	R98358 Somatostatin-like rec	2.07e-35
38	496	22.3	355	10	R52749 C-C chemokine recepto	4.07e-34
39	496	22.3	355	23	W25751 Human MIP-1alpha/RANT	4.07e-34
40	490	22.0	363	12	R66934 Mouse AT2 receptor.	1.45e-33
41	471	21.1	355	18	W03376 CC-chemokine receptor	8.18e-32
42	471	21.1	355	22	W10100 Human C-C chemokine r	8.18e-32
43	467	21.0	325	15	R48730 G-protein coupled boy	1.91e-31
44	468	21.0	355	23	W27124 Human chemokine recep	1.54e-31
45	468	21.0	355	18	W03377 CC-chemokine receptor	1.54e-31

ALIGNMENTS

RESULT 1
ID R67672 standard; Protein; 295 AA.
AC R67672;
DT 18-AUG-1995 (first entry)
DE Human kappa opioid receptor partial protein.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeric; assay; probe.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Misc_difference 169
FT /label= Any amino acid
FT Misc_difference 181
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FT Misc_difference 265
FT /label= Any amino acid
FT Misc_difference 269
FT /label= Any amino acid
FN W09428132-A.
PD 08-DEC-1994.
PE 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR N-PSDB; Q75931.
PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 12; Page 236-239; 300pp; English.
CC The partial amino acid sequence of the novel human kappa opioid receptor.
CC The corresponding gene was isolated from a human brain hippocampus cDNA
CC library using a probe from the mouse kappa opioid receptor gene (Q75926).
CC The gene is missing the N-terminal sequence. The C-terminal sequence is
CC very similar to the mouse kappa opioid receptor sequence. Of the
CC C-terminal 293 amino acids, 281 residues are identical and 6 residues
CC have conservative substitutions. The gene encoding the human opioid
CC receptor can be placed in a suitable expression vector for production of
CC the protein in a cell. The opioid receptors thus produced are useful for
CC the development of novel assays designed to select or improve substances,
CC capable of interacting with the opioid receptor proteins, for use in
CC diagnosis, drug design and therapeutic applications.

SQ	Sequence	295 AA;						
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QY	1	YTKMKTATNIYIFNLALADALVTTT	MPFQSTVYLNMSWPGDYLCKIVISIDY	YNNFTSI	60			
Db	61	ftltmsvdryiavchp	vkaldfrt	plkakini	ciwlssvgisaivlg	tkvregvd	120	
QY	61	FTLTMSVDRIYAVCHP	VKALDERTPLKAKIINICWLSSVGISAIVLG	TKVREDVD	120			
Db	121	viecclqfpddysw	dlfmkicvfifafv	ipvllivcytlmlrlk	xvrllsgsrek	180		
QY	121	VIECCLOFPDDYSW	WDLFMKICVFIFAFVIPVLLI	VCYTLMLRLKXVRL	SGSREKD	180		
Db	181	xnlrritrlv	lvvavfvvcwtp	pihifilveal	gstshstaalssy	fcialgytnssln	240	
QY	181	XNLRITRLVLVVAVFVVCWTP	PIHIFILVEALGSTSHSTAALSSYFCIALGYT	NSSLN	240			
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ID	R88722	standard;	Protein;	380	AA.			
AC	R88722;							
DT	04-SEP-1996	(first entry)						
DE	Human	kappa opioid receptor.						
KW	Human;	kappa opioid receptor; psychiatric disorder; cardiovascular; neurology; diagnosis.						
KM	Homo sapiens.							
OS	WO9601898-A1.							
PD	25-JAN-1996.							
PF	07-JUL-1995;	F00912.						
PR	11-JUL-1994;	FR-008531.						
PA	(UYST-) UNIV PASTEUR STRASBOURG LOUIS.							
PI	Kieffer B, Simonin F;							
DR	WPI; 96-097628/10.							
DR	N-PSDB; T12550.							
PT	New nucleic acid encoding the human Kappa opioid receptor - useful in diagnosis and therapy, and for isolating receptor ligands and							
PT	modulators							
PS	Claim 7; Page 13-15; 30pp; French.							
CC	The sequence coding for the human kappa opioid receptor was							
CC	obtained from two overlapping cDNA fragments isolated from a							
CC	human placental cDNA library. The fragments were amplified from							
CC	the library using PCR primers based on the sequence of human							
CC	genomic clones which hybridised with a murine delta receptor cDNA							
CC	probe. Nucleotide probes derived from the kappa opioid receptor							
CC	coding sequence are useful for diagnosis of neurological, cardio-							
CC	vascular and psychiatric disorders associated with opioid							
CC	receptors. The receptor can be used for identifying e.g. agonists							
CC	of its activity for potential use as analgesics.							
SQ	Sequence	380	AA;					
	Query Match	98.3%;	Score 2192;	DB 17;	Length 380;			
	Best Local Similarity	97.6%;	Pred. No. 4.42e-196;					
	Matches	288;	Conservative	1;	Mismatches 5; Indels 1; Gaps 1;			
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QY	1	YTKMKTATNIYIFNLALADALVTTT	MPFQSTVYLNMSWPGDYLCKIVISIDY	YNNFTSI	60			
Db	147	ftltmsvdryiavchp	vkaldfrt	plkakini	ciwlssvgisaivlg	tkvredvd	206	
QY	61	FTLTMSVDRIYAVCHP	VKALDERTPLKAKIINICWLSSVGISAIVLG	TKVREDVD	120			
Db	207	viacsllqfpddysw	dlfmkicvfifafv	ipvllivcytlmlrlk	svrllsgsrek	266		
QY	207	VIACSLQFPDDYSW	DLFMKICVFIFAFVIPVLLI	VCYTLMLRLKSVRL	SGSREK	266		

QY	121	VIECCLQFPDDISW	WDLFMKICVFIFAFVIPVLLI	VCYTLMLRLKXVRL	SGSREKD	180	
Db	267	nrlrritrlv	lvvavfvvcwtp	pihifilveal	gstshstaalssy	fcialgytnssln	326
QY	181	XNLRITRLVLVVAVFVVCWTP	PIHIFILVEALGSTSHSTAALSSYFCIALGYT	NSSLN	240		
Db	327	pilyaflden	fkrcfrdfc	plkmmxerxstsr	vrntvgdpayl	reidgm-nkpv	380
QY	241	PILYAFLDENFKRCFRDFCPLKMMXERXSTSRVRNTVQDPAYLREIDGM	NKPV	295			
RESULT	3						
ID	R67669	standard; Protein; 380	AA.				
AC	R67669;						
DT	17-AUG-1995	(first entry)					
DE	Mouse kappa opioid receptor MOR1.						
KW	Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;						
KM	transmembrane domain; somatostatin; receptor; human; expression vector;						
KW	truncate; chimeric; assay; probe.						
OS	Mus musculus.						
PN	WO9428132-A.						
PD	08-DEC-1994.						
PF	20-MAY-1994; U05747.						
PR	20-MAY-1993; US-066296.						
PR	30-JUL-1993; US-100694.						
PR	05-NOV-1993; US-147592.						
PA	(ARCH-) ARCH DEV CORP.						
PI	Bell GI, Reisine T, Yasuda K;						
DR	WPI; 95-022804/03.						
DR	N-PSDB; Q75926.						
PT	Polynucleotides and peptides derived from opioid receptor						
PT	polypeptides - for use in therapeutic compositions and in						
PT	screening assays for useful drug substances.						
PS	Claim 8; Page 207-211; 300pp; English.						
CC	The amino acid sequence of the novel mouse kappa opioid receptor MOR1.						
CC	The corresponding gene was isolated from a mouse brain cDNA library using						
CC	a fragment (amplified from the cDNA library with primers Q75929-30) as a						
CC	probe. The primers are based on the conserved sequences present in the						
CC	second and third transmembrane domains of somatostatin (SRIF) receptor						
CC	subtypes SST1, SST2 and SST3. The 1.2 kb PstI fragment from the mouse						
CC	kappa opioid receptor clone, lambda ms1-1, was subcloned into the CMV						
CC	promoter-based expression vector pCMV-6b. The resultant construct						
CC	pCMV-ms1-1 was transfected into COS-1 cells for protein production. The						
CC	gene encoding the opioid receptor can be used to produce complete, the						
CC	truncated or chimeric opioid receptor proteins. The opioid receptors						
CC	thus produced are useful for the development of novel assays designed to						
CC	select or improve substances, capable of interacting with the opioid						
CC	receptor proteins, for use in diagnosis, drug design and therapeutic						
CC	applications.						
SQ	Sequence	380	AA;				
Query Match	95.8%; Score 2136; DB 12; Length 380;						
Best Local Similarity	92.9%; Pred. No. 1.15e-190;						
Matches	274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;						
Db	87	ytkmktatniyifnlaladalvt	ltmpfgsavylnmswpgdv	lckivisidyymftsi	146		
QY	1	YTKMKTATNIYIFNLALADALVTT	MPFQSTVYLNMSWPGDYLCKIVISIDY	YNNFTSI	60		
Db	147	ftltmsvdryiavchp	vkaldfrt	plkakini	ciwlssvgisaivlg	tkvredvd	206
QY	61	FTLTMSVDRIYAVCHP	VKALDERTPLKAKIINICWLSSVGISAIVLG	TKVREDVD	120		
Db	207	viacsllqfpddysw	dlfmkicvfafavip	lvllivcytlmlrlk	svrllsgsrek	266	
QY	121	VIECCLQFPDDISW	WDLFMKICVFIFAFVIPVLLI	VCYTLMLRLKXVRL	SGSREKD	180	
Db	267	nrlrritrlv	lvvavfvvcwtp	pihifilveal	gstshstaalssy	fcialgytnssln	326
QY	181	XNLRITRLVLVVAVFVVCWTP	PIHIFILVEALGSTSHSTAALSSYFCIALGYT	NSSLN	240		
Db	327	pilyaflden	fkrcfrdfc	plkmmxerxstsr	vrntvgdpasmr	dvngm-nkpv	380
QY	327	PILYAFLDENFKRCFRDFCPLKMMXERXSTSRVRNTVQDPASMR	DVNGM	NKPV	380		


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QY      241 PILYAFLDENKRCFRDCEPFLKMMERXSTSRVNTVQDPAYLREIDGMNKPV 295
RESULT      4
ID      R72591 standard; Protein; 380 AA.
AC      R72591;
DE      01-DEC-1995 (first entry)
KW      Mammalian kappa opioid receptor protein.
KW      Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;
OS      amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
FH      Rattus rattus.
FT      Key      Location/Qualifiers
FT      CDS      111..1253
FT      /tag= a
FT      /product= kappa opioid receptor
FT      /product= kappa opioid receptor
PN      J07070191-A.
PD      14-MAR-1995.
PF      30-JUL-1993; 190261.
PR      09-JUL-1993; JP-170591.
PA      (TAKE ) TAKEDA CHEM IND LTD.
DR      WPI; 95-144857/19.
DR      N-PSDB; Q86725.
PI      Kappa opioid receptor protein and cells expressing it - useful
PI      for the screening of compounds for analgesic and hypnotic
PI      properties
PS      Claim 2; Page 9-10; 15pp; Japanese.
CC      The amino acid sequence of the novel mammalian kappa opioid receptor.
CC      The gene was isolated by amplifying a fragment from rat brain mRNA by
CC      reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
CC      the mouse delta-opioid receptor gene. This fragment was cloned into the
CC      plasmid pCRIT to produce pRI1. The plasmid pRI1 was used to probe a rat
CC      brain DNA library in lambda ZAP11 to obtain a clone of the rat kappa
CC      opioid receptor gene, designated pKOPR2. This clone was introduced into
CC      E.coli JM109 for production of the receptor protein. The receptor protein
CC      is useful for screening of analgesic and hypnotic compounds including
CC      peptides and proteins.
SQ      Sequence 380 AA;

Query Match      95.6%; Score 2132; DB 13; Length 380;
Best Local Similarity 92.5%; Pred. No. 2.79e-190;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db      87 ytkmktatniyifnlaladalvtttmpfgsavylnmswpfgdvickivisidyymftsi 146
QY      1 YTKMKTATNIYIFNLALADALVTTTMPFGSVIYIMNSWPFGDVLCIKIVISIDYNNMFTSI 60
Db      147 ftltmmsvdryiaavchpvcaldfrtbpkakiniciwllassvgisaivlggtkvredvd 206
QY      61 FTLTMMSVDRYIAVCHPVCALDFRTPLKAKINICIWLLSSSVGISAIVLGGTKVREDVD 120
Db      207 viecslqfpddeswldfmkicvfafvfpvllivcytlmllrksvrlisgsrekd 266
QY      121 VIECCLQFPDDDYSWWDLFMKICVFIFAFVFPVLLIIVCYTILMLRLKXVRLISGSREKD 180
Db      267 nllrritklivlvavfliowtphihflvealgstshstavlssyfcialgytnssln 326
QY      181 XNLRIRITRLVLVAVFVVCWTPIHIFILVEALGSTSHSTALSSYFCIALGYTNSSLN 240
Db      327 pvllyafldenfkrcfrdfcfpikmmergstnrvrntvgdpasmrdivgm-nkpv 380
QY      241 PILYAFLDENKRCFRDCEPFLKMMERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT      5
ID      R76783 standard; Protein; 380 AA.
AC      R76783;
DE      11-DEC-1995 (first entry)
DE      Rat kappa opiate receptor.
KW      Kappa opiate receptor; mu opiate receptor; hMOR; opiate agonist;
KW      opiate antagonist; drug abuse; analgesic.
OS      Rattus sp.
PN      W09520667-A1.
PD      03-AUG-1995.
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PF      30-JAN-1995; U01144.
PR      28-JAN-1994; US-188275.
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA      (USSH ) US SEC DEPT HEALTH.
PI      Johnson PS, Persico AM, Uhl G, Wang J;
DR      WPI; 95-275452/36.
PT      New DNA encoding human mu opiate receptor - used esp. for screening
PT      cpds. for activity as opiate agonists or antagonists
PS      Disclosure; Page 29-30; 49pp; English.
CC      hMOR cDNA was obtd. from a human cerebral cortical cDNA library
CC      screened with fragments of a rat mu opiate receptor. The encoded
CC      protein showed homology to rat mu, delta and kappa opiate
CC      receptors (R76781-83).
SQ      Sequence 380 AA;

Query Match      95.6%; Score 2132; DB 13; Length 380;
Best Local Similarity 92.5%; Pred. No. 2.79e-190;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db      87 ytkmktatniyifnlaladalvtttmpfgsavylnmswpfgdvickivisidyymftsi 146
QY      1 YTKMKTATNIYIFNLALADALVTTTMPFGSVIYIMNSWPFGDVLCIKIVISIDYNNMFTSI 60
Db      147 ftltmmsvdryiaavchpvcaldfrtbpkakiniciwllassvgisaivlggtkvredvd 206
QY      61 FTLTMMSVDRYIAVCHPVCALDFRTPLKAKINICIWLLSSSVGISAIVLGGTKVREDVD 120
Db      207 viecslqfpddeswldfmkicvfafvfpvllivcytlmllrksvrlisgsrekd 266
QY      121 VIECCLQFPDDDYSWWDLFMKICVFIFAFVFPVLLIIVCYTILMLRLKXVRLISGSREKD 180
Db      267 nllrritklivlvavfliowtphihflvealgstshstavlssyfcialgytnssln 326
QY      181 XNLRIRITRLVLVAVFVVCWTPIHIFILVEALGSTSHSTALSSYFCIALGYTNSSLN 240
Db      327 pvllyafldenfkrcfrdfcfpikmmergstnrvrntvgdpasmrdivgm-nkpv 380
QY      241 PILYAFLDENKRCFRDCEPFLKMMERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT      6
ID      R65188 standard; Protein; 356 AA.
AC      R65188;
DE      19-APR-1995 (first entry)
DE      Murine mu-subtype opioid receptor.
KW      Mu-subtype opioid receptor; MSOR; drug addiction.
OS      Rattus rattus.
FH      Key      Location/Qualifiers
FT      Modified_site 10..12
FT      /note= "putative N-linked glycosylation site"
FT      Modified_site 230
FT      /note= "Threonine residue especially favourable
FT      for protein kinase A phosphorylation"
FT      Region 25..48
FT      /note= "hydrophobic membrane spanning region"
FT      Region 58..78
FT      /note= "hydrophobic membrane spanning region"
FT      Region 96..118
FT      /note= "hydrophobic membrane spanning region"
FT      Region 139..166
FT      /note= "hydrophobic membrane spanning region"
FT      Region 187..212
FT      /note= "hydrophobic membrane spanning region"
FT      Region 236..257
FT      /note= "hydrophobic membrane spanning region"
FT      Region 274..294
FT      /note= "hydrophobic membrane spanning region"
PN      EP-612845-A.
PD      09-FEB-1994; 101968.
PR      26-FEB-1993; US-026140.
PA      (AMCY ) AMERICAN CYANAMID CO.
PI      Corbett MJ, Eppler CM, Shieh H, Zysk JR;
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DR WPI; 94-265963/33.
DR N-PSDB; Q79199.
PT Pure mu-type opioid receptor protein - and nucleic acid coding
PT for it
PS Claim 2; Fig 9; 39pp; English.
CC R65188 is the rat mu-subtype opioid receptor protein purified
CC from rat brain membranes, with biotinyl-b-endorphin (R5666)
CC as its ligand. It is encoded by the nucleotide sequence Q79199
CC which was synthesised using Q71022 and Q71023 as PCR primers.
CC R65188 is useful for identifying other receptor subtypes, for
CC screening new opioid ligands, and for studying mechanisms of
CC opioid action, e.g. drug addiction.
SQ Sequence 356 AA;

Query Match	68.38;	Score 1522;	DB 11;	Length 356;
Best Local Similarity	66.18;	Pred. No. 1.81e-131;		
Matches 191;	Conservative 45;	Mismatches 49;	Indels 4;	Gaps 4;

D6 54 yckmktatniyifnlaladalatsclpfqsvnylmgtwfpfctllckivisisdyymftsi 113
| | | | | | | | | | : : | | | | : | | | | | | | | | |
QY 1 YTKMKRATNIYIFNLALADALVTPMPFQSTVYLMSWPFQGVLCIKIVISIDYYNMFTSI 60

```
Dd      114 ftlctmsvdryiaavchpvkaldftprnakivncwmlssaiglpvmfmatkkyrg-s 172
        ||| ||||| ||||| ||||| :|||:| |:|||:|::: :|||:
Qy      61 fTlPMMSVDRYIAVCHPVKALDFRFLAKAIINICIMWLSSSVGISAIVLGSTKRVREVD 120
```

```

D6 173 -idcltftshptw-ywenllkicvfifafimpvllitvcyglmllrksvmlsgsked 230
    | : | | : | : | | | | | | | | | | | | | | | | | | | | | | | |
QY 121 VIECCLQEPDDDYSWMDLFMKICVFTEAFVLPVLIIVCYTLMILRLKXVRLSGSREND 180

```

Db 231 mrnrllmvlvavafivcwtpihyikalitipettfgtvswhfialgytscln 2900
 |||||:|||||:|||||::: ||::: || ||||| ||
 QY 181 xnlrrlplvllvavfvcwcpqlhffllvealgstshstlaalssyfcialglttssln 2400

```
D8 291 pvljafldentkrcfrefcipcrlstsllegqnstrvrgntrephstantvd 3339
QY 241 PILYAFLEDNFKRCRDFCFPLKMMXMRSTSRVR-NTVQDPALUREID 288
```

RESULT	7
ID	R76781 standard; Protein; 398 AA.

DT 11-DEC-1995 (first entry)
DE Rat mu opiate receptor.
KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
KW drug abuse; analgesic.

OS	Rattus sp.
PN	W09520667-A1.

PD 03-AUG-1995.
PF 30-JAN-1995; U01144.

PR 28-JAN-1994; US-188275.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA (USSH) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;

PT	New DNA encoding human mu opiate receptor - used esp. for screening
DR	WPI; 95-275452/36.

PI cpsds for activity as opiate agonists or antagonists
PS Disclosure; Page 26-28; 49pp; English.

CC screened with fragments of a rat mu opiate receptor. The encoded

CC protein showed homology to rat mu, delta and kappa opiate
CC receptors (R76781-83).

50 Sequence 398 AA;

Query Match	68.3%;	Score 1522;	DB 13;	Length 398;
Best Local Similarity	66.1%;	Pred. No. 1.81e-131;		
Matches 191;	Conservative 45;	Mismatches 49;	Indels 4;	Gaps 4;

Dd 96 ytkmktatniyifnladalastlplfqsvnylmgtwfpqtilckivisidqymftsi 155
||||| :||| :||| :||| :|||
Qy 1 YTKMKTATNIYIFNLADALVITLTPFQSTVYLMSNPEGDVLCKIVISIDYYNNFTSI 60

Db 156 ftlctmsvdryiavchpvkaldftrprnakivvnwnilssaiglpvmfmattkyrg-s 214

QY	61	FTLTMSVBYIAVCHPKALDFRPLKAKIINICIWLTSSSGISAIVLGGTKRBDVD	120
Db	215	-idctltfshptw-ywenllkicvifafimpvlliltvcyglmllrlksvrmlsskcd	272
QY	121	VIECCIOFEDDDYSWMDLFMKICVFIFAFVIVPVLIIIVCYIIMILRLKXVRLLSGSRKED	180
Db	273	nrlrlrtmvlvavavfivcwtbplhlylalkalitipetltfqvshfcialgythscln	332
QY	181	XNLRRIIRLVLVYAVFVVCWPIPIHFIILVEALGSTSHSTALSSYFCIALGYTNSSLN	240
Db	333	pvllyafldcnfkrcfrefcipcststieqgnstrvrqntbrehstantvd	381
QY	241	PILYATLDEMFKRCFRDFCFPLKXMKMERKXSTSRVR-NIVQDPAVYLREID	288

RESULT	8
ID	R71966 standard; Protein; 400 AA.

DT 20-OCT-1995 (first entry)
DE Human mu opioid receptor.
KW Mu opioid receptor; MOR; gene therapy; diagnostic.

OS Homo sapiens.
PN W09507983-A.
PD 23-MAR-1995.

PF 13-SEP-1994; U10358.
PR 13-SEP-1993; US-120601.

PA (INDV) UNIV INDIANA FOUND.
PI YU L;

DR WPI; 95-131351/17.
DR N-PSDB; Q89226.

PT New nucleic acid encoding new human mu opioid receptor - and related vectors, transformed cells, antibodies etc., useful in

PT	diagnosis, treatment and drug screening.
PS	Claim 4; Page 211-214; 266pp; English.

cc A cDNA library constructed from human caudate nucleus mRNA was
cc screened with rat mu opioid receptor cDNA under conditions of

low stringency. One positive clone included the sequence given in Q89226, encoding a mu opiod receptor MOR (R/71964). The cdna

CC is used for prodn. of recombinant MOR, in gene therapy, etc.
SQ Sequence 400 AA;

Query Match	68.3%;	Score 1522;	DB 13;	Length 400;
Best Local Similarity	67.1%;	Pred. No. 1.81e-131;		
Matches 188;	Conservative 43;	Mismatches 46;	Indels 3;	Gaps 3;

```
Db      98 ytkmktatniyifnladalatalstlpfgsvnylmgtwpfqtilckivisidqynmfts i 157
        |||||
QY      1 YTKMKIATNIYIFNLALADALVTTTTPFQSTVIYLMNSWPGDVLCCKIVISIDYYNMF TSI 60
```

```
Db 158 ftlctmsvdrylavchpvpkala6ftprnakiiinvcnwllssaiglpvmfmatkxyrg-s 215
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 FTLTMSVDRYIAVCHPVPKALDFRPLKAKIINICIMWLSSSVGISAIVLGGTKYRQEDVD 120
```

Dd 217 -idcrltfsnptw-ywenllkicvifafimpvlitvcyglmllrklsvmlsgsked 274
| : | | : | : : | | | | | : | | | | | | | | | : | | | | |
Qy 121 VIECCIQEPDDDEYSWMDLFMKICVFIFAFAVLPVLIIIVCYLIMILRLKXVRLLSSGREKD 180

```
Db 275 nrlrriatmvlvavavifvewcpihiylikaltvitpeltfqtswhfciagytnscln 334
    |||||:|||||:|||||::: || : : : | ||||| ||
QY 181 xnlrritrlvllvavfvewcpihiflllvealgstshstlaalssyyfcialgttnssln 240
```

Db 335 pvl yafldenfkr cfr efcip tsnie qnstrir qntr d 374

241 PIIYAFIDENFKRCFRCFPLKMMERASTSRVANTVÖD 2800

ID	R71964 standard; Protein; 398 AA.
AC	R71964;
DT	20-OCT-1995 (first entry)

KW Mu opioid receptor; MOR-1; gene therapy; diagnostic.

OS Rattus sp.
PN W09507983-A.
PD 23-MAR-1995.
PF 13-SEP-1994; U10358.
PR 13-SEP-1993; US-120501.
PA (INDV) UNIV INDIANA FOUND.
PI Ya L,
DR WPI; 95-131351/17.
PT N-PSDB; Q89222.
PT New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.
PS Disclosure; Page 190-194; 266pp; English.
PC A 365 bp fragment of the mouse delta opioid receptor was used to
CC screen a rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in Q89222, encoding a
CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in
CC transfected CHO cells.
SQ sequence 398 AA;

Query Match	58.2%;	Score 1520;	DB 13;	Length 398;
Best Local Similarity	65.7%;	Pred. No. 2.82e-131;		
Matches 190;	Conservative 46;	Mismatches 49;	Indels 4;	Gaps 4;

```
Db      96 ytkmktatnuyifnaladalatalstipfgsvnylmgtwpfctickivisisdyymftsi    155
        ||||| ||||| ||||| : : ||| | | : ||| ||||| ||||| |||||
QY      1 YTKMKIATNUIYIFNLALADALTITMPFQSTVYIMNSWPFGBVLCKIVISIDYYNMFTSI    60
Ddb     156 ftltcmvadyiaavchpykaldfrtprnakivncwmlssalglyvmfmattkkyrg-s    214
        ||| ||||| ||||| ||||| : ||| : | : ||| : : : || :
QY      61 FTLTMSVDXYIAVCHPYKALDFRTPRLAKIINICIMWLSSSGISAIVLGGTKVREYD    120
Db      215 -idcrlfshptw-ywenllkicvfafimpillitvcyglmllrksvrmlsgsked    272
        ||| | | : : : ||||| ||||| : ||| ||||| ||||| |||
QY      121 VIECCLQFPDDDYSMWDLFMKICVFIFAFAVIPVLIITVCYTTLMLRLKXVRLLSGSREKD    180
Db      273 mnlrritmwlvvavafivcwtpbhivyilikalitipettftqvswhfcialgytuscjn    332
        ||||| : ||||| : ||||| : ||| : : : | ||||| ||||| ||
QY      181 XNLRRTIRLVVVAVPVVCWPPIHILFLVEALGSTSHSTAALSSYFCIALGYTINSLN    240
Db      333 pvlvyafldenfkrcrfrefcipsstsieqgnstrvrgntrebpstantvd    381
        |:|:||||| ||||| : ||| : : ||| || : | :
QY      241 PILYAFLDENFKRCRFDECFPLKMXMERKXSTSRRV-NIVQDPAYLREID    288
```

	RESULT	10
ID	R76780	standard; Protein; 400 AA.
AC	R76780;	
DT	11-DEC-1995	(first entry)
DE	Human mu opiate receptor.	
KW	Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;	
KW	drug abuse; analgesic.	
OS	Homo sapiens.	
FS	Key	Location/Qualifiers
FT	Modified_site	9
FT	/label= Glycosylation	
FT	/note= "N-linked glycosylation site"	
FT	Modified_site	11
FT	/label= Glycosylation	
FT	/note= "N-linked glycosylation site"	
FT	Modified_site	32
FT	/label= Glycosylation	
FT	/note= "N-linked glycosylation site"	
FT	Modified_site	40
FT	/label= Glycosylation	
FT	/note= "N-linked glycosylation site"	
FT	Modified_site	48
FT	/label= Glycosylation	
FT	/note= "N-linked glycosylation"	
FT	Domain	68..87
FT	/label= Transmembrane_domain	
FT	Domain	107..125
FT	/label= Transmembrane_domain	

FT Domain 144..165
FT /label= Transmembrane_domain
FT Domain 188..208
FT /label= Transmembrane_domain
FT Domain 236..256
FT /label= Transmembrane_domain
FT Domain 284..304
FT /label= Transmembrane_domain
FT Domain 322..341
FT /label= Transmembrane_domain
PN W09520667-A1.
PD 03-AUG-1995.
PF 30-JAN-1995; U01144.
PR 28-JAN-1994; US-188275.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
DR WPI; 95-275452/36.
N-PSDB; Q93102.
PT New DNA encoding human mu opiate receptor - used esp. for screening
PT cpds. for activity as opiate agonists or antagonists
PS Claim 1; Page 25-26; 49pp; English.
CC hMorl cDNA was obtd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. Expression
CC of hMorl in COS cells revealed high affinity recognition of the mu
CC opiate specific ligand. Recombinant hMorl can be used to screen
CC compounds for analgesic activity.
SQ Sequence 400 AA;

Query Match	68.2%;	Score 1520;	DB 13;	Length 400;
Best Local Similarity	67.1%;	Pred. No. 2.82e-131;		
Matches 188;	Conservative 43;	Mismatches 46;	Indels 3;	Gaps 3;

```
Dd      98 ytkmktatniyifnlaladalastlpgfsgvnylmgtwfpglclckivisidyymftsi 157
        ||||| | | | | | : : | | | | | : | | | | : | | | | | 
QY      1 xTKMKtATNIXIFNLALADALAVITTMPEqSVXYIMNSWPFEGDVLCKIVISIDYYNMFTSI 60

Db      158 fltlctmsvdryiaavchpvkaldfrtpnakinvcnwllssaiglpvmfmattkyrgg-s 216
        ||| | | | | | | | | | | | | | : | | | | : | | | | : : : | | | :
QY      61 FTLLMMSVDRYIAVCHPVKALDFRTPLKAKIINICLMLSSSVGISAIVLGGTKVRDVD 120

Db      217 -idcrltfshptw-ywenlvkicvfifaafimpvjltwcyclmlrlrksvrmlsgskekd 274
        |:| | | : | : : | | | | | : | | | | | ||| ||| ||| | | : | | | : | | |
QY      121 VIECCLEPDDDDYSWMDLFMKICVFIFAFAVIPVLIITVCYTLMILRLKXVRLLSGSREKD 180

Db      275 nrlrrlcmvlvvavfvicwtppihiyilkalvatlpettfqtswhfcialgytnscln 334
        ||||| : | | | | | : | | | | | : : : | | : : : | | | | | ||| |||
QY      181 XNLRRITRLVVVAVFVWCWPPIHIFILVEALGSTISHSTAALLSSYYFCIALGYTNSLN 240

Db      335 pvllyafidenfkrcfrefoiciptsniegnstrirgntrd 374
        |:| | | | | | | | | | | : | | : | : : | | : : | |
QY      241 PIIAFLDENFKRCFRDFOCFPLKMXMERXSTSRVYNTVOD 280
```

RESULT 11
ID R76782 standard; Protein; 372 AA.
AC R76782;
DT 11-DEC-1995 (first entry)
DE Rat delta opiate receptor.
KW Delta opiate receptor; mu opiate receptor; hMOR; opiate agonist;
KW opiate antagonist; drug abuse; analgesic.
OS Rattus sp.
PN W09520667-A1.
PD 03-AUG-1995.
PF 30-JAN-1995; U01144.
PR 28-JAN-1994; US-188275.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PI (USSH) US SEC DEPT HEALTH.
PI Johnson ES, Persico AM, Uhl G, Wang J;
DR WPI; 95-275452/36.
PT New DNA encoding human mu opiate receptor - used esp. for screening
PT cpds. for activity as opiate agonists or antagonists
PS Disclosure;Page 28-29; 49pp; English.

Query Match	65.0%;	Score 1448;	DB 12;	Length 372;
Best Local Similarity	68.8%;	Pred. No. 2.33e-124;		
Matches	179;	Conservative	44;	Mismatches 33; Indels 4; Gaps 4;
Db	77	ytklktatniyiflnaladalatsltlpfgsakylmetwpgfelickavlsidymfts	136	
QY	1	YTKMKTATNIYIFLNALADALVTITMPFQSTVYLYMNSWPFGEVLCKIVISIDYNNMFTSI	60	
Db	137	ftltmmsvdryiaavchpyxaldfrtpakakliniciwvlasgvygypimvmavtqprdga-	195	
QY	61	FTLTMSVDRYIAVCHPYXALDFRTPKAKIINICIMWLLSSSGISAIVLGTKVREDVD	120	
Db	196	vv-cmlqfpspsw-ywdtvbkicvflfafvvpililitvcyglmllrlsrlljsgskekd	253	
QY	121	VIECCIQFPDDDSWMDLKMKICVFIFAFVIPVLIIVCYITMLRLKXVRLLSGSREXD	180	
Db	254	rsllritrmvllvvvgafavvcwaphifviwvltvdiinrrdplvvaalhlcialgyanssl	313	
QY	181	XNLRRIITRLVLLVVAVFVVCWTFPIHIFILVEALGSTSHSTA-ALSSYYFCIALGYTNSSL	239	
Db	314	npvlyafldenfkrcfrqlc	333	
QY	240	NPILYAFLDENFKRCFRDFC	259	

RESULT 14
ID R66503 standard; Protein; 371 AA.
AC R66503;
DT 19-JAN-1995 (first entry)
DE Murine delta opioid receptor.
KW delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain
KW drug addiction; neurological disorder; psychiatric; disorder;
KW cardiovascular disorder.
OS Mus musculus.
PN FR2697850-A.
PD 13-MAY-1994.
PF 10-NOV-1992; 013526.
PR 10-NOV-1992; FR-013526.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUTIS.
PI Kieffer B;
DR WPI; 94-178255/22.
DR N-PSDB; Q66656.
PT New nucleic acid encoding opioid receptor - and related
PT polypeptide, antisense nucleic acid, probes, recombinant cells
PT and ligands, useful in diagnosis and treatment of e.g.
PT neurological disorders
PS Claim 8; Page 19-20; 29pp; French.
CC A CDNA bank constructed from hybridoma NG108-15, was used to
CC transfect COS-1 cells. The cells were tested for ability to bind
CC tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or
CC absence of the opioid antagonist naloxone. Clone K56 was isolated
CC from a positive colony and found to contain a 2216bp insert. This
CC cDNA encodes a delta opioid (enkephalin) receptor with apparent
CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
SQ Sequence 371 AA;

Query Match	60.5%;	Score 1348;	DB 10;	Length 371;
Best Local Similarity	66.9%;	Pred. No. 9.17e-115;		
Matches 174;	Conservative	45;	Mismatches 36;	Indels 5;
				Gaps 5;

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Db      77  ytklktatniyiflnaladalatsltlfpqsakylmetwlpfgellckavlsidyymfts! 136
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QY      1  YTKMKTATNIIYIFNLALADALVTTTMEFQSTVYLLNSMWPFGDVLCKIIVISIDYYNMFTSI 60

Db      137  ftltmmsvdr̄yiaavchpvcakaldfr̄tpcakalinīciwlasgvavpim̄mayta-p̄gmwq 195
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61  FTLTMSVDR̄YIAVCHPVCALDFR̄TPCAKALINIC̄IWLSSSVGISAIVLTGGTKVREDVD 120

Db      196  wyacs-ssp̄vq-lvl-dt̄vbkic̄vfīfafv̄p̄il̄it̄vcygl̄ml̄rl̄sr̄vll̄sgsk̄ed̄ 252
      | : | ||||:||||:|||| ||| |||:||||:|||||
QY      121  VIECCLŌFPDD̄DYSWWDLĒMKIC̄VFĪFAV̄IPV̄LIIV̄CYT̄LMIL̄RL̄KXV̄RL̄L̄SGS̄REK̄D 180

Db      253  rsl̄rl̄it̄rm̄vl̄vw̄gaf̄vcw̄ap̄h̄it̄v̄l̄wt̄l̄vd̄in̄rr̄dp̄l̄v̄aal̄h̄ic̄ial̄gȳaans̄l 312

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QY	181	XLRLRITRLVLVVAVFVVCWCTPIHIFILVEALGSTSHSTA-ALSSYYFICIALGYTNSSL	239
D5	313	npv\yafldenfkrcfrqlc	332
QY	240	NPILYAFLDENFKRCFRDFC	259

RESULT 15
 ID R71968 standard; Protein; 367 AA.
 AC R71968;
 DT 20-OCT-1995 (first entry)
 DE Rat opioid receptor.
 KW Opioid receptor; gene therapy; diagnostic.
 OS Rattus sp.
 PN W09507983-A.
 PD 23-MAR-1995.
 PF 13-SEP-1994; U10358.
 PR 13-SEP-1993; U5-120501.
 PA (INDY) UNIV INDIANA FOUND.
 PI Yu L;
 DR WPI; 95-131351/17.
 DR N-PSDB; Q89233.
 PT New nucleic acid encoding new human mu opioid receptor - and
 PT related vectors, transformed cells, antibodies etc., useful in
 PT diagnosis, treatment and drug screening.
 PS Example 9; Page 218-222; 266pp; English.
 CC The cDNA given in Q89233 was isolated from a rat brain library by
 CC low stringency hybridization with rat mu opioid receptor cDNA
 CC (Q89222). The clone encoded a 367-amino acid protein (R71968)
 CC that showed high homology with mu, kappa and delta opioid receptors
 CC but lacked affinity for their ligands, suggesting it to be
 CC a novel member of the opioid receptor family.
 SQ Sequence 367 AA;

Query Match	60.38;	Score 1345;	DB 13;	Length 367;
Best Local Similarity	62.18;	Pred. No. 1.78e-114;		
Matches 174;	Conservative	46;	Mismatches 55;	Indels 5;
			Gaps	5;

[illegible]

Search completed: Thu Apr 16 13:41:27 1998
Job time : 81 secs.

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Db 267 RNLRRITRLVLVWVAVFWCWPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSLN 326
QY 181 XNLRITRLVLVWVAVFWCWPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSLN 240
Db 327 PILYAFLDENFKRCRDFCFPLKMMERQSTSRVNTVQDPAYLRDIDGM-NKPV 380
QY 241 PILYAFLDENFKRCRDFCFPLKMMERKXSTSRVNTVQDPAYLRDIDGMNKPV 295

RESULT 2
ID JC2338 STANDARD; PRT; 380 AA.
AC xxxxxx
XX 01-JAN-1900
DE TOIG of: jc2338 check: 8304 from: 1 to: 380.
XX
CC TOIG of: jc2338 check: 8304 from: 1 to: 380
CC

>P1:JC2338
kappa opioid receptor - human
C/Species: Homo sapiens (man)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 10-Sep-1997
C/Accession: JC2338; A55354
C/R/Mansson, E.; Bare, L.; Yang, D.
CC Biochem. Biophys. Res. Commun. 202, 1431-1437, 1994
CC A/Title: Isolation of a human kappa opioid receptor cDNA from placenta.
CC A/Reference number: JC2338
CC A/Accession: JC2338
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <MAN>
CC A/Experimental source: placenta
CC R/Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhl, G.R.
CC J. Biol. Chem. 269, 25966-25969, 1994
CC A/Title: Human kappa opiate receptor second extracellular loop elevates dynorphin
CC A/Reference number: A55354
CC A/Accession: A55354
CC A/Status: preliminary
CC A/Molecule type: mRNA
CC A/Residues: 136-279 <MAN>
CC A/Cross-references: GB:I36130; NID:g598184; PID:g598185
CC C/Comment: This receptor preferentially binds to dynorphins.
CC C/Keywords: G protein-coupled receptor; receptor; transmembrane protein
CC F:60-85/Domain: transmembrane #status predicted <TM1>
CC F:95-114/Domain: transmembrane #status predicted <TM2>
CC F:133-154/Domain: transmembrane #status predicted <TM3>
CC F:177-199/Domain: transmembrane #status predicted <TM4>
CC F:228-251/Domain: transmembrane #status predicted <TM5>
CC F:275-296/Domain: transmembrane #status predicted <TM6>
CC F:311-333/Domain: transmembrane #status predicted <TM7>
SQ SEQUENCE 380 AA; 42659 MW; 802911 CN;

Query Match 98.38; Score 2192; DB 2; Length 380;
Best Local Similarity 97.68; Pred. No. 4.74e-191;
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

Db 87 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPEGDVLCIKIVISIDYYNMFTSI 146
QY 1 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPEGDVLCIKIVISIDYYNMFTSI 60
Db 147 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIMWLLSSVGISAIVLGTKVREDVD 206
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIMWLLSSVGISAIVLGTKVREDVD 120
Db 207 VTECSLQFPDDYSWMDLFMKICVFIFAFAVIPVLLITVCTIMILRLKSVRLSGSREKD 266
QY 121 VTECSLQFPDDYSWMDLFMKICVFIFAFAVIPVLLITVCTIMILRLKSVRLSGSREKD 180
Db 267 RNLRRITRLVLVWVAVFWCWPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSLN 326
QY 181 XNLRITRLVLVWVAVFWCWPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSLN 240

Db 327 PILYAFLDENFKRCRDFCFPLKMMERQSTSRVNTVQDPAYLRDIDGM-NKPV 380
QY 241 PILYAFLDENFKRCRDFCFPLKMMERKXSTSRVNTVQDPAYLRDIDGMNKPV 295

RESULT 3
ID A55259 STANDARD; PRT; 380 AA.
AC xxxxxx
XX 01-JAN-1900
DE TOIG of: a55259 check: 7081 from: 1 to: 380.
XX
CC TOIG of: a55259 check: 7081 from: 1 to: 380
CC

>P1:A55259
kappa opioid receptor - guinea pig
C/Alternate names: dynorphin receptor
C/Species: Cavia porcellus (guinea pig)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 10-Sep-1997
C/Accession: A55259
CC R/Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A
CC Proc. Natl. Acad. Sci. U.S.A. 91, 3779-3783, 1994
CC A/Title: Primary structure and functional expression of a guinea pig kappa opio
CC A/Reference number: A55259
CC A/Accession: A55259
CC A/Status: preliminary
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <XIE>
CC A/Cross-references: GB:U04092; NID:g476106; PID:g476107
CC C/Keywords: transmembrane protein
SQ SEQUENCE 380 AA; 42736 MW; 800736 CN;

Query Match 96.88; Score 2157; DB 2; Length 380;
Best Local Similarity 94.68; Pred. No. 1.01e-187;
Matches 279; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Db 87 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPEGDVLCIKIVISIDYYNMFTSI 146
QY 1 YTKMKTATNIYIFNLALADALVTTMPFQSTVYLMNSWPEGDVLCIKIVISIDYYNMFTSI 60
Db 147 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIMWLLSSVGISAIVLGTKVREDVD 206
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIMWLLSSVGISAIVLGTKVREDVD 120
Db 207 IIECSLQFPDDYSWMDLFMKICVFIFAFAVIPVLLITVCTIMILRLKSVRLSGSREKD 266
QY 121 IIECSLQFPDDYSWMDLFMKICVFIFAFAVIPVLLITVCTIMILRLKSVRLSGSREKD 180
Db 267 RNLRRITRLVLVWVAVFWCWPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSLN 326
QY 181 XNLRITRLVLVWVAVFWCWPPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSLN 240
Db 327 PILYAFLDENFKRCRDFCFPLKMMERQSTSRVNTVQDPAYLRDIDGM-NKPV 380
QY 241 PILYAFLDENFKRCRDFCFPLKMMERKXSTSRVNTVQDPAYLRDIDGMNKPV 295

RESULT 4
ID MESPIQIFRGDPGPTCPSACLLPNSSSWFPNMAESDSNGSVGSEDQLESAAHISPAIPVITAVSVVF STAND
AC xxxxxx
XX 01-JAN-1900
DE This is a DE line.
XX
SQ SEQUENCE 310 AA; 35247 MW; 528594 CN;

Query Match 95.88; Score 2136; DB 2; Length 310;
Best Local Similarity 92.98; Pred. No. 1.01e-185;
Matches 274; Conservative 13; Mismatches 7; Indels 1; Gaps 1;

Db 17 YTKMKTATNIIYIFNLALADALVTTTTPQSAVYLMNSWPEGDVLCIVISIDYYNMTSI 76
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QY 1 YTKMKTATNIIYIFNLALADALVTTTTPQSTVYLMNSWPFQDVLCIVISIDYYNMTSI 60
77 FTLTMSVDRIYAVCHPVKALDFRTPPKAKIINICIWLASSVGISAIVLGTKVREDVD 136
|||||
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPPKAKIINICIWLSSVGISAIVLGTKVREDVD 120
137 VIECLOFPDDDEYSWDLFMKICVFEAFVIVPVLIIIVCYTLMILRLKSVRLLSGSREXD 196
|||||
QY 121 VIECLOFPDDDYSWWDLFMKICVFIFAIVIPVLIIVCYTLMILRLKXVRLLSGSREXD 180
197 RNLRRITKLVLVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYFCIALGYTNSLN 256
|||||
QY 181 XNLRRIITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFCIALGYTNSLN 240
257 PVLVAFLDENFKRCFRDCEFPFKMRMERQSTNRVNTVQDPASMRDYGGM-NKPV 310
|:|||||
QY 241 PILVAFLDENFKRCFRDCEFPFKMXMERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT 5 STANDARD; PRT; 380 AA.
ID S36143
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A/Accession: S36143.
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CC A/Accession: S36143
CC A/Status: preliminary
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <NIS>
CC R/Chen, Y.; Mestek, A.; Liu, J.; Yu, L.
CC Biochem. J. 295, 625-628, 1993
CC A/Title: Molecular cloning of a rat kappa opioid receptor reveals sequence similar
CC A/Reference number: S38825
CC A/Accession: S38825
CC A/Status: preliminary
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <CHE>
CC A/Cross-references: GB:L22001; NID:g409236; PID:g409237
CC R/Minami, M.; Toya, T.; Katano, Y.; Nakamura, S.; Onogi, T.; Kaneko, S
CC FEBS Lett. 329, 291-295, 1993
CC A/Title: Cloning and expression of a cDNA for the rat kappa-opioid receptor.
CC A/Reference number: S36102
CC A/Accession: S36102
CC A/Molecule type: mRNA
CC A/Residues: 1-41, 'L', 43-380 <MIN>
CC R/Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Deriel, J.K.; Ashby, B.; Liu-Chen, L.Y.
CC Biochem. J. 295, 629-633, 1993
CC A/Title: Molecular cloning and expression of a rat kappa opioid receptor.
CC A/Reference number: S39015
CC A/Accession: S39015
CC A/Molecule type: mRNA
CC A/Residues: 1-344, 'Y', 346-380 <LIS>
CC R/Meng, F.; Xie, G.
CC Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958, 1993
CC A/Title: Cloning and pharmacological characterization of a rat kappa opioid recept
CC A/Reference number: A48789; MUID:94052210
CC A/Accession: A48789
CC A/Status: preliminary; translated from GB/EMBL/DBD
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <RES>
CC A/Cross-references: EMBL:U00442; NID:g403486; PID:g403487
CC C/Keywords: G protein-coupled receptor; transmembrane protein
SQ SEQUENCE 380 AA; 42688 MW; 808499 CN;

Query Match 95.6%; Score 2132; DB 2; Length 380;
Best Local Similarity 92.5%; Pred. No. 2, 43e-185;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 87 YTKMKTATNIIYIFNLALADALVTTTTPQSAVYLMNSWPEGDVLCIVISIDYYNMTSI 146
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QY 1 YTKMKTATNIIYIFNLALADALVTTTTPQSTVYLMNSWPFQDVLCIVISIDYYNMTSI 60
147 FTLTMSVDRIYAVCHPVKALDFRTPPKAKIINICIWLASSVGISAIVLGTKVREDVD 206
|||||
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPPKAKIINICIWLSSVGISAIVLGTKVREDVD 120
207 VIECLOFPDDDEYSWDLFMKICVFEAFVIVPVLIIIVCYTLMILRLKSVRLLSGSREXD 266
|||||
QY 121 VIECLOFPDDDYSWWDLFMKICVFIFAIVIPVLIIVCYTLMILRLKXVRLLSGSREXD 180
267 RNLRRITKLVLVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYFCIALGYTNSLN 326
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QY 181 XNLRRIITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFCIALGYTNSLN 240
327 PVLVAFLDENFKRCFRDCEFPFKMRMERQSTNRVNTVQDPASMRDYGGM-NKPV 380
|:|||||
QY 241 PILVAFLDENFKRCFRDCEFPFKMXMERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT 6 STANDARD; PRT; 380 AA.
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XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A/Accession: JC2434.
XX
CC A/Accession: JC2434
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <NIS>
CC A/Cross-references: DDBJ:D31663
CC C/Genetics:
CC A/Map position: 1A2-3
CC A/Introns: 86/2; 204/1
CC C/Keywords: receptor
SQ SEQUENCE 380 AA; 42630 MW; 803251 CN;

Query Match 94.8%; Score 2114; DB 2; Length 380;
Best Local Similarity 92.5%; Pred. No. 1.25e-183;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

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QY 1 YTKMKTATNIIYIFNLALADALVTTTTPQSTVYLMNSWPFQDVLCIVISIDYYNMTSI 60
147 FTLTMSVDRIYAVCHPVKALDFRTPPKAKIINICIWLASSVGISAIVLGTKVREDVD 206
|||||
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPPKAKIINICIWLSSVGISAIVLGTKVREDVD 120
207 VIECLOFPDDDEYSWDLFMKICVFEAFVIVPVLIIIVCYTLMILRLKSVRLLSGSREXD 266
|||||
QY 121 VIECLOFPDDDYSWWDLFMKICVFIFAIVIPVLIIVCYTLMILRLKXVRLLSGSREXD 180
267 RNLRRITKLVLVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYFCIALGYTNSLN 326
|||||
QY 181 XNLRRIITRLVLVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFCIALGYTNSLN 240
327 PVLVAFLDENFKRCFRDCEFPFKMRMERQSTNRVNTVQDPASMRDYGGM-NKPV 380
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QY 241 PILVAFLDENFKRCFRDCEFPFKMXMERXSTSRVNTVQDPAYLREIDGMNKPV 295

RESULT 7 STANDARD; PRT; 398 AA.
ID A57510
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX


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CC A:Residues: 1-398 <ROS>  
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CC A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1  
CC C:Genetics:  
CC A:Gene: MOR-1  
CC A:Introns: 95/2; 213/1; 386/3  
CC C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane  
CC SEQUENCE 398 AA; 44421 MW; 862989 CN;  
  
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Best Local Similarity 65.7%; Pred. No. 1.15e-127;  
Matches 190; Conservative 47; Mismatches 48; Indels 4; Gaps 4;  
  
Db 96 YTKMKTATNIYIFNLALDALATSTLPFQSVNYLMGTMPFGNIIICKIVISIDYNNMTSI 155  
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QY 1 YTKMKTATNIYIFNLALDALATSTLTMPFQSTVYLMSWPFGLCKIVISIDYNNMTSI 60  
  
Db 156 FTLCTMSVDRIAVCHPYKALDERTPRNAKIVNCNWITSSAIGLPVMFMATTKYRG-S 214  
| | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |  
QY 61 FTLLTMSVDRIAVCHPYKALDERTPLKAKIINICIMLSSSVGISAIVLGGIKVRDVD 120  
  
Db 215 -IDCTLTFSHPTW-YWENILKICVFIFAIFIMPVLITYCYGMLIRLKSVRLSGSREKD 272  
| : | | | : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
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Db 333 PLYLAFLDENFKRCFRFCIPTSTIEQNSARIRONTREHPSTANTVD 381  
| : | | | | | | | | | | | | | | | : | : : : | | : | : |  
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RESULT 3 STANDARD; PRT; 400 AA.  
ID I56553  
AC xxxxxx  
DT 01-JAN-1900  
XX A:Accession: I56553.  
DE  
XX  
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CC A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ  
CC A:Molecule type: mRNA  
CC A:Residues: 1-400 <RES>  
CC A/Cross-references: GB:L29301; NID:g459831; PID:g459832  
CC R,Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.R  
CC submitted to GenBank, August 1994  
CC A:Reference number: A38991  
CC A:Accession: A38991  
CC A:Status: translated from GB/EMBL/DDBJ  
CC A:Molecule type: mRNA  
CC A:Residues: 1-50,'N',52-233,'V',235-400 <WAN>  
CC A/Cross-references: GB:L25119; PID:g452073  
CC R,Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.R  
CC FEBS Lett. 338, 217-222, 1994  
CC A>Title: Human mu opiate receptor. cDNA and genomic clones, pharmacologic character  
CC A:Reference number: S41075  
CC A:Accession: S41075  
CC A:Status: nucleic acid sequence not shown  
CC A:Molecule type: mRNA  
CC A:Residues: 1-50,'N',52-400 <WA2>  
CC R,Bare, L.A.; Mansson, E.; Yang, D.  
CC FEBS Lett. 354, 213-216, 1994  
CC A>Title: Expression of two variants of the human mu opioid receptor mRNA in SK-N-SH  
CC A:Reference number: S51215  
CC A:Accession: S51215
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[illegible]

[illegible]

CC Biochem. Biophys. Res. Commun. 209, 563-574, 1995
CC A>Title: Complementary DNA cloning of a mu-opioid receptor from rat peritoneal
CC A>Reference number: I52314; MUID:95251654
CC A>Accession: I52314
CC A>Status: preliminary
CC A>Molecule type: mRNA
CC A>Residues: 101-340 <SED>
CC A>Cross-references: GB:S77863; NID:g998526
CC A>Experimental source: Sprague Dawley, peritoneal macrophages
CC R>Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
CC FEBS Lett. 327, 311-314, 1993
CC A>Title: Primary structures and expression from cDNAs of rat opioid receptor de
CC A>Reference number: S34592
CC A>Accession: S34593
CC A>Molecule type: mRNA
CC A>Residues: 1-244, 'V', 246-398 <FUK>
CC R>Wang, J.
CC Proc. Natl. Acad. Sci. U.S.A. 90, 10230-10234, 1993
CC A>Title: Mu opiate receptor: cDNA cloning and expression.
CC A>Reference number: A48799; MUID:94052137
CC A>Accession: A48799
CC A>Status: preliminary; translated from GB/EMBL/DBJ
CC A>Molecule type: mRNA
CC A>Residues: 1-244, 'V', 246-398 <WAN>
CC A>Cross-references: GB:L20684; NID:g409149; PID:g409150
CC R>Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.

RESULT	10		
ID	I56517	STANDARD;	PRT; 398 AA.
XX			
AC	xxxxxxx		
XX			
DI	01-JAN-1900		
XX			
DE	TOIG of: I56517	check: 8374	from: 1 to: 398.
XX			
CC	TOIG of: I56517	check: 8374	from: 1 to: 398

CC A>Title: Cloning and pharmacological characterization of a rat mu opioid receptor
CC A:Reference number: I58154; MUID:94059560
CC A:Accession: I58154
CC A>Status: preliminary; translated from GB/EMBL/DBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-244, 'V', 246-398 <THO>
CC A:Cross-references: GB:L22455; NID:g437671; PID:g437672
CC C:Genetics:
CC A:Gene: MUOR1
CC C:Keywords: G protein-coupled receptor; transmembrane protein
SQ SEQUENCE 398 AA; 44508 MW; 870781 CN;

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CC >P1;I56517
CC mu-opioid receptor - rat
CC C:Species: Rattus norvegicus (Norway rat)
CC C:Date: 26-Jul-1996 #sequence revision 26-Jul-1996 #text change 13-Mar-1997
CC C:Accession: I56517; I57951; A49680; I52314; S34593; A48799; I58154
CC C:R:Runzow, J.R.; Zhang, G.; Bouvier, C.; Saez, C.; Ronnekleiv, O.K.; Kelly, M.J.; G
CC C: J. Neurochem. 64, 14-24, 1995
CC C:A:Title: Characterization and distribution of a cloned rat mu-opioid receptor.
CC C:A:Reference number: I56517; MUID:95096825
CC C:A:Accession: I56517
CC C:A:Status: preliminary; translated from GB/EMBL/DBJ
CC C:A:Molecule type: mRNA
CC C:A:Residues: 1-398 <RES>
CC C:A:Cross-references: EMBL:U02083; NID:g403573; PID:g403574
CC C:R:Chen, Y.; Mestek, A.; Liu, J.; Hurley, J.A.; Yu, L.
CC C:Mol. Pharmacol. 44, 8-12, 1993
CC C:A:Title: Molecular cloning and functional expression of a mu-opioid receptor from
CC C:A:Reference number: I57951; MUID:93341493
CC C:A:Accession: I57951
CC C:A:Status: preliminary; translated from GB/EMBL/DBJ
CC C:A:Molecule type: mRNA
CC C:A:Residues: 1-398 <RES>
CC C:A:Cross-references: GB:LI3069; NID:g348250; PID:g348251
CC C:R:Eppler, C.M.; Hulmes, J.D.; Wang, J.B.; Johnson, B.; Corbett, M.; Luthin, D.R.;
CC C: J. Biol. Chem. 268, 26447-26451, 1993
CC C:A:Title: Purification and partial amino acid sequence of a mu opioid receptor from
CC C:A:Reference number: A49680; MUID:94075333
CC C:A:Accession: A49680
CC C:A:Status: preliminary
CC C:A:Molecule type: protein
CC C:A:Residues: 272-291 <EPP>
CC C:A:Experimental source: brain membranes
CC C:A>Note: sequence extracted from NCBI backbone (NCBIP:140841)
CC C:R:Sedgt, M.; Roy, S.; Ramakrishnan, S.; Elde, R.; Ich, H.H.

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Query Match          68.2%; Score 1520; DB 2; Length 398;
Best Local Similarity 65.7%; Pred. No. 2.74e-127;
Matches 190; Conservative 45; Mismatches 49; Indels 4; Gaps 4;

Db      96  YTKMKTATNIYIFNLALADALATSTLPFQSVNYLMGTWPEGLTICKIVISIDYNNMETSI 155
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      1  YTKMKTATNIYIFNLALADALATSTLPFQSTVYIMNSWPFQDVLCRIVISIDYNNMETSI 60

Db      156  FTLICTMSVDRIYAVCHPVKALDERTPRNAKIVNVCNWISSAIGLPMEMATTKYRQG-S 214
        |||  ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      61  FTLTMSVDRIYAVCHPVKALDERTPRNAKIIINICIWLLSSVGTSAIVLGTKVREDVD 120

Db      215  -IDCTLTFPSHPTW-YWENILKICVFIFAFIMPIIITVQYGLMILRLKSVRLSGSKEKD 272
        ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
QY      121  VTECCLQFPDDDYSWWDLFMKICVFIFAFIVPVLIIVCYTELMILRLKXVRLLSGSREKD 180

Db      273  RNLRIRTRMVLVVAVFIVCWPPIHIYVITIKALITIPETTFQVSWHFCIALGYTNSCLN 332
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      181  XNLRIRIRLVVVAVFVVCWPIHIFILVEALGSTSHSTAALSSYFCIALGYTNSSLN 240

Db      333  PVLVAFLDENEFKRCFREFCIPSTSLIEQONSTRVRONTREHPSTANTVD 381
        |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
QY      241  PVLVAFLDENEFKRCFREFCIPKMKMEXRSTSRVR-NTVQDPAYLREID 288

RESULT  11
ID      156504      STANDARD;      PRT;      398 AA.
XX
AC      xxxxxx
XX
DE      01-JAN-1900
XX
DE      TOIG of: 156504      check: 8604      from: 1      to: 398.
XX

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CC      TOIG of: I56504      check: 8604      from: 1      to: 398
CC
CC      >P1:I56504
CC      mu oploid receptor - rat
CC      C/Species: Rattus norvegicus (Norway rat)
CC      C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
CC      C/Accession: I56504
CC      R/Zastawny, R.L.; George, S.R.; Nguyen, T.; Cheng, R.; Tsatsos, J.; Briones-Urbina
CC      J. Neurochem. 62, 2099-2105, 1994
CC      A/Title: Cloning, characterization, and distribution of a mu-opioid receptor in rat
CC      A/Reference number: I56504; MUID:94246380
CC      A/Accession: I56504
CC      A/Status: preliminary; translated from GB/EMBL/DBD/J
CC      A/Molecule type: mRNA
CC      A/Residues: 1-398 <RES>
CC      A/Cross-references: EMBL:U35424; NID:g1017731; PID:g1017732
CC      SEQUENCE      398 AA: 44403 MW: 871809 CN/
SQ

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Query Match	67.58;	Score 1505;	DB 2;	Length 398;
Best Local Similarity	65.78;	Pred. No. 7.18e-126;		
Matches 190;	Conservative 45;	Mismatches 50;	Indels 4;	Gaps 4;

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D6      96 YTKMKTAFTNIYIENLALADALATSTLPFQSVNLYLMGTWPEGLICKIVISIDYYNMFTSI   155  
        ||| | ||||| ||||| : |: ||||| ||| : ||||| ||||| |||||  
OY       1 YTKMKTATNTIYIENTLALADALTPTNNMFQSTVYLMSNWPEGDVLCIKIVISIDYYNMFTSI   60
```

Db 156 FTTCIMSVDRYIAVCHPVKALDFERTENAKIVNVCNWLSSAIGLPMEMATTXYRQ-S 214
||| ||||| ||||| ||||| :|||:| :|||:|: : : || :
Qy 61 FTTFMMSVDRYIAVCHPVKALDFERTPLAKIINICIMWLSSSVGISAIYVLGTVKREDDV 120C

Db 215 -IDCTLESHPTW-YWENLKIICVGFIAFIMPVLIITVCYGLMILRLKSVRLSGSKRED 2722

Qy 121 VIECCLOEPDDDDYSWMDLEMKICVLEIFAVIPVLIITVCYGLMILRLKXVRLSGSKRED 1800

D0 273 RNLRRITMVLVWVAVFIVCWTPHVIILKALITIPETPQTVSWHECIALGYTNSCLN 33Z
| | | | | : | | | | | : | | : | : | | | | | | |
OY 181 XNLRRTRLVLVWVAVFVWCPTPIHTFLIVEALGSTSHSTALSSYYFCIALGYTNSCLN 240

[illegible]

RESULT	12	
ID	I38657	STANDARD; PRT; 372 AA.

AC
XXXXXXXX

DT 01-JAN-1900

DE A; Accession: I38657.

CC A; Accession: I38657

A;Molecule type: mRNA

CC A;Cross-references: EMBL:U10504; NID:g501144; PID:g501145
SEQUENCE 372 AA; 40368 MW; 725194 CN;

Query Match	65.4%;	Score 1458;	DB 2;	Length 372;
Best Local Similarity	69.2%;	Pred. No. 1.97e-121;		
Matches 180;	Conservative	43;	Mismatches 33;	Indels 4;
			Gaps	4;

D6
77 YTKMTATNIYIFNLALADALATSTLPFQSAKYIMETWPGELLCKAVLSIDYYNMFTSI 136
|||||
1 YTKMTATNIYIFNLALADALVTTTTFPQSTVYLMSWGVDLCKIVISIDYYNMFSTI 60

D_b

137 IITLTMSVDRIYAVCHPVKALDERTPAKAKLINICIWVLAISGVGPIMMVAVTTRPDCA - 195
| | | | | | | | | | | | : : : : : : : : : : : : : : : : : : :
OY 61 ITLTMSVDRIYAVCHPVKALDERTPLKAKIINICICIWLSSSVGISAIVLGCTKVREDDV 120

Dd 196 VV-CMLQFPSPSM-YWDIVKICVELFAFVPILITFYGIMLLRLRSVRLSGSKND 253

| : | | | | | | | | | : | | | | | | | | | | | | :

QY 121 VIECCLQFEDDDYSWMDLFMKICVYIFAFAVIVPLIIIVCYITLMIIRLKXVRLLSGSREKD 180

Db 254 RSLRRITRFAVLVYVGAFVVCWAPRHHFVIVWTLVDIDRDEPLVVAALHLCIALGYANSSL 313
:|||||:|||||:|||||:|: : : : :|:|||||:|||||

QY 181 XNLRRTIRLVVYVAVFVVCWTPRHIFILVEALGSTSHSTA-ALSSYYFCIALGYTNSSL 239

Db 314 NPVLVAFLDENFKRCFRQLC 333
||:|||||:|||||:|:|

QY 240 NPILVAFLDENFKRCFRDFC 259

RESULT	13
ID	534592
STANDARD;	PRT;
	372 AA

AC
XXXXXXXXXX

DT 01-JAN-1900

DE TOIG of: s34592 check: 2221 from: 1 to: 372.

TOIG of: s34592 check: 2221 from: 1 to: 372

CC >P1;S34592

C;Species: Rattus norvegicus (Norway rat)

CC C;Accession: S34592; I56571

CC FEBS Lett. 327, 311-314, 1993

CC A;Reference number: S34592

CC A;Molecule type: mR

CC R;Abood, M.E.

CC A;Title: Molecular cloning and expr

CC A/Accession: I56571

CC A;Molecule type: mRNA
CC A;Def:Accession: 1-379 chrms

CC A/Cross-references: EMBL:U00475; NID:g403488; PTD:g514211
CC A/Cross-references:

CC A;Gene: dor

SQ SEQUENCE 372 AA; 40449 MW; 719618 CN;

Query Match	65.18;	Score 1452;	DB 2;	Length 372;
Best Local Similarity	68.8%;	Pred. No. 7.27e-121;		
Matches	179;	Conservative	44;	Mismatches 33;
			Indels 4;	Gaps 4;

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Db      77 YTKLKVATNIYIFNLALADALATSTLPFQSAKYLMEIWPFGILLCKAVLSIDYYNMTSTI 136
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy      1 YTKMKVATNIYIFNLALADALVPTMPFQSTVYLMSWPFEGYLVCKIVISIDYYNMTSTI 60

```

D6 137 FTLTMSVDRYIAVCHPVKALDFRTPAKAKLINICIWLASGVGPIMWAVTQPRDGA- 195

QY 61 FTLTMSVDRYIAVCHPVKALDFRPLKAKLINICIWLSSSGISAIVLGTKVREYD 120

D₆ 196 VV-CTIQFPPSPW-YWDITVTKICVELEAFVVPILITVQYGLMLRLRSVRLLSGSKEKD 2533
 121 VIECCLEQEPDDDDYSWMDLEMKICVLEAFVIVPILITVQYGLMLRLKXVRLLSGSREKD 1800

Db 254 RSLRRTRMVLVVGAFVVCWAPTHIFVIVWTLVDINRRDPLVVAALHLCIALGYANSSL 3133
:|||||:||||:||||:|: : : : :
QY 181 XNLRRTIRLVVVAVFVVCWCPHIFILVEALGSTSHSTA-ALSSYYFCIALGYTNSSL 2339

```
Db      314  NPVLYAFLDENFKRCFRQLC 333
        ||:|||||:|||||:|
QY      240  NPILYAFLDENFKRCFRDFC 259
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```
RESULT 14
ID B48227 STANDARD; PRT; 372 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: b48227 check: 3372 from: 1 to: 372.
XX
CC TOIG of: b48227 check: 3372 from: 1 to: 372
CC
CC >P1;B48227
CC delta opioid receptor 1 - mouse
CC C:Species: Mus musculus (house mouse)
CC C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 10-Sep-1997
CC C:Accession: B48227; S37807; A48685; S36745
CC R:Yasuda, K.; Raynor, K.; Kong, H.; Breder, C.D.; Takeda, J.; Reisine, T.; Bell, G
CC Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740, 1993
CC A:Title: Cloning and functional comparison of kappa and delta opioid receptors fr
CC A:Reference number: A48227
CC A:Accession: B48227
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 1-372 <YAS>
CC A:Cross-references: GB:L11064; NID:g348246; PID:g348247
CC R:Kieffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
CC submitted to the EMBL Data Library, February 1993
CC A:Reference number: S37807
CC A:Accession: S37807
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 1-372 <KIE>
CC A:Cross-references: EMBL:I06322; NID:g192942; PID:g192943
CC R:Bzdega, T.; Chin, H.; Kim, H.; Jung, H.H.; Kozak, C.A.; Klee, W.A.
CC Proc. Natl. Acad. Sci. U.S.A. 90, 9305-9309, 1993
CC A:Title: Regional expression and chromosomal localization of the delta opiate rece
CC A:Reference number: A48685; MUID:94022364
CC A:Accession: A48685
CC A:Status: preliminary
CC A:Molecule type: mRNA
CC A:Residues: 8-372 <BZD>
CC A:Experimental source: NG108-15 hybrid cells
CC A:Note: sequence extracted from NCBI backbone (NCBIN:138618, NCBIP:138619)
CC R:Kieffer, B.L.; Befort, K.; Gaveriaux-Ruff, C.; Hirth, C.G.
CC Proc. Natl. Acad. Sci. U.S.A. 89, 12048-12052, 1992
CC A:Title: The delta-opioid receptor: isolation of a cDNA by expression cloning and
CC A:Reference number: S36745
CC A:Accession: S36745
CC A:Molecule type: mRNA
CC A:Residues: 1-189, 'N', 191, 'GMVQ', 207-208, 'ACSSSPVQLVL', 210-372 <KIW>
CC A:Cross-references: EMBL:I06322
CC C:Keywords: brain; G protein-coupled receptor; glycoprotein; phosphoprotein; trans
SQ SEQUENCE 372 AA; 40561 MW; 727422 CN;

Query Match 65.0%; Score 1448; DB 2; Length 372;
Best local Similarity 68.8%; Pred. No. 1.73e-120;
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

DB 77 YTKLTATNTYIFNLALADALATSTLPFQSAKIMETWPFGELLCKAYLSIDYNNMTSI 136
QY 1 YTKMKTATNTYIFNLALADALVTTTMTPEQSYIYLMNSWPFQDVLCIKIVISIDYNNMTSI 60

DB 137 FTLTMSVDRYIAVCHPYKALDFRTPAKAKLINICIVLASGVGPIMVMAVTQPRDGA- 195
QY 61 FTLTMSVDRYIAVCHPYKALDFRTPLAKAKLINICIVLSSSVGISALVIGTKVREDVD 120

DB 196 VV-CMLQFPSPSW-WMDTVTKICVFLFAFVVPILITVQYGLMLRLRSVRLSGSKEKD 253
QY 121 VIECCLQFPDDDSYMWDLFMKICVFIFAFVLPVLIITVCYTIMILRLKXVRLSGSREKD 180

DB 254 RSLRITRMVIVVGAFFVVCWAPIHIFVIVWLVLDINRQDPLVVAALHLCIALGYANSSL 313
QY 181 XNLRITRLVIVVAVFVVCWTPIHIFILVEALGSTSHSTA-ALSSYFCTALGYTNSSL 239
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```
DB 314 NPVIYAFIDENFKRCFROLG 333
QY 240 NPVIYAFIDENFKRCFRDFC 259

RESULT 15
ID I56520 STANDARD; PRT; 367 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE A:Accession: I52654.
XX
CC A:Accession: I52654
CC A:Status: preliminary; translated from GB/EMBL/DDBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-367 <RE2>
CC A:Cross-references: GB:L29419; NID:g510718; PID:g510719
CC C:Keywords: G protein-coupled receptor; transmembrane protein
SQ SEQUENCE 367 AA; 40523 MW; 720655 CN;
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Query Match 60.3%; Score 1345; DB 2; Length 367;
Best local Similarity 62.1%; Pred. No. 8.99e-111;
Matches 174; Conservative 46; Mismatches 55; Indels 5; Gaps 5;

DB 77 TKMKTATNTYIFNLALADTLVLLTLFPGQIDILLGFWPFGNALCKRYIAIDYNNMTSTF 136
QY 2 TKMKTATNTYIFNLALADALVTTTMTPEQSYIYLMNSWPFQDVLCIKIVISIDYNNMTSIF 61

DB 137 TLTMSVDRYIAVCHPIRALDVRTSSKAQAVNAIHALASVGVPAIMGSAQV-EDDEE- 194
QY 62 TLTMSVDRYIAVCHPYKALDFRTPLAKAKLINICIVLSSSVGISALVIGTKVREDVDV 121

DB 195 IECLVEIPADQY-WGPVFA-ICIFLFSFIIPVLIISVCYSLMIRLRGVRLSGSREKD 252
QY 122 IECLQFPD-DDYSWDLFMKICVFIFAFVLPVLIITVCYTIMILRLKXVRLSGSREKD 180

DB 253 RNLRRITRLVIVVAVFVVCWTPVQVFEVLVQGLGVQPGSETAVALLPCTALGYVNSCLN 312
QY 181 XNLRITRLVIVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYFCTALGYTNSSLN 240

DB 313 PILYAFIDENFKRCFKCCASSLHREMQVSDRVRSIAKD 352
QY 241 PILYAFIDENFKRCFRDFCFPLKMXMERXSTRVNTVQD 280
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Search completed: Thu Apr 16 13:39:47 1998
Job time : 55 secs.

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FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
FT CONFLICT 2 2 E -> D (IN REF. 2 AND 3).
SQ SEQUENCE 380 AA; 42659 MW; 1980629E CRC32;
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Query Match 98.3%; Score 2192; DB 1; Length 380;
Best Local Similarity 97.6%; Pred. No. 0.00e+00;
Matches 288; Conservative 1; Mismatches 5; Indels 1; Gaps 1;

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Db 87 YTKMKTATNIVIFNLALADALVTTTTFQSTVYLMNSWPFQDVLCKIVISIDYNNMFTSI 146
1 YTKMKTATNIVIFNLALADALVTTTTFQSTVYLMNSWPFQDVLCKIVISIDYNNMFTSI 60

Db 147 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIWLSSVGISAIVLGGTKVREDVD 206
61 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIWLSSVGISAIVLGGTKVREDVD 120

Db 207 VTECSLQFPDDYSWMDLFMKICVFIFAFVIVPVLIIIVCYTLMILRLKSVRLSGSREKD 266
121 VTECSLQFPDDYSWMDLFMKICVFIFAFVIVPVLIIIVCYTLMILRLKSVRLSGSREKD 180

Db 267 RNLRRITRLVLYVAVFVVCWTPPIHIFILVEALGSTSHSTALSSYFICIALGYTNSSLN 326
181 XNLRRITRLVLYVAVFVVCWTPPIHIFILVEALGSTSHSTALSSYFICIALGYTNSSLN 240

Db 327 PILYAFLDENKRCRDFCEPLKMRMEROSTSRVNTVQDPAYLRIDGM-NKPV 380
241 PILYAFLDENKRCRDFCEPLKMRMERKSTSRVNTVQDPAYLRIDGMNKNPV 295

QY
```

RESULT 2
ID OPRK_CAVPO STANDARD; PRT; 380 AA.
AC P41144;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN OPRK1.
OS CAVIA PORCELLUS (GUINEA PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY; TISSUE=BRAIN;
RX MEDLINE; 94224825.
RA XIE G.X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEEN M.T.,
RA GOLDSTEIN A., WATSON S.J., AKIL H.;
RA PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U04092; G476107; -.
DR GCRDB; GCR_0991; -.
DR PROSITE; PS00237; G-PROTEIN-RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.

```
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
SQ SEQUENCE 380 AA; 42736 MW; F9F34C4C CRC32;
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Query Match 96.8%; Score 2157; DB 1; Length 380;
Best Local Similarity 94.6%; Pred. No. 0.00e+00;
Matches 279; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

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Db 87 YTKMKTATNIVIFNLALADALVTTTTFQSTVYLMNSWPFQDVLCKIVISIDYNNMFTSI 146
1 YTKMKTATNIVIFNLALADALVTTTTFQSTVYLMNSWPFQDVLCKIVISIDYNNMFTSI 60

Db 147 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIWLSSVGISAIVLGGTKVREDVD 206
61 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIWLSSVGISAIVLGGTKVREDVD 120

Db 207 IIECSLQFPDDYSWMDLFMKICVFVFAFVIVPVLIIIVCYTLMILRLKSVRLSGSREKD 266
121 IIECSLQFPDDYSWMDLFMKICVFVFAFVIVPVLIIIVCYTLMILRLKSVRLSGSREKD 180

Db 267 RNLRRITRLVLYVAVFVVCWTPPIHIFILVEALGSTSHSTALSSYFICIALGYTNSSLN 326
181 XNLRRITRLVLYVAVFVVCWTPPIHIFILVEALGSTSHSTALSSYFICIALGYTNSSLN 240

Db 327 PILYAFLDENKRCRDFCEPLKMRMEROSTSRVNTVQDPAYLRVNDGV-NKPV 380
241 PILYAFLDENKRCRDFCEPLKMRMERKSTSRVNTVQDPAYLRVNDGMNKNPV 295

QY
```

RESULT 3
ID OPRK_MOUSE STANDARD; PRT; 380 AA.
AC P33534;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).
GN OPRK1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 93342064.
RA YASUDA K., RAYNOR K., KONG H., BREDDER C.D., TAKEDA J., REISINE T.,
RA BELL G.T.;
RA PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95100967.
RA NISHI M., TAKEISHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95251663.
RA LIU H.C., LU S., AUGUSTIN L.B., FELSHEIM R.F., CHEN H.C.,

Query Match	Best Local Similarity	Score	DB 1;	length	380;
Matches	274;	Conservative	13;	Mismatches	7;
			Indels	1;	Gaps
					1;
Db 87	YTKMKTATNIYIFNLALADALVTMTMPQSAVYIMNSWPFQDVLCKIVISIDYNNMFTSI	146			
QY 1	YTKMKTATNIYIFNLALADALVTMTMPQSTVYIMNSWPFQDVLCKIVISIDYNNMFTSI	60			
Db 147	FLITMMSVDRIYAVCHPVRKALDERTPPLKAKIINICITWLLASSVGSIAIVLGSTKVRDVD	206			
QY 61	FLITMMSVDRIYAVCHPVRKALDERTPPLKAKIINICITWLLASSVGSIAIVLGSTKVRDVD	120			
Db 207	VIECSLQFPDDEYSWMDLFMKICVFVFAFVIPVLITIVCYITLMLIRKSVRLLSGSREKD	266			
QY 121	VIECSLQFPDDEYSWMDLFMKICVFVFAFVIPVLITIVCYITLMLIRKSVRLLSGSREKD	180			
Db 267	RNLKRITKLVLVVAVFTICWPIHIFILVEALGSTSHSTAALSYFCIALGYTNSLN	326			
QY 181	RNLKRITKLVLVVAVFTICWPIHIFILVEALGSTSHSTAALSYFCIALGYTNSLN	240			

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Db      327 PVLYAFLDENFKRCFRDCEPIKMRMERQSTNRVRNTYQDPASMRDYVGM-NKPV 380
       1:|||||
Qy      241 PIIYAFLDENFKRCFRDCEPIKMXMERXSTSRRVNTYQDPALIREIDGMNKPV 295

RESULT 4
ID OPER_RAT STANDARD; PRT; 380 AA.
AC P34975;
DI 01-FEB-1994 (REL. 28, CREATED)
DI 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DI 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN OPRL OR KOR-D.
OS RATUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94059008.
RA CHEN Y., MESTEK A., LIU J., YU L.;
RL BIOCHEM. J. 295:625-628(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93374033.
RA MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,
RA KANEKO S., SATOH M.;
RL FEBS LETT. 329:291-295(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 94059009.
RA LI S., ZHU J., CHEN C., CHEN Y.-W., DERIEL J.K., ASHBY B.,
RA LIU-CHEN L.-Y.;
RL BIOCHEM. J. 295:629-633(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 94052210.
RA MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,
RA WATSON S.J., AKIL H.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=BRAIN;
RX MEDLINE; 93380575.
RA NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.;
RL FEBS LETT. 330:77-80(1993).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE; 95204422.
RA YAKOVLEV A.G., KRUEGER K.E., FADEN A.I.;
RL J. BIOL. CHEM. 270:6421-6424(1995).
CC -|- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
CC AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -|- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L22001; G409237; -.
DR EMBL; D16829; G404116; -.
DR EMBL; L22536; G425189; -.
DR EMBL; U00442; G403487; -.
DR EMBL; D16534; G415310; -.
DR EMBL; U17995; G727260; -.
DR EMBL; U17993; G727260; JOINED.
DR EMBL; U17994; G727260; JOINED.
DR PIR; S36143; S36143.
DR PIR; S38825; S38825.
DR GCDB; GCR_0636; -.
DR GCDB; GCR_0724; -.

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DR	GCRDE; GCR_0790; -. .
DR	GCRD3; GCR_0804; -. .
DR	PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT	DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 59 85 1 (POTENTIAL).
FT	DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 96 117 2 (POTENTIAL).
FT	DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 133 154 3 (POTENTIAL).
FT	DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 174 196 4 (POTENTIAL).
FT	DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 223 247 5 (POTENTIAL).
FT	DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 276 299 6 (POTENTIAL).
FT	DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 312 333 7 (POTENTIAL).
FT	DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT	DISULFID 131 210 BY SIMILARITY.
FT	LIPID 345 345 PALMITATE (POTENTIAL).
FT	CARBOXYD 25 25 POTENTIAL.
FT	CARBOXYD 39 39 POTENTIAL.
FT	CONFLICT 42 42 V -> L (IN REF. 2).
FT	CONFLICT 345 345 C -> Y (IN REF. 3).
SEQ	380 AA; 42688 MW; EE858A46 CRC32;

Query Match	95.6%;	Score 2132;	DB 1;	Length 380;
Best Local Similarity	92.5%;	Pred. No. 0.00e+00;		
Matches 273;	Conservative	13;	Mismatches 8;	Indels 1;
				Gaps 1;

Db	87	YTKMKIATINXIENLALADALVTITMPFQSAVYILMNSWPEGDVLCXIVISIDYYNMFSTI	146
QY	1	YTKMKIATINXIENLALADALVTITMPFQSTVYILMNSWPEGDVLCXIVISIDYYNMFSTI	60
Db	147	FTLTMASVDRIYAVCHPVKALDERPLKAKIINICIMLASSVGISATVLGGTKVREYD	206
QY	61	FTLTMASVDRIYAVCHPVKALDERPLKAKIINICIMLASSVGISATVLGGTKVREYD	120
Db	207	VIECSIQEPDDDEYSWMDLFMKICGVFAFVIPVLIIVCYTILMLRLKSVRLSSGREK	266
QY	121	VIECCIQEPDDDEYSWMDLFMKICGVFAFVIPVLIIVCYTILMLRLKSVRLSSGREK	180
Db	267	RNLRRITKVLVWVAVEIICWPIHIFILVEALGSTSHSTAYLSSYFYCIALGYTNSLN	326
QY	181	XNLRRITKVLVWVAVEVVCWPIHIFILVEALGSTSHSTAYLSSYFYCIALGYTNSLN	240
Db	327	PVLTAFLDENEFKRCFRDCEPIKMMERQSTNRVRNTVQDPAASMDVGGM-NKPV	380
QY	241	PVLTAFLDENEFKRCFRDCEPIKMMERKXSTSRVRNTVQDPAVLYREIDGMNKPV	295

RESULT	5		
ID	OPRM_MOUSE	STANDARD;	PRT; 398 AA.
AC	P42866; Q60768;		
DT	01-NOV-1995 (REL. 32, CREATED)		
DT	01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)		
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)		
DE	MU-TYPE OPIOID RECEPTOR (MOR-1).		
GN	OPRM1 OR OPRM OR MOR.		
OS	MUS MUSCULUS (MOUSE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; RODENTIA.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6; TISSUE=LIVER;		
RX	MEDLINE; 94377496.		
RA	MIN B.H., AUGUSTIN L.B., FELSHEIM R.F., FUCHS J.A., LOH H.H.;		
RL	PROC. NATL. ACAD. SCI. U.S.A. 91:9081-9085(1994).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=BRAIN;		

RX	MEDLINE; 95377399.		
RA	ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.;		
RA	FEBS LETT. 369:192-196(1995).		
RL	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BALB/C; TISSUE=BRAIN;		
RC	MEDLINE; 95318184.		
RA	KADEMAN D.L., KEITH D.E., ANTON B., TIAN J., MAGENDZO K.,		
RA	NEWMAN D., TRAN T., LEE D.S., WEN C., XIA Y., LUSIS A.J.,		
RA	EVANS C.J.;		
RL	J. BIOL. CHEM. 270:15877-15883(1995).		
CC	-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM		
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR		
CC	FOR BETA-ENDORPHIN.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
DR	EMBL; U10561; G565069; -.		
DR	EMBL; U10558; G565069; JOINED.		
DR	EMBL; U10559; G565069; JOINED.		
DR	EMBL; U10560; G565069; JOINED.		
DR	EMBL; U26915; G1055231; -.		
DR	EMBL; U19380; G885865; -.		
DR	MGD; MGI:97441; OPRM.		
KR	PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.		
DR	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;		
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.		
FT	DOMAIN 1 64 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 65 94 1 (POTENTIAL).		
FT	DOMAIN 95 103 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 104 121 2 (POTENTIAL).		
FT	DOMAIN 122 143 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 144 163 3 (POTENTIAL).		
FT	DOMAIN 164 193 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 194 209 4 (POTENTIAL).		
FT	DOMAIN 210 234 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 235 257 5 (POTENTIAL).		
FT	DOMAIN 258 280 CYTOPLASMIC (POTENTIAL).		
FT	TRANSMEM 281 303 6 (POTENTIAL).		
FT	DOMAIN 304 311 EXTRACELLULAR (POTENTIAL).		
FT	TRANSMEM 312 328 7 (POTENTIAL).		
FT	DOMAIN 329 398 CYTOPLASMIC (POTENTIAL).		
FT	DISULFID 140 217 BY SIMILARITY.		
FT	LIPID 351 351 PALMITATE (POTENTIAL).		
FT	CARBOHYD 9 9 POTENTIAL.		
FT	CARBOHYD 31 31 POTENTIAL.		
FT	CARBOHYD 38 38 POTENTIAL.		
FT	CARBOHYD 46 46 POTENTIAL.		
FT	CONFLICT 22 22 C -> W (IN REF. 3).		
SO	SEQUENCE 398 AA; 44421 MW; C0211489 CRC32;		

Query Match	68.4%;	Score 1524;	DB 1;	Length 398;
Best Local Similarity	65.7%;	Pred. No. 2.16e-282;		
Matches 190;	Conservative 47;	Mismatches 48;	Indels 4;	Gaps 4

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Db      96 YTKMKIATNIYIFNLALADALATSIHPQSVNYLGMWPKGNILCKIVISIDYYNMFSTI    155
        | | | | | | | | | | | | | | : | : | | | | | | | : | | | | | | | | | | | | | |
QY      1 YTKMKIATNIYIFNLALADALVITTFMEFQSTVYLMSNWPEGDVLCKIVISIDYYNMFTSI    60
Ddb     156 FTLCIMSVDRYAUCHPVKALDFRPNRAKIVNVCCNWLLSSAIGLPVMFMATTKYRQG-S    214
        | | | | | | | | | | | | | | : | | : | | : | | : : : | | : |
QY      61 FTLIMMSVDRYAVCHPVKALDFRPDLAKIINICIMWLSSSVGISAIVLGTXKREYD       120
Ddb     215 - IDCTLFESHPTW-YMENLKICVFIFAIFIMPVLIIITYCYGLMIIRLKSVRMLSGSKEKD    272
        | : | | | : | : : | | | | | : | | | | | | | | | | | | | | | | | |
QY      121 VIECLOQEPDDDYSWMDLEFKICVFIFAFAVIPVLIIITYCYGLMIIRLKSXRLLSGSKEKD    180
Ddb     273 RNLRRIITRNVLVVAVFIVCWPIIHVIILKALITIPETFEQTYSWHFCIALGYTNSCLN    332
        | | | | | : | | | | | : | | | | : : : | | : : : | | | | | | | | | |
QY      181 XNLRRIITRNVLVVAVFVVCWPPIHFIILVEALGSTSHSTAALSSYFCIALGYTNSCLN    240
Ddb     333 PVLIAFLDENFKCFREFECIPTTSITEQONSARIRONTRHEHSTANTVD 381
        | : | | | | | | | | | : | | : : : | | | : | | : |
QY      241 PILYAFLEDENFKCFRDECFPLKMXMERXSTSRRV-NIVQDAVYLREID 288
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RA	UHL C.R.;		
RL	FEBS LETT. 338:217-222(1994).		
RN	[2]		
RC	SEQUENCE FROM N.A.		
RA	TTSUE=BRIN;		
RA	MESTER A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M.,		
RA	CHEN Y., YU L.;		
CC	SUBMITTED (XXX-1994) TO EMBL/GENEBANK/DBJ DATA BANKS.		
CC	-I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM		
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR		
CC	FOR BETA-ENDORPHIN.		
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
DR	EMBL; L25119; G452073; -.		
DR	EMBL; L29301; G459832; -.		
DR	GCRDB; GCR_0985; -.		
DR	GCRDB; GCR_0966; -.		
DR	MM; 600018; -.		
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.		
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;		
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.		
FT	DOMAIN	1	66
FT	TRANSMEM	67	96
FT	DOMAIN	97	105
FT	TRANSMEM	106	123
FT	DOMAIN	124	145
FT	TRANSMEM	146	165
FT	DOMAIN	166	195
FT	TRANSMEM	196	211
FT	DOMAIN	212	236
FT	TRANSMEM	237	259
FT	DOMAIN	260	282
FT	TRANSMEM	283	305
FT	DOMAIN	306	313
FT	TRANSMEM	314	330
FT	DOMAIN	331	400
FT	DISULFID	142	219
FT	LIPID	353	353
FT	CARBOHYD	9	9
FT	CARBOHYD	12	12
FT	CARBOHYD	33	33
FT	CARBOHYD	40	40
FT	CARBOHYD	48	48
FT	POTENTIAL.	51	51
FT	CONFLICT	234	234
FT	CONFLICT	234	234
FT	SEQUENCE	400 AA;	44764 MW; 3E40D610 CRC32;

Query Match	68.2%;	Score 1520;	DB 1;	Length 400;
Best Local Similarity	67.1%;	Pred. No. 1.50e-281;		
Matches	188;	Conservative	43;	Mismatches 46;
			Indels	3;
			Gaps	3;

Db	98	YTKMKLATNIYIENLALADALATSTPEQSVNLYMGTWPEGLTICKIVISIDYNNMFTSI	157
QY	1	YTKMKLATNIYIENLALADALATVTIMPEQSTVYLMNSWPEGVCKIVISIDYNNMFTSI	60
Db	158	FTLCITMSVDRIYAVCHPVKALDERTPRNAKIINVCNWILSSAIGLPVEMMATTKYRQG-S	216
QY	61	FTLTMSVDRIYAVCHPVKALDERPRLKAKIINICIMWLSSSVGISALVLGGTKYREYD	120
Db	217	-IDCTLFPSHPTW-YWENLVKICVETFAFIMPVLIITVCYGLMILRLKSVRMLSGSEKED	274
QY	121	VIECCIQEPDDDYXSWMDLFMKICVETFAFVITPVLIITVCYGLMILRLKXVRLLSGSEKED	180
Db	275	RNLRRITRMYLVVAVFIVCWPETHIYIILKALVITPETEQTVSWHFCIALGYNNSCLN	334
QY	181	XNLRRIITRLVYLVAVFVVCWPIETHIFILVEALGSTSHSTALSSYFCIALGYNNSCLN	240
Db	335	PVLXAFILDENEKRCFREFCIPITSSNIEQONSTRIRONTRD	374
QY	241	PILYAFILDENEKRCFREFCIPITSSNIEQONSTRIRONTRD	280

RESULT 3

ID	OPRM_PIG	STANDARD;	PRT;	401 AA.
AC	095247;			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	MU-TYPE OPIOID RECEPTOR (MOR-1).			
OS	OPRM1.			
OS	SUS SCROFA (PIG).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; ARTIODACTYLA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-CEREBRAL CORTEX;			
RA	PAMPUSCH M.P., OSINSKI M.A., BROWN D.R., MURTAUGH M.P.;			
RL	SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.			
CC	-I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM			
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR			
CC	FOR BETA-ENDOPHIN.			
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL; U38645; G1553057; -.			
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.			
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;			
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.			
FT	DOMAIN	1	67	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	68	97	1 (POTENTIAL).
FT	DOMAIN	98	106	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	107	124	2 (POTENTIAL).
FT	DOMAIN	125	146	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	147	166	3 (POTENTIAL).
FT	DOMAIN	167	196	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	197	212	4 (POTENTIAL).
FT	DOMAIN	213	237	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	238	260	5 (POTENTIAL).
FT	DOMAIN	261	283	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	284	306	6 (POTENTIAL).
FT	DOMAIN	307	314	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	315	331	7 (POTENTIAL).
FT	DOMAIN	332	401	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	143	220	BY SIMILARITY.
FT	LIPID	354	354	PALMITATE (POTENTIAL).
FT	CARBOHYD	9	9	POTENTIAL.
FT	CARBOHYD	12	12	POTENTIAL.
FT	CARBOHYD	34	34	POTENTIAL.
FT	CARBOHYD	41	41	POTENTIAL.
FT	CARBOHYD	49	49	POTENTIAL.
SQ	SEQUENCE	401 AA;	45098 MW;	6786FD94 CRC32;

Query Match	68.1%;	Score 1518;	DB 1;	Length 401;
Best Local Similarity	67.1%;	Pred. No. 3.96e-281;		
Matches	188;	Conservative	43;	Mismatches 46;
			Indels	3;
			Gaps	3;

Db	99	YTKMKTATNIXIENLALADALATSTEEQOSVNYLMGTWPEGLTICKIVISIDYNNMFTSI	158
QY	1	YTKMKTATNIXIENLALADALATTTTEMBEQSTVYLMNSWPEGDYLCIKIVISIDYNNMFTSI	60
Db	159	FTLCMTMSVDRYLAVCHPVKALDFRTPRRAKIIINVCNWLISSAIGLPVFMFMATTKYRNG-S	217
QY	61	FTLTMSVDRYLAVCHPVKALDFRTPRRAKIIINVCNWLISSAIGLAVLGTKVREYD	120
Db	218	-IDCALTFSHPTW-YWENLLKICVPIFAFIMPVLIITVCYGLMILRLKSVRMLSGSKEKD	275
QY	121	VIECCLOGFPPDDXSWMDLFMKICVFIFAFAVIVPVIITVCYTLMLRLKXVRLLSGSKEKD	180
Db	276	RNLRRITRMVIVVAVFIVCWTPIHIVIIKALITIPETPQTVSWHFCIALGYTNSCLN	335
QY	181	XNLRRIITRLVIVVAVFVVCWTPIHIFILVEALGSTSHSTAALSSYYFCIALGYTNSCLN	240
Db	336	PVLYAFILDENMKRCFRFCIPTSTSTIEQONSARIRONTRD	375
QY	241	PILYAFILDENMKRCFRFCPLKMKMERKXSTSRVRNTVQD	280


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RESULT      9
ID          OPRD_HUMAN      STANDARD;      PRT;      372 AA.
AC          P41143;
DT          01-FEB-1995 (REL. 31, CREATED)
DI          01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DI          01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE          DELTA-TYPE OPIOID RECEPTOR (DOR-1).
GN          OPRD1 OR OPRD.
OS          HOMO SAPIENS (HUMAN).
OC          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC          EUTHERIA; PRIMATES.
RN          [1]
RP          SEQUENCE FROM N.A.
RC          TISSUE=CEREBRAL CORTEX, AND STRIATUM;
RX          MEDLINE; 94260835.
RA          KNAPP R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M.,
RA          SANTORO G., VARGA E.V., HRUBY V.J., ROESKE W.R., YAMAMURA H.I.;
RL          LIFE SCI. 54:463-469(1994).
RN          [2]
RP          SEQUENCE FROM N.A.
RX          MEDLINE; 95107267.
RA          SIMONIN F., BEFORT K., GAVERIAUX-RUFF C., MATTHES H., NAPPET V.,
RA          LANNES B., MICHELETTI G., KIEFFER B.;
RL          MOL. PHARMACOL. 46:1015-1021(1994).
CC          -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC          ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC          STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC          -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC          -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR          EMBL; U07882; G497314; -.
DR          EMBL; U10504; E162517; -.
DR          MIM; 165195; -.
DR          PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW          G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW          PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT          FT          DOMAIN          1          45          EXTRACELLULAR (POTENTIAL).
FT          TRANSSEM          46          75          1 (POTENTIAL).
FT          DOMAIN          76          84          CYTOPLASMIC (POTENTIAL).
FT          TRANSSEM          85          102          2 (POTENTIAL).
FT          DOMAIN          103          124          EXTRACELLULAR (POTENTIAL).
FT          TRANSSEM          125          144          3 (POTENTIAL).
FT          DOMAIN          145          174          CYTOPLASMIC (POTENTIAL).
FT          TRANSSEM          175          190          4 (POTENTIAL).
FT          DOMAIN          191          215          EXTRACELLULAR (POTENTIAL).
FT          TRANSSEM          216          238          5 (POTENTIAL).
FT          DOMAIN          239          261          CYTOPLASMIC (POTENTIAL).
FT          TRANSSEM          262          284          6 (POTENTIAL).
FT          DOMAIN          285          293          EXTRACELLULAR (POTENTIAL).
FT          TRANSSEM          294          310          7 (POTENTIAL).
FT          DOMAIN          311          372          CYTOPLASMIC (POTENTIAL).
FT          CARBOHYD          18          18          POTENTIAL.
FT          CARBOHYD          33          33          POTENTIAL.
FT          DISULFID          121          198          BY SIMILARITY.
FT          LIPID          333          333          PALMITATE (POTENTIAL).
FT          CONFLICT          27          27          F -> C (IN REF. 2).
FT          CONFLICT          40          41          PG -> AR (IN REF. 2).
FT          CONFLICT          348          348          P -> A (IN REF. 2).
FT          CONFLICT          370          370          R -> A (IN REF. 2).
SQ          SEQUENCE          372 AA; 40450 MW; CFF92985 CRC32;

Query Match          65.4%; Score 1458; DB 1; Length 372;
Best Local Similarity 69.28; Pred. No. 1.62e-268;
Matches 180; Conservative 43; Mismatches 33; Indels 4; Gaps 4;

Db          77          YTKMKTATNIYIFNLALADALATSTLRFQSAKYLMETWPGELLCKAYLSIDYYNMTSTI 136
          |||||
          1          YTKMKTATNIYIFNLALADALVTTIMPFQSTVYLMNSWPGDYLCIKIVISIDYYNMTSTI 60
Db          137          FTLTMSVDRIYAVCHPYKALDFRTPAKAKLINICIVWLASGVGVPIMYMAVTRPRDGA- 195
          |||||
          61          FTLTMSVDRIYAVCHPYKALDFRTPLKAKIINICIWLLSSVGSIAIVLGGTKVREDVD 120
Db          196          VV-CMLQFPSPSW-YWDIYTKICVFLFAFVVPILITIVCYGLMLLRISVRLLSGSKKED 253

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QY      121  VIECCLQFPDDYSWMDLFMKICVFIFAFLVPLLIIVCYTLMELRLKXVRLLSGSREKD 180
Db      254  RSLRRTIRMLVVGAEVVGCAPIHIFIVITWTLVDIDRRDPLVVALHLCIALGYANSSI 313
QY      181  XNLRRITRLVLVVAEVVVCWPIHIFIVLVEALGSTSHSTA-ALSSYFCIALGYTNSSL 235
Db      314  NPVLVAFIDENFKRCFRQLC 333
QY      240  NPVLVAFIDENFKRCFRDQC 259

RESULT 10
ID      OPRL_RAT      STANDARD;      PRT;      372 AA.
AC      P33533;
DT      01-FEB-1994 (REL. 28, CREATED)
DT      01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT      01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE      DELTA-TYPE OPIOID RECEPTOR (DOR-1) (OPIOID RECEPTOR A).
GN      OPRD1 OR KOR-A.
OS      RATTUS NORVEGICUS (RAT).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; RODENTIA.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=BRAIN;
RX      MEDLINE: 93351652.
RA      FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
RL      FEBS LETT. 327:311-314(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX      MEDLINE: 94322412.
RA      ABOOD M.E., NOEL M.A., FARNSWORTH J.S., TAO Q.;
RL      J. NEUROSCI. RES. 37:714-719(1994).
CC      -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC      ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC      STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR      EMBL: D16348; G391865; -.
DR      EMBL: U00475; G514211; -.
DR      PIR: S34592; S34592.
DR      GCRDB: GCR_0638; -.
DR      GCRDB: GCR_0805; -.
DR      PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.
KW      G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW      PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT      DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 46 75 1 (POTENTIAL).
FT      DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 85 102 2 (POTENTIAL).
FT      DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 125 144 3 (POTENTIAL).
FT      DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 175 190 4 (POTENTIAL).
FT      DOMAIN 191 215 5 (POTENTIAL).
FT      TRANSMEM 216 238 5 (POTENTIAL).
FT      DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM 262 284 6 (POTENTIAL).
FT      DOMAIN 285 293 EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM 294 310 7 (POTENTIAL).
FT      DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).
FT      CARBOHYD 311 372 18 POTENTIAL.
FT      CARBOHYD 18 18 18 POTENTIAL.
FT      CARBOHYD 33 33 33 BY SIMILARITY.
FT      DISULFID 121 198 198 PALMITATE (POTENTIAL).
FT      LIPID 333 333 333
SQ      SEQUENCE 372 AA; 40449 MW; 59F5EE50 CRC32;

Query Match 65.1%; Score 1452; DB 1; Length 372;
Best local Similarity 68.8%; Pred. No. 2,95e-267;
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

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Db 77 YTKLKTATNIYIFNLADALATSTLPFQSAKYIMETWPFGEILLCKAVLSIDYNNMFTSI 136
QY 1 YTKMKTATNIYIFNLADALATSTLPFQSTVYIMNSWPFQDVLCKIVISIDYNNMFTSI 60
Db 137 FTLTMSVDRIYAVCHPVKALDFRTPAKAKLINICIVWLASGVGPIMVMAVTPRDGA- 195
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIMWLSSVGSISAIVLGKTKYREDVD 120
Db 196 VV-CMLQFPSPSW-YWDIVTKICVFLFAFVVPILITVCGIMLLRLRSVRLSGSKEKD 253
QY 121 VIECCLOFPDDYSWMDLFMKICVFIFAFVLPVLIITVCGITMLIRLKXVRLSGSREKD 180
Db 254 RSLRITRMVLYVVGAFVVCWAPIHIFVIVTWLVDIRRDPVLVVALHLGIALGYANSSL 313
QY 181 XNLRITRLVLYVAVFVVCWTPIHIFILVEALGSTSHSTA-ALSSYFCIALGYTNSSL 239
Db 314 NPVLYAFLDENFKRCFRQLC 333
QY 240 NPILYAFLDENFKRCFRDFC 259

RESULT 11
ID OPRL MOUSE STANDARD; PRT; 372 AA.
AC P32300;
DT 01-OCT-1993 (REL. 27, CREATED)
DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE DELTA-TYPE OPIOID RECEPTOR (DOR-1) (K56) (MSL-2).
GN OPRL.
OS MUS MUSCULUS (MOUSE).
OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RA MEDLINE; 93101664.
RA KIEFFER B.L., BEFORT K., GAVERIAUX-RUFF C., HIRTH C.G.;
RA PROC. NATL. ACAD. SCI. U.S.A. 89:12048-12052(1992).
RN [2]
RA MEDLINE; 93110361.
RA EVANS C.J., KEITH D.E. JR., MORRISON H., MAGENDZO K., EDWARDS R.H.;
RA SCIENCE 258:1952-1955(1992).
RN [3]
RA MEDLINE; 93342064.
RA YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
RA BELL G.I.;
RA PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
RN [4]
RA KEITH D.E. JR., ANTON B., EVANS C.J.;
RA PROC. WEST. PHARMACOL. SOC. 36:299-306(1993).
RN [5]
RA MEDLINE; 94022364.
RA BZDEGA T., CHIN H., KIM K., JUNG H.H., KOZAK C.A., KLEE W.A.;
RA PROC. NATL. ACAD. SCI. U.S.A. 90:9305-9309(1993).
RN [6]
RA 3D-STRUCTURE MODELLING.
RA MEDLINE; 97001837.
RA ALKORTA I., LOEW G.H.;
RA PROTEIN ENG. 9:573-583(1996).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE BASAL
CC GANGLIA AND LIMBIC REGIONS.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L06322; G192943; -;
DR EMBL; L07271; -; NOT_ANNOTATED_CDS.
DR EMBL; L11064; G348247; -;

DR EMBL; S65335; G442326; -;
DR EMBL; S66181; G435782; -;
DR PIR; S37807; S37807.
DR PIR; B48227; B48227.
DR GCRDB; GCR_0229; -;
DR GCRDB; GCR_0493; -;
DR GCRDB; GCR_0634; -;
DR GCRDB; GCR_0842; -;
DR MGD; MGI:97438; OPRL.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45
FT TRANSMEM 46 75
FT DOMAIN 76 84
FT TRANSMEM 85 102
FT DOMAIN 103 124
FT TRANSMEM 125 144
FT DOMAIN 145 174
FT TRANSMEM 175 190
FT DOMAIN 191 215
FT TRANSMEM 216 238
FT DOMAIN 239 261
FT TRANSMEM 262 284
FT DOMAIN 285 293
FT TRANSMEM 294 310
FT DOMAIN 311 372
FT CARBOHYD 18 18
FT CARBOHYD 33 33
FT DISULFID 121 198
FT LIPID 333 333
SQ SEQUENCE 372 AA; 40561 MW; 514022F5 CRC32;

Query Match 65.0%; Score 1448; DB 1; Length 372;
Best Local Similarity 68.8%; Pred. No. 2.04e-266;
Matches 179; Conservative 44; Mismatches 33; Indels 4; Gaps 4;

Db 77 YTKLKTATNIYIFNLADALATSTLPFQSAKYIMETWPFGEILLCKAVLSIDYNNMFTSI 136
QY 1 YTKMKTATNIYIFNLADALATSTLPFQSTVYIMNSWPFQDVLCKIVISIDYNNMFTSI 60
Db 137 FTLTMSVDRIYAVCHPVKALDFRTPAKAKLINICIVWLASGVGPIMVMAVTPRDGA- 195
QY 61 FTLTMSVDRIYAVCHPVKALDFRTPLKAKIINICIMWLSSVGSISAIVLGKTKYREDVD 120
Db 196 VV-CMLQFPSPSW-YWDIVTKICVFLFAFVVPILITVCGIMLLRLRSVRLSGSKEKD 253
QY 121 VIECCLOFPDDYSWMDLFMKICVFIFAFVLPVLIITVCGITMLIRLKXVRLSGSREKD 180
Db 254 RSLRITRMVLYVVGAFVVCWAPIHIFVIVTWLVDIRRDPVLVVALHLGIALGYANSSL 313
QY 181 XNLRITRLVLYVAVFVVCWTPIHIFILVEALGSTSHSTA-ALSSYFCIALGYTNSSL 239
Db 314 NPVLYAFLDENFKRCFRQLC 333
QY 240 NPILYAFLDENFKRCFRDFC 259

RESULT 12
ID OPRL RAT STANDARD; PRT; 367 AA.
AC P35370;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
DE RECEPTOR) (KOR-3) (ROR-C) (XOR1).
GN OPRL OR OOR.
OS RATTUS NORVEGICUS (RAT).
OC EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RA SEQUENCE FROM N.A.
RA STRAIN=WISTAR; TISSUE=BRAIN;

RX	MEDLINE; 94215703.
RA	FUJUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H., IWABE N.,
RA	MIYATA T., HOUTANI T., SUGIMOTO T.;
RL	FEBS LETT. 343:42-46(1994).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=HIPPOCAMPUS;
RA	MENG F., XIE G., ALFRED M., THOMPSON R., HOVERSTEN M., WATSON S.,
RA	AKIL H.;
RL	SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX	MEDLINE; 94307401.
RA	BUNZOW J.R., SAEZ C., MORTFJD M., BOUVIER C., WILLIAMS J.T., LOW M.
RA	GRANDY D.K.;
RL	FEBS LETT. 347:284-288(1994).
RN	[4]
RP	SEQUENCE FROM N.A.
RX	MEDLINE; 94307400.
RA	CHEN Y., FAN Y., LIU J., MESTEK A., TIAN M., KOZAK C.A., YU L.;
RL	FEBS LETT. 347:279-283(1994).
RN	[5]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RX	MEDLINE; 95096849.
RA	LACHOWICZ J.E., SHEN Y., MONSMA F.J. JR., SIBLEY D.R.;
RL	J. NEUROCHEM. 64:34-40(1995).
RN	[6]
RP	SEQUENCE FROM N.A.
RC	TISSUE=BRAIN;
RX	MEDLINE; 94298959.
RA	WANG J.B., JOHNSON P.S., IMAI Y., PERSICO A.M., OZENBERGER B.A.,
RA	EPPLER C.M., UHL G.R.;
RL	FEBS LETT. 348:75-79(1994).
RN	[7]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX	MEDLINE; 95182817.
RA	WICK M.J., MINNERATH S.R., LIN X., ELDE R.P., LAW P.Y., LOH H.H.;
RL	BRAIN RES. MOL. BRAIN RES. 27:37-44(1994).
CC	-1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
CC	HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC	INCLUDING INSTINCTIVE BEHAVIOURS AND EMOTIONS. THE ACTIVITY OF
CC	THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC	CYCLASE.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SEVERAL BRAIN AREAS.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR	EMBL; D16438; G5333355; -
DR	EMBL; U05239; G451844; -
DR	EMBL; U01913; G487965; -
DR	EMBL; L28144; G4962220; -
DR	EMBL; U07871; G606803; -
DR	EMBL; L33916; G557200; -
DR	EMBL; L29419; G510719; -
DR	PIR; S46238; S46238.
DR	PIR; S43655; S43655.
DR	GCRDB; GCR_0834; -
DR	GCRDB; GCR_0898; -
DR	GCRDB; GCR_0912; -
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT	DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 48 74 1 (POTENTIAL).
FT	DOMAIN 75 84 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 85 106 2 (POTENTIAL).
FT	DOMAIN 107 121 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 122 143 3 (POTENTIAL).
FT	DOMAIN 144 162 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 163 185 4 (POTENTIAL).
FT	DOMAIN 186 208 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM      209      233      5 (POTENTIAL).
FT DOMAIN        234      261      CYTOPLASMIC (POTENTIAL).
FT TRANSMEM      262      285      6 (POTENTIAL).
FT DOMAIN        286      297      EXTRACELLULAR (POTENTIAL).
FT TRANSMEM      298      319      7 (POTENTIAL).
FT DOMAIN        320      366      CYTOPLASMIC (POTENTIAL).
FT DISULFID      120      197      BY SIMILARITY.
FT LIPID         331      331      PALMITATE (POTENTIAL).
FT CARBOHYD      21      21      POTENTIAL.
FT CARBOHYD      26      26      POTENTIAL.
FT CARBOHYD      36      36      POTENTIAL.
FT CONFLICT      105      105      G -> R (IN REF. 2).
FT CONFLICT      226      226      L -> V (IN REF. 2).
FT CONFLICT      246      246      S -> P (IN REF. 2).
FT CONFLICT      348      348      S -> T (IN REF. 3).
SQ SEQUENCE      367 AA; 40523 MW; 7FD40CCC CRC32;

Query Match          60.3%; Score 1345; DB 1; Length 367;
Best Local Similarity 62.1%; Pred. No. 8.24e-245;
Matches 174; Conservative 46; Mismatches 55; Indels 5; Gaps 5;

Db    77 TKMKTATNIXIENLALADILVLLLPFGQTDILLGFWPFGNALCKTVIAIDYNNMTSTF 136
      ||| ||||| ||||| ||||| ||| : ||| : | : ||| ||| ||| ||| ||| |||
QY   2 TKMKTATNIXIENLALADALVTITMPQSTVYLMSWPFQDVLCIKIVISIDYNNMTSIF 61

Db    137 TLTAMSVDRYVAICHPIRALDVRTSSKAQAVNVAIMALASVGVPAALMGSAQV-EDEF- 194
      || ||||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
QY   62 TLTAMSVDRYIAVCHPVKALDFRTPDKAKIINICIMWLSSSVGISAIVLGGTKVEDVDV 121

Db    195 IECLVEIPAPQDY-WGPVFA-IGTFLESFIIPLLIISVCYSIMIRLRGVRLLSGSREKD 252
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY   122 IECLQEPD-DDYSWMDLFMKICVFIFAFTVPVLIITVCYTMLRLKXVRLLSGSREKD 180

Db    253 RNLRRTRLVLVNAVFVGCPVQVFLVQGLGVQPGESEVAALLRCTALGYNSCLN 312
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||
QY   181 XNLRRTRLVVVAAVFVVCWPTPHIFILVEALGSTSHSLALSYYFCIALGYTNSSLN 240

Db    313 PILYAFLDENFKACFRKFCCASSLHREMÖVSDRVRSIAKD 352
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||
QY   241 PILYAFLDENFKRCFRDCEPLKMXMERXSISRVRTVQD 280

RESULT 13
AC OPBX MOUSE STANDARD; PRG: 367 AA.
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DE 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
DE RECEPTOR) (KOR-3) (ORGC) (K3 OPIATE RECEPTOR).
OS OPR1 OR OPR1 OR OOR.
OS MUS MUSCULUS (MOUSE).
OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6N; TISSUE=BRAIN;
RA YASUDA K., JONES E., REISINE T., BELL G.I.;
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBDJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95100967.
RA NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA MATTHEWS H.W.D.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBDJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A.
RA PAN Y.X., XU J., PASTERNAK G.W.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBDJ DATA BANKS.
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Db 140 TLTMSVDRYVAICHPIRALDVRTSSKAQAVNAIWALASVGVPAIMGSAQV-EDEE- 197
QY 62 TLTMSVDRYIAVCHPVKALDFRTPUKAKIINICIWLLSSSVGISAIVLGGTKVREDVDV 121
Db 198 IECLVEIPDPQDY-WGPVFA-ICIFLFSFVIVPVLIISVCYSLMIRRLRGVRLSGSREKD 255
QY 122 IECCIQFPD-DDYSWMDLFMKICVFIFAFLVPLIIVCYTLMILRLKXVRLLSGSREKD 180
Db 256 RNLRRITRLVLYVVAVFVGCWTPVQVFLVQGLGVQPSSETAVAILRFTALGYVNSCLN 315
QY 181 XNLRRITRLVLYVVAVFVGCWTPHIHIFILVEALGSTSHSTALSSYYFCIALGYTNSLN 240
Db 316 PILYAFIDENFKACFRKFCASALRRDQVSDRVRSIAKDVA 357
QY 241 PILYAFIDENFKRCFRDFCFPLKXMERXSTSRVNTVQDPA 282

RESULT 15
ID OPRX_PIG STANDARD; PRT; 370 AA.
AC P79292;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID RECEPTOR) (KOR-3) (ORGC) (K3 OPIATE RECEPTOR).
GN OPRIL.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX;
RA OSINSKI M.A., PAMPUSCH M.S., BROWN D.R., MURTAUGH M.P.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.
CC HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC INCLUDING INSTINCTIVE BEHAVIORS AND EMOTIONS. THE ACTIVITY OF
CC THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL
CC CYCLASE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U72758; G1763257; -
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 50
FT TRANSMEM 51 77
FT DOMAIN 78 87
FT TRANSMEM 88 109
FT DOMAIN 110 124
FT TRANSMEM 125 146
FT DOMAIN 147 165
FT TRANSMEM 166 188
FT DOMAIN 189 211
FT TRANSMEM 212 236
FT DOMAIN 237 264
FT TRANSMEM 265 288
FT DOMAIN 289 300
FT TRANSMEM 301 322
FT DOMAIN 323 370
FT DISULFID 123 370
FT LIPID 334 334
FT CARBOHYD 21 21
FT CARBOHYD 28 28
FT CARBOHYD 39 39
SQ SEQUENCE 370 AA; 40610 MW; E1050DAC CRC32;

Query Match 59.5%; Score 1327; DB 1; Length 370;
Best Local Similarity 61.3%; Pred. No. 4.85e-241;
Matches 173; Conservative 46; Mismatches 58; Indels 5; Gaps 5;

Db 80 TKMKTATNIYIFNLALADTAVLLTLPFQGDVLLGFWPFGNALCKAVIAIDYYNMTSAP 139

QY 2 TKMKTATNIYIFNLALADALVYTTMPFQSTVYLLMSWPEGDYLCKIVISIDYINMTSIF 61
Db 140 TLTMSVDRYVAICHPIRALDVRTSSKAQAVNAIWALASVGVPAIMGSAQV-EDEE- 197
QY 62 TLTMSVDRYIAVCHPVKALDFRTPUKAKIINICIWLLSSSVGISAIVLGGTKVREDVDV 121
Db 198 IECLVEIPAPQDY-WGPVFA-VCIFLFSFVIVPVLIISVCYSLMVRRLRGVRLLSGSREKD 255
QY 122 IECCIQFPD-DDYSWMDLFMKICVFIFAFLVPLIIVCYTLMILRLKXVRLLSGSREKD 180
Db 256 RNLRRITRLVLYVVAVFVGCWTPVQVFLVQGLGVQPSSETAVAILRFTALGYVNSCLN 315
QY 181 XNLRRITRLVLYVVAVFVGCWTPHIHIFILVEALGSTSHSTALSSYYFCIALGYTNSLN 240
Db 316 PILYAFIDENFKACFRKFCAPTRRREMOVSDRVRSIAKDVA 357
QY 241 PILYAFIDENFKRCFRDFCFPLKXMERXSTSRVNTVQDPA 282

Search completed: Thu Apr 16 13:38:32 1998
Job time : 30 secs.

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M E E E E
(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 16 13:36:28 1998; MasPar time 15.63 Seconds
794.520 Million cell updates/sec
Tabular output not generated.

Title: >US-08-292-694A-12
Description: (1-295) from US08292694A.pep
Perfect Score: 2229
Sequence: 1 YTKMKTATNIYIFNLALADA.....NTVQDPAYLRIDGMNKPV 295

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vertebrate
13:sp_unclassified

Statistics: Mean 46.849; Variance 117.237; scale 0.400

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	1520	68.2	392	2	Q12930 MU OPIOID RECEPTOR VAR	1.74e-225
2	1489	66.8	401	4	P79350 MU OPIOID RECEPTOR.	2.90e-220
3	1461	65.5	383	12	O42324 MU-OPIOID RECEPTOR.	1.50e-215
4	1328	59.6	240	10	Q64120 MU-OPIOID RECEPTOR MOR	3.34e-193
5	856	38.4	117	10	Q60733 KAPPA OPIOID RECEPTOR	1.17e-114
6	643	28.8	119	10	Q64206 DELTA OPIOID RECEPTOR/	6.90e-80
7	635	28.5	98	10	P97266 MU-OPIOID RECEPTOR (FR	1.35e-78
8	522	23.4	372	10	O08726 GALANIN RECEPTOR TYPE	1.74e-60
9	483	21.7	354	10	O35313 CCR5.	2.60e-54
10	474	21.3	354	10	P97405 BETA CHEMOKINE RECEPTO	6.81e-53
11	473	21.2	352	4	O02746 CHEMOKINE RECEPTOR CCR	9.79e-53
12	473	21.2	354	10	P97308 C-C CHEMOKINE RECEPTOR	9.79e-53
13	472	21.2	359	12	P79785 ANGIOTENSIN II RECEPTO	1.41e-52
14	470	21.1	359	10	O35210 ANGIOTENSIN II RECEPTO	2.90e-52
15	468	21.0	352	2	O14705 CCR5 RECEPTOR (FRAGMEN	5.98e-52
16	468	21.0	354	10	O35891 CC CHEMOKINE RECEPTOR-	5.98e-52
17	467	21.0	361	10	O35811 G-PROTEIN COUPLED RECE	8.59e-52
18	461	20.7	333	2	O14694 CCR5 RECEPTOR (FRAGMEN	7.53e-51
19	462	20.7	352	2	O14697 CCR5 RECEPTOR (FRAGMEN	5.24e-51
20	462	20.7	352	2	O14692 CCR5 RECEPTOR (FRAGMEN	5.24e-51

21	462	20.7	352	4	O18770 CCR5 RECEPTOR (FRAGMEN	5.24e-51
22	461	20.7	352	2	O14702 CCR5 RECEPTOR (FRAGMEN	7.53e-51
23	461	20.7	352	2	O15538 CCR5 RECEPTOR (FRAGMEN	7.53e-51
24	461	20.7	352	2	O14699 CCR5 RECEPTOR (FRAGMEN	7.53e-51
25	461	20.7	352	2	O14701 CCR5 RECEPTOR (FRAGMEN	7.53e-51
26	461	20.7	352	2	O14707 CCR5 RECEPTOR (FRAGMEN	7.53e-51
27	461	20.7	352	2	O14700 CCR5 RECEPTOR (FRAGMEN	7.53e-51
28	461	20.7	352	2	O14704 CCR5 RECEPTOR (FRAGMEN	7.53e-51
29	462	20.7	362	12	O91383 ANGIOTENSIN II RECEPTO	5.24e-51
30	459	20.6	352	4	O02778 CC CHEMOKINE RECEPTOR	1.55e-50
31	459	20.6	352	2	O14695 CCR5 RECEPTOR (FRAGMEN	1.55e-50
32	458	20.5	352	2	O14706 CCR5 RECEPTOR (FRAGMEN	2.22e-50
33	457	20.5	352	4	O18772 CCR5 RECEPTOR (FRAGMEN	3.19e-50
34	455	20.4	352	2	O14696 CCR5 RECEPTOR (FRAGMEN	6.57e-50
35	454	20.4	352	2	O14703 CCR5 RECEPTOR (FRAGMEN	9.43e-50
36	453	20.3	352	2	O14693 CCR5 RECEPTOR (FRAGMEN	1.35e-49
37	450	20.2	383	11	O89609 G PROTEIN-COUPLED RECE	3.99e-49
38	449	20.1	352	4	O18771 CCR5 RECEPTOR (FRAGMEN	5.72e-49
39	448	20.1	352	2	O14698 CCR5 RECEPTOR (FRAGMEN	8.20e-49
40	445	20.0	344	2	O15133 PURINERGIC RECEPTOR P2	2.42e-48
41	444	19.9	352	2	O14708 CCR5 RECEPTOR (FRAGMEN	3.46e-48
42	442	19.8	678	3	O94736 TACHYKININ-LIKE RECEPT	7.11e-48
43	436	19.6	353	12	P79960 MESENCHYME-ASSOCIATED	6.15e-47
44	415	18.6	238	12	O92158 ANGIOTENSIN II RECEPTO	1.14e-43
45	415	18.6	360	4	O18793 CHEMOKINE RECEPTOR.	1.14e-43

ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	392 AA.
AC	Q12930;			
DI	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DI	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DI	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	MU OPIOID RECEPTOR VARIANT.			
GN	MORL.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RX	MEDLINE; 95046336.			
RA	BARE L.A., MANSON E., YANG D.;			
RL	FEBS LETT. 354:213-216(1994).			
RN	[2]			
RP	SEQUENCE OF 1-388 FROM N.A.			
RC	TISSUE=BRAIN;			
RX	MEDLINE; 94139928.			
RA	WANG J.B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,			
RA	UHL G.R.;			
RL	FEBS LETT. 338:217-222(1994).			
DR	EMBL; U12569; G607912; .			
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.			
FT	VARIANT 40 D -> N (IN REF. 2).			
FT	VARIANT 51 D -> N (IN REF. 2).			
FT	VARIANT 207 I -> M (IN REF. 2).			
FT	VARIANT 234 L -> V (IN REF. 2).			
SO	SEQUENCE 392 AA; 43939 MW; 3359DDB4 CRC32;			
Query Match				
Best Local Similarity 68.2%; Score 1520; DB 2; Length 392;				
Matches 188; Conservative 43; Mismatches 46; Indels 3; Gaps 3;				
Db	98 YTKMKTATNIYIFNLALADALATSTLPFGQSYNYIMGWTPFGTTLCKIYISIDYNNMTSI	157		
QY	1 YTKMKTATNIYIFNLALADALVTTIMPFQSTIYILMSWPFQDVLCIYISIDYNNMTSI	60		
Db	158 FTLCMSVDRIYAVCHPVKALDFRIPRNKILINVCNWLSSAIGLPVFIATTKYRG-S	216		
QY	61 FTLTMSVDRIYAVCHPVKALDFRIPRNKILINVCNWLSSAIGLPVFIATTKYRG-S	120		


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Db      217 -IDCITLTHSHPTW-YWENLKKICVFIEAFIMPVLIITVCYXGIMILRLKSVRMJSGSKEXD 274
      | : | | : | : : | | | | | : | | | | | | : | | : | |
QY      121 VTECCTLPDPDDYSWMDLFMKICVFIEAFVIVPLIITVCYTLMLRLKXVRLJSGSREKD 180
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      275 RNLRRITRMVLVWVAVFIVCWTPIHIVYIKALVTIPETTFQIVSWHFCIALGYTNSCLN 334
      | | | | | | | | | | | | | | | : : | : | | | | | | | |
QY      181 XNLRRIITRYLVWVAVFVVCWTPIHITLLVEALGSTSHSTALSSYYFCIALGYTNSCLN 240
      | | | | | | | | | | | | | | | : : | : | | | | | | | |
Db      335 PVLVAFLEDNFKRCFRBFCIPTSSNTEQONSTRIRQNTRPD 374
      | : | | | | | | | | | | | | | : : | : : | : | : |
QY      241 PIIYAFLEDNFKRCFRDFCFPLKMXMERKXSTSRVRYNTVQD 280

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RESULT	2		
ID	P79350	PRELIMINARY;	PRT; 401 AA.
AC	P79350;		
DT	01-MAY-1997	(TREMBLREL. 03, CREATED)	
DT	01-MAY-1997	(TREMBLREL. 03, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998	(TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE	MU OPIOID RECEPTOR.		
OS	BOS TAURUS (BOVINE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; ARTIODACTYLIA.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=STRIATUM;		
RA	SIMON E.J., VILLEM S., ANDRIA M., ONOPRISHVILI I., HILLER J.M.;		
RL	SUBMITTED (MAR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
DR	EMBL; 089677; GI881731; -.		
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.		
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.		
SQ	SEQUENCE 401 AA; 45045 MW; 5673B9B8 CRC32;		

Query Match	66.8%;	Score 1489;	DB 4;	Length 401;
Best Local Similarity	66.1%;	Pred. No. 2.90e-220;		
Matches	185;	Conservative	45;	Mismatches 47;
			Indels	3;
			Gaps	3;

Db	99	YTKMKTATNIXIFENFALADALATSTLPFQSVNylmgTWpEgTlCKIVISIDYNNMFTSI	158
QY	1	YTKMKTATNIXIFENFALADALATSTLPFQSVNylmNSWpEGDVLCKIVISIDYNNMFTSI	60
Db	159	FTLCMSVDXYIACVCHPVKALDERTPRNAKIINICNWIITSSATGLPVMFMATKRYRQG-S	217
QY	61	FTLCMSVDXYIACVCHPVKALDERTPTLKAKITINICWLTSSVGISAIVLGGTKREDVD	120
Db	218	-IDSTTFESHPTW-YWENLKTQVEIFAFIMPLILITVYCGLMILRKSVRMLSGSKEKD	275
QY	121	VIECQLQEPDDDYSSWMDLEMKICVFIFAFVIPVLITIVCYTLMILRLKXVRLLSGSREKD	180
Db	276	RNLRTITRMVLVVAVFIVCWMPIHIYVILKALITIPETTFQIVSWHFCIALGYNSSCLN	335
QY	181	XNLRTITRLVLVVAVFVVCWMPHIFILVYALGSTSHSTAALSSYFCIALGYNSSSLN	240
Db	336	PVLYAFLDENFKRCFRECIPITSSTIEQNSTRIKQNRD	375
QY	241	PVLYAFLDENFKRCFRECIPPLKMXMERKXSTSRVRNTYQD	280

RESULT	3		
ID	042324	PRELIMINARY;	PRT; 363 AA.
AC	042324;		
DT	01-JAN-1998 (TREMBLREL. 05, CREATED)		
DT	01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)		
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)		
DE	MU-OPIOID RECEPTOR.		
OS	CATOSTOMUS COMMERSONI (WHITE SUCKER).		
OC	EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; PISCES; GNATHOSTOMATA;		
OC	OSTEICHTHYES; ACTINOPTERYGII; CYPRINIFORMES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=CNS;		
RA	DARLISON M.G., HARVEY R.J., GRETEN F.R., KREIENKAMP H.J., ZWIERS H.,		

RA STEINER T., LEDERIS K., RICHTER D.;
RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; Y10904; E1169530; -!
DR DR PROTEIN; PS00237; G-PROTEIN RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SQ SEQUENCE 383 AA; 43232 MW; 00BDCBD CRC32;

Query Match	65.5%;	Score 1461;	DB 12;	Length 383;
Best Local Similarity	65.1%;	Pred. No. 1.50e-215;		
Matches	183;	Mismatches 42;	Indels 6;	Gaps 4;

Db	85	YTKMKTATNIYIFNNLALADALATSTLEFQSYNXYLMGTWPEFGDVYCKIWMSIDYNNMTSTI	144
QY	1	YTKMKTATNIYIFNNLALADALVTTTMEFQSTVYLLMNSWPEFGVLCCKIIVISIDYNNMFTSI	60
Db	145	FTLTMTSDIRYIAVCHPVKALDFRTPRNAKIVNCWNLISSAIGLPVYMWMASTTIENONS	204
QY	61	FTLTMTMSVDRIYAVCHPVKALDFRTPRLAKIINICIMWLTSSSVGISATVLGGTKV-RED-	118
Db	205	PLQVSNEDCTLLFPHPPW-YWETLLIKICVEILAFIMPVLITTYCYGIMLRKXVRMTSG	263
QY	119	-VDV-IECLOQFPDDDYSWWDEMKICVFIFAFVIVPVLIIYCYTILMLRLKXVRMTSG	175
Db	264	SKEKDRNLRTTRMVLVNVVAVEFICWTPPIHIFVILKALVTPINSLFQVTWHEFCIALGYT	323
QY	176	SREKDXNLRTRTLRVLVVVAVEVCWTPPIHIFILVEALGSTSHSTAALSSYYFCIALGYT	235
Db	324	NSCLNFPVLYAFLDENFKRCFREFCVPSPSVLDLQNSTRNNSN	364
QY	236	NSSLNPILYAFLDENFKRCFRDECFPLKMXMERXSTSRVRN	276

RESULT	4	
ID	Q64120	PRELIMINARY; PRT; 240 AA

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE MU-OPIOID RECEPTOR MOR (FRAGMENT).
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95251654.
RA SEDQI M., ROY S., RAMAKRISHNAN S., ELDE R., IOH H.H.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 209:563-574(1995).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; S77863; E199500; ~.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT NON_TER 1 1
SQ SEQUENCE 240 AA; 27408 MW; D3C58BFF CRC32;

Query Match	59.6%;	Score 1328;	DB 10;	Length 240;
Best Local Similarity	68.38;	Pred. No. 3.34e-193;		
Matches	166;	Conservative	36;	Mismatches 38;
			Indels	3;
			Gaps	3;

[illegible]

QY 186 ITRVLVWVAVFVWCWTPRIHIFLVEALGSTSHSTAALSYEFCIALGYTNSLNPLLYA 245
Db 238 FLD 240
QY 246 FLD 248

RESULT 5
ID Q60733 PRELIMINARY; PRT; 117 AA.
AC Q60733;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE KAPPA OPIOID RECEPTOR (FRAGMENT).
GN OPRK1.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA GRANDY D.K.;
RL SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; U16998; G595937; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT NON_TER 1 1
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13071 MW; FCGF68EI CRC32;

Query Match 38.4%; Score 856; DB 10; Length 117;
Best Local Similarity 96.6%; Pred. No. 1.17e-114;
Matches 113; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 YTKMKATNIYIFNLADALVTTTTFQSAVYLMNSWPEGVLCIKIVISIDYNNFTSI 60
QY 1 YTKMKATNIYIFNLADALVTTTTFQSTVYLMNSWPEGVLCIKIVISIDYNNFTSI 60
Db 61 FTLLTMSVDRIYAVCHPVKALDFRTPKAKIINICIWLLASSVGSAILVLGTVRE 117
QY 61 FTLLTMSVDRIYAVCHPVKALDFRTPKAKIINICIWLLSSVGSAILVLGTVRE 117

RESULT 6
ID Q64206 PRELIMINARY; PRT; 119 AA.
AC Q64206;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (TREMBLREL. 01, LAST ANNOTATION UPDATE)
DE DELTA OPIOID RECEPTOR/DOR (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA ROY S., SEDOI M., RAMAKRISHNAN S., BARKE R.A., LOH H.H.;
RL CELL. IMMUNOL. 169:271-277(1996).
DR EMBL; S81965; E257299; -.
FT NON_TER 1 1
SQ SEQUENCE 119 AA; 13380 MW; DFC85C30 CRC32;

Query Match 28.8%; Score 643; DB 10; Length 119;
Best Local Similarity 66.9%; Pred. No. 6.90e-80;
Matches 81; Conservative 18; Mismatches 19; Indels 3; Gaps 3;

Db 1 IFTLLTMSVDRIYAVCHPVKALDFRTPKAKIINICIWLLASGVYPIVMVAVTQPRDGA 60
QY 60 IFTLLTMSVDRIYAVCHPVKALDFRTPKAKIINICIWLLSSVGSAILVLGTVRE 119
Db 61 -LV-CMLQPPSPSW-YWDIVTKICVELFAVVPILITVYGLMLRLRSVRLSGSKEK 117
QY 120 DVIECCLOFPDDYSWMDLFMKICVFIFAFVIFVLIITVCTIMILRLKXVRLLSGSREK 179

Db 118 D 118
QY 180 D 180

RESULT 7
ID P97266 PRELIMINARY; PRT; 98 AA.
AC P97266;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE MU-OPIOID RECEPTOR (FRAGMENT).
OS CAVIA PORCELLUS (GUINEA PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA RONNEKLEIV O.K., BOSCH M.A., CUNNINGHAM M.J., WAGNER E.J.,
RA GRANDY D.K., KELLY M.J.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL; U67928; G1763013; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT NON_TER 1 1
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11161 MW; 28F749E6 CRC32;

Query Match 28.5%; Score 635; DB 10; Length 98;
Best Local Similarity 81.6%; Pred. No. 1.35e-78;
Matches 80; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Db 1 YTKMKATNIYIFNLADALATSTLFPQSVNYIMGTWPFGLICKIVISIDYNNFTSI 60
QY 1 YTKMKATNIYIFNLADALVTTTTFQSTVYLMNSWPEGVLCIKIVISIDYNNFTSI 60
Db 61 FTLLTMSVDRIYAVCHPVKALDFRTPKAKIINICIW 98
QY 61 FTLLTMSVDRIYAVCHPVKALDFRTPKAKIINICIW 98

RESULT 8
ID O08726 PRELIMINARY; PRT; 372 AA.
AC O08726;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE GALANIN RECEPTOR TYPE 2.
GN GALR2.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HYPOTHALAMUS;
RA HOWARD A.D., TAN C., SHIAO L.L., PALYHA O.C., MCKEE K.K.,
RA WEINBERG D.H., FEIGNER S.D., CASCIERI M.A., SMITH R.G., PLOEG L.H.T.,
RA SULLIVAN K.A.;
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RA SMITH K.E., FORRAY C., WALKER M.W., JONES K.A., TAMM J.A., BARD J.,
RA BRANCHER T.A., LINEMEYER D.L., GERALD C.;
RL J. BIOL. CHEM. 272:24612-24616(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA SMITH K.E., FORRAY C., WALKER M., JONES K.A., TAMM J.A., BARD J.,
RA BRANCHER T.A., LINEMEYER D.L., GERALD C.;
RL SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A.
RA WANG S., HASHEMI T., HE C., STREADER C., BAYNE M.,
RL MOL. PHARMACOL. 52:337-343(1997).

Db 1 mespiqifrgdpgptcpsacilpnssswfpuwaesdngsvgsedqqlsahispaipv 60
QY 1 MESPIQIFRGDPGPTCPSACILPNSSSWFPNWAESDSNGSVGSEDQQLSAHISPAPV 60
Db 61 itavysvfvvlgvlgvnslymfviirytktmktatniyifnlaladalvtttmpfgsavy1 120
QY 61 IITAVYSVFEVVGVLGNSLYMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFGSAVYL 120
Db 121 mnswpfgdvclckivisidyymftsiflttmmsvdryiavchpvpkaldfrtbpkakiini 180
QY 121 MNSWPFEGDVLCKIVISIDYYNMTSIFLTMTMSVDRIYAVCHPVPKALDFRTPKAKIINI 180
Db 181 ciwllassvgisaivlgtkvredvdviesclqfpddeyswdlfmkicvfvfafvipvl 240
QY 181 CIWLLASSVGISAIVLGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFVIPVL 240
Db 241 iivcytlmilrlksvrlsgsrekdrnlrritklvlyvvavfiicwtpihifilvealg 300
QY 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVLVYVAVFIICWTPIHIFILVEALG 300
Db 301 stshstaalssyyfcialgytnsslnpvyafldenfkrcfrdfcfpikmmergstnrv 360
QY 301 STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMMERGSTNRV 360
Db 361 rntvqdpasmrdvggmkrpv 380
QY 361 RNTVQDPASMRDVGGMKRPV 380

RESULT 2
ID R76783 standard; Protein; 380 AA.
AC R76783;
DT 11-DEC-1995 (first entry)
DE Rat kappa opiate receptor.
KW Kappa opiate receptor; mu opiate receptor; hMOR; opiate agonist;
KW opiate antagonist; drug abuse; analgesic.
OS Rattus sp.
PN W09520667-A1.
PD 03-AUG-1995.
PF 30-JAN-1995; U01144.
PR 28-JAN-1994; US-188275.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
DR WPI; 95-275452/36.
PT New DNA encoding human mu opiate receptor - used esp. for screening
PT cpds. for activity as opiate agonists or antagonists
PS Disclosure; Page 29-30; 49pp; English.
CC hMOR cDNA was obt'd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. The encoded
CC protein showed homology to rat mu, delta and kappa opiate
CC receptors (R76781-83).
SQ Sequence 380 AA;

Query Match 99.6%; Score 2829; DB 13; Length 380;
Best Local Similarity 98.9%; Pred. No. 7.76e-256;
Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 mespiqifrgepgptcapsacilpnssswfpuwaesdngsvgsedqqlsahispaipv 60
QY 1 MESPIQIFRGDPGPTCPSACILPNSSSWFPNWAESDSNGSVGSEDQQLSAHISPAPV 60
Db 61 itavysvfvvlgvlgvnslymfviirytktmktatniyifnlaladalvtttmpfgsavy1 120
QY 61 IITAVYSVFEVVGVLGNSLYMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFGSAVYL 120
Db 121 mnswpfgdvclckivisidyymftsiflttmmsvdryiavchpvpkaldfrtbpkakiini 180
QY 121 MNSWPFEGDVLCKIVISIDYYNMTSIFLTMTMSVDRIYAVCHPVPKALDFRTPKAKIINI 180
Db 181 ciwllassvgisaivlgtkvredvdviesclqfpddeyswdlfmkicvfvfafvipvl 240
QY 181 CIWLLASSVGISAIVLGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFVIPVL 240

Db 241 iivcytlmilrlksvrlsgsrekdrnlrritklvlyvvavfiicwtpihifilvealg 300
QY 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVLVYVAVFIICWTPIHIFILVEALG 300
Db 301 stshstaalssyyfcialgytnsslnpvyafldenfkrcfrdfcfpikmmergstnrv 360
QY 301 STSHSTAALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMMERGSTNRV 360
Db 361 rntvqdpasmrdvggmkrpv 380
QY 361 RNTVQDPASMRDVGGMKRPV 380

RESULT 3
ID R72591 standard; Protein; 380 AA.
AC R72591;
DT 01-DEC-1995 (first entry)
DE Mammalian kappa opioi'd receptor protein.
KW Mammalian kappa opioi'd receptor; mouse delta opioi'd receptor; analgesic;
KW amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
FH Key location/Qualifiers
FT CDS 111..1253
FT /*tag= a
FT /product= kappa opioi'd receptor
PN J07070191-A.
PD 14-MAR-1995.
PE 30-JUL-1993; 190261.
PR 09-JUL-1993; JP-170591.
PA (TAKE) TAKEDA CHEM IND LTD.
DR WPI; 95-144857/19.
DR N-PSDB; Q86725.
PT Kappa opioi'd receptor protein and cells expressing it - useful
PT for the screening of compounds for analgesic and hypnotic
PT properties
PS Claim 2; Page 9-10; 15pp; Japanese.
CC The amino acid sequence of the novel mammalian kappa opioi'd receptor.
CC The gene was isolated by amplifying a fragment from rat brain mRNA by
CC reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
CC the mouse delta-opioi'd receptor gene. This fragment was cloned into the
CC plasmid pCRII to produce pRII. The plasmid pRII was used to probe a rat
CC brain DNA library in lambda ZAPII to obtain a clone of the rat kappa
CC opioi'd receptor gene, designat'd pKOPR2. This clone was introduced into
CC E.coli JM109 for production of the receptor protein. The receptor protein
CC is useful for screening of analgesic and hypnotic compounds including
CC peptides and proteins.
SQ Sequence 380 AA;

Query Match 99.4%; Score 2823; DB 13; Length 380;
Best Local Similarity 98.7%; Pred. No. 2.94e-255;
Matches 375; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Db 1 mespiqifrgepgptcapsacilpnssswfpuwaesdngsvgsedqqlsahispaipv 60
QY 1 MESPIQIFRGDPGPTCPSACILPNSSSWFPNWAESDSNGSVGSEDQQLSAHISPAPV 60
Db 61 itavysvfvvlgvlgvnslymfviirytktmktatniyifnlaladalvtttmpfgsavy1 120
QY 61 IITAVYSVFEVVGVLGNSLYMFVIIRYTKMKTATNIYIFNLALADALVTTTMPFGSAVYL 120
Db 121 mnswpfgdvclckivisidyymftsiflttmmsvdryiavchpvpkaldfrtbpkakiini 180
QY 121 MNSWPFEGDVLCKIVISIDYYNMTSIFLTMTMSVDRIYAVCHPVPKALDFRTPKAKIINI 180
Db 181 ciwllassvgisaivlgtkvredvdviesclqfpddeyswdlfmkicvfvfafvipvl 240
QY 181 CIWLLASSVGISAIVLGTKVREDVDVIECSLQFPDDEYSWDLFMKICVFVFAFVIPVL 240
Db 241 iivcytlmilrlksvrlsgsrekdrnlrritklvlyvvavfiicwtpihifilvealg 300
QY 241 IIVCYTLMILRLKSVRLSGSREKDRNLRRITKLVLVYVAVFIICWTPIHIFILVEALG 300

Db 301 stshstaviessyfciaiglytnsslmpvlyafidenfkrcfrdfcfplkmmmergstnr 360
QY 301 STSHSTAALSSYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMMERQSTNRV 360
Db 361 rntvqdpasmrdrvqgmknkp 380
QY 361 RNTVQDPASMRDVGGMKNKP 380

RESULT 4

ID R88722 standard; Protein; 380 AA.
AC R88722;
DT 04-SEP-1996 (first entry)
DE Human kappa opioid receptor.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular; neurology; diagnosis.
OS Homo sapiens.
PN WO9601898-A1.
PD 25-JAN-1996.
PF 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B, Simonin F;
DR WPI; 96-097628/10.
DR N-PSDB; T12550.
PT New nucleic acid encoding the human Kappa opioid receptor - useful in diagnosis and therapy, and for isolating receptor ligands and modulators
PT Claim 7; Page 13-15; 30pp; French.
PS The sequence coding for the human kappa opioid receptor was obtained from two overlapping cDNA fragments isolated from a human placental cDNA library. The fragments were amplified from the library using PCR primers based on the sequence of human genomic clones which hybridised with a murine delta receptor cDNA probe. Nucleotide probes derived from the kappa opioid receptor coding sequence are useful for diagnosis of neurological, cardiovascular and psychiatric disorders associated with opioid receptors. The receptor can be used for identifying e.g. agonists of its activity for potential use as analgesics.
SQ Sequence 380 AA;

Query Match 96.7%; Score 2746; DB 17; Length 380;
Best Local Similarity 93.7%; Pred. No. 7.80e-248;
Matches 356; Conservative 18; Mismatches 6; Indels 0; Gaps 0;

Db 1 mdsplqifrgpgptcspacplpnssawfpgwaepdngsagsedaglepahispaip 60
QY 1 MESPIQIFRGDPTCSPACLLPNSSSWFPMWAESDSNGSVGEDQLESAAHISPAIPV 60
Db 61 iitavysvfvvglyvgnslvmfviirymkktatniyifnlaladalvttmpfgstvy 120
QY 61 IITAVYSVYVVGVLGNSLVMFVIRYTKMTATNIYIFNLALADALVTTMPFGSAVYL 120
Db 121 mnswpfgdvclckivisidyymftsifltmmsvdryiaavchpvkaldftrtlkakini 180
QY 121 MNSWPFGDVCLCKIVISIDYNNMFTSIFLTMMSVDRYIAVCHPVKALDERTPPLKAKIINI 180
Db 181 ciwlsssvgisaiivlgtkvredvdiacsqfipddyswdlfnkicvfifafvipy 240
QY 181 CIWLSSVGISAIIVLGGTKVREDVDIECSLQFPDDEYSWWDLFMKICVFVEAFVIPVL 240
Db 241 iivvcytlmlrlksvrlsgrsrekdrnlrrltrlvavavfvcwpphifilvealg 300
QY 241 IIVVCYTLMLRLKSVRLSGRSREKDRNLRLTRLVAVAVFVLCWPIPHIFILVEALG 300
Db 301 stshstaalssyfciaiglytnsslmpvlyafidenfkrcfrdfcfplkmmmergst 360
QY 301 STSHSTAALSSYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFCFPIKMMERQSTNRV 360
Db 361 rntvqdpaylridigmkp 380
QY 361 RNTVQDPASMRDVGGMKNKP 380

RESULT 5
ID R67672 standard; Protein; 295 AA.
AC R67672;
DT 18-AUG-1995 (first entry)
DE Human kappa opioid receptor partial protein.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify; transmembrane domain; somatostatin; receptor; human; expression vector; truncate; chimeraic; assay; probe.
OS Homo sapiens.
FH Key Location/Qualifiers

FT Misc_difference 169
FT /label= Any amino acid
FT Misc_difference 181
FT /label= Any amino acid
FT Misc_difference 265
FT /label= Any amino acid
FT Misc_difference 269
FT /label= Any amino acid
PN WO9428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR N-PSDB; Q75931.
PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in screening assays for useful drug substances.
PS Claim 12; Page 236-239; 300pp; English.
CC The partial amino acid sequence of the novel human kappa opioid receptor.
CC The corresponding gene was isolated from a human brain hippocampus cDNA library using a probe from the mouse kappa opioid receptor gene (Q75926).
CC The gene is missing the N-terminal sequence. The C-terminal sequence is very similar to the mouse kappa opioid receptor sequence. Of the C-terminal 293 amino acids, 281 residues are identical and 6 residues have conservative substitutions. The gene encoding the human opioid receptor can be placed in a suitable expression vector for production of the protein in a cell. The opioid receptors thus produced are useful for the development of novel assays designed to select or improve substances, capable of interacting with the opioid receptor proteins, for use in diagnosis, drug design and therapeutic applications.
SQ Sequence 295 AA;

Query Match 75.0%; Score 2130; DB 12; Length 295;
Best Local Similarity 92.5%; Pred. No. 1.53e-168;
Matches 273; Conservative 13; Mismatches 8; Indels 1; Gaps 1;

Db 1 ytkmktatniyifnlaladalvttmpfgstvylnmswpfgdvclckivisidyymfts 60
QY 87 YTKMKTATNIYIFNLALADALVTTMPFGSAVYIMNSWPFGDVCLCKIVISIDYNNMFTSI 146
Db 61 fltmmvsdryiaavchpvkaldftrtlkakiniiciwlsssvgisaiivlgtkvregvd 120
QY 147 FLTMMVSDRYIAVCHPVKALDFTRTLKAKIINICIWLLASSVGISAIVLGGTKVREDVD 206
Db 121 vieccldfipddyswdlfnkicvfifafvipyliiivvcytlmlrlksvrlsgrsrek 180
QY 121 VIECCLDIFPDDYSWDLFNKICVFIFAFVIPPYLIIVVCYTLMLRLKSVRLSGSREKD 266
Db 207 viecsldfipddeswldfmkicvveafvipyliiivvcytlmlrlksvrlsgrsrek 266
QY 207 VIECSLDFIPDDEYSWDLFMKICVVEAFVIPPYLIIVVCYTLMLRLKSVRLSGSREKD 266
Db 181 xnlrrltrlvavavfvcwpphifilvealgstshstaalssyfciaiglytnssl 240
QY 181 RNLRLTRLVAVAVFVLCWPIPHIFILVEALGSTSHSTAALSSYFCIALGYTNSSLN 326
Db 241 pilayafidenfkrcfrdfcfplkmmmerxstsrvtvqdpaylreidgmknkp 295
QY 241 PILYAFIDENFKRCFRDFCFPIKMMERQSTNRVNTVQDPASMRDVGGM-NKPV 380

RESULT 6

ID	R65188	standard; Protein; 356 AA.
AC	R65188;	
DT	19-APR-1995	(first entry)
DE	Murine mu-subtype opioid receptor.	
KW	Mu-subtype opioid receptor; MSOR; drug addiction.	
OS	Rattus rattus.	
FH	Key	Location/Qualifiers
FT	Modified_site	10..12
FT	/note= "putative N-linked glycosylation site"	
FT	Modified_site	230
FT	/note= "Threonine residue especially favourable for protein kinase A phosphorylation"	
FT	Region	25..48
FT	/note= "hydrophobic membrane spanning region"	
FT	Region	58..78
FT	/note= "hydrophobic membrane spanning region"	
FT	Region	96..118
FT	/note= "hydrophobic membrane spanning region"	
FT	Region	139..166
FT	/note= "hydrophobic membrane spanning region"	
FT	Region	187..212
FT	/note= "hydrophobic membrane spanning region"	
FT	Region	236..257
FT	/note= "hydrophobic membrane spanning region"	
FT	Region	274..294
FT	/note= "hydrophobic membrane spanning region"	
PN	EP-612845-A.	
PD	31-AUG-1994.	
PR	09-FEB-1994; 101968.	
PI	26-FEB-1993; US-026140.	
PA	(AMCY) AMERICAN CYANAMID CO.	
DR	Corbett MJ, Eppler CM, Shieh H, Zysk JR; MPI; 94-265963/33.	
DR	N-PDB; Q79199.	
PT	Pure mu-type opioid receptor protein - and nucleic acid coding for it	
PS	Claim 2; Fig 9; 39pp; English.	
CC	R65188 is the rat mu-subtype opioid receptor protein purified from rat brain membranes, with biotinyl-D-endorphin (R56666) as its ligand. It is encoded by the nucleotide sequence Q79199 which was synthesised using Q71022 and Q71023 as PCR primers. R65188 is useful for identifying othe receptor subtypes, for screening new opioid ligands, and for studying mechanisms of opioid action, e.g. drug addiction.	
SQ	Sequence	356 AA;

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Query Match          59.3%; Score 1683; DB 11; Length 356;
Best Local Similarity 62.8%; Pred. No. 1.15e-145;
Matches 213; Conservative 60; Mismatches 62; Indels 4; Gaps 4;

Dd      3 septlgndslcpqtgspsmvtaitalmlysiwcvglfngflvmvivrytkmkatn 62
        |:| |:| :|:| | :|:| |:|:|:| | ||| | |||:|:| |||||
Qy      36 SDSNGSVGSEDDQLESAHSIPAIPVITTAIVSYVFVGVGLVGNLSVMFEVIIRYTKMKATN 95
Dd      63 iylfnlaladalatstlpfqswnylmgtpwfgtlilcklvisidyyrnftsiftlctmsvd 122
        ||||||| ||| |:|:| | | | |||:|:| ||||| ||||| |||
Qy      96 IYIFNLALADALVTTPMPFQSAAVYLIMNSWPFGDVLCKIYISIDYYNMFTSIFTLTMSVD 155
Dd      123 ryiaavchpykaldfrtprnakivncwilssaiqlpymfmattkyrg-s-idctlfs 180
        ||||||| ||||| |:|:| | |:|:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy      156 RYIAVCHPYKALDFRPPLAKIINICIMWLASSVGISAIVIGSTKVREDVDVIECSIQFP 215
Dd      181 hptw-ywenllkiavifafimpvliitvcyglmrlrksvrmlsgskekdnlrritm 239
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy      216 DDEYSWMWDLFMKICVEFAFVIPVLIITVCYTIMITRLKSRYLLSGSRKDRNLRRITKL 275
Dd      240 vlvvvavfiwcwtpihlyvikalilitipettftqtswhfcialgytnsclnpylaflde 299
        ||||||| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy      276 VLVVVAVFIICWTPIHIFILVEALGSTSHSTAALLSSYFCIALGYTNSSLNPVLYAFLDE 335
Dd      300 nfkrcrfeciptsstlegqnstrvrntrehpstantv 338
        ||||||| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Qy      336 NEKRRCFRDFCFPIKRMEROSTNRVR-NTVQDPASMRDV 373

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RESULT      7
ID      R71966 standard; Protein; 400 AA.
AC      R71966;
DT      20-OCT-1995 (first entry)
DE      Human mu opioid receptor.
KW      Mu opioid receptor; MOR; gene therapy; diagnostic.
OS      Homo sapiens.
PN      WO9507983-A.
PD      23-MAR-1995.
PF      13-SEP-1994; U10358.
PR      13-SEP-1993; US-120601.
PA      (INDV ) UNIV INDIANA FOUND.
PI      Yu L;
DR      WPI; 95-131351/17.
DR      N-PSDB: Q89226.
PT      New nucleic acid encoding new human mu opioid receptor - and
PT      related vectors, transformed cells, antibodies etc., useful in
PT      diagnosis, treatment and drug screening.
PS      Claim 4; Page 211-214; 266pp; English.
CC      A cDNA library constructed from human caudate nucleus mRNA was
CC      screened with rat mu opioid receptor cDNA under conditions of
CC      low stringency. One positive clone included the sequence given in
CC      Q89226, encoding a mu opioid receptor MOR (R71964). The cDNA
CC      is used for prodn. of recombinant MOR, in gene therapy, etc.
SQ      Sequence 400 AA;

Query Match      59.1%; Score 1677; DB 13; Length 400;
Best Local Similarity 66.6%; Pred.No.4.31e-145;
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

Db 70 aitimalysivcvgglfgnfiymyivirytkmktatniyifnaladalatstlpfgsvn 129
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 59 FVITAVYSVFEVGLVGNSTLMEFVIRYTKMKTATNIYIFNLADALVTTPMFOSAV 118
   130 ylmgtwpgftlclckivisiayymftsiftlctmsvdryiavchpykaldfrtpnakil 189
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 119 YLMSWPEFGDYLCKIVISIDYNNMFTSIFTLTMSVDRIYAVCHPYKALDERTPKAKII 178
   190 nvcnwllssaiglpymfmatkkyrg-s-idctltfsbptw-ywenllkicvfifafimp 246
   ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 179 NICIWLLASSVGISAIVLGGIKVREDVDVIECSLQFPDDEYSWMDLFMKICVFVFAFVIR 238
   247 vliitvcyglmrlrksvmlsgskekdnlrritrmvlyvvavfiwcwtpbihyviika 305
   |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 239 VLIITVCYTLMLRLKSVRLLSGSRKDRNLRRITKVLVYVAVFIICWTPIHIFILVEA 298
   Db 307 lvtipettftvswfhciaigytnsclnpvllyafldenfkrcfrcfciptsnieqgst 366
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 299 LGSTSHSTAALSSYFCIALGYTNSSLNPVLYAFLDENFKRCFRDFOPIKRMEROSTN 358
   Db 367 rirgntrdhps 377
   |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 359 RVRNIVQDPAS 369

RESULT      8
ID      R76781 standard; Protein; 398 AA.
AC      R76781;
DT      11-DEC-1995 (first entry)
DE      Rat mu opiate receptor.
KW      Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
KW      drug abuse; analgesic.
OS      Rattus sp.
PN      WO9520667-A1.
PD      03-AUG-1995.
PF      30-JAN-1995; U01144.
PR      28-JAN-1994; US-188275.
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA      (USSH ) US SEC DEPT HEALTH.
PI      Johnson PS, Persico AM, Uhl G, Wang J;
WPI: 95-275452/36.

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PI New DNA encoding human mu opiate receptor - used esp. for screening
PI cpds. for activity as opiate agonists or antagonists
PS Disclosure, Page 26-28; 49pp; English.
CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. The encoded
CC protein showed homology to rat mu, delta and kappa opiate
CC receptors (R76781-83).
SQ Sequence 398 AA;

Query Match	59.0%;	Score 1676;	DB 13;	Length 398;
Best Local Similarity	66.1%;	Pred. No. 5.37e-145;		
Matches	209;	Mismatches 50;	Indels 4;	Gaps 4;

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Db 68 aialmalysivcvgvlfgnflvmyvlyvtlkmktatniyifnlaladlatstlpfgsvn 127
QY 59 PVIITAVYSVWFVWGLVGNLSYMHVYIRYTKMKTATNIYIFNLALADALVTITMPQOSAV 118
Db 128 ylmgtwpgftlclckivisidymnftsiftlctmsvdryiavchpvkalftrpnakiv 187
QY 119 YIMNSWPFPGDVLCKIVISIDYXNMFTSIFTLTMSVDRIYAVCHPVKALDFRTPKAKII 178
Db 188 nvcnwilssaiglpvmfmatkkyrgs-idctltfshtw-ywenllkicvifafimp 244
QY 179 NICIWLASSVGISAIVLGITKVRBDVDYIECSLQFPDDEXSWWDLFMKICVFVEAFVIP 238
Db 245 vlitvcyglmilrlksvrmllsgskekdnlrritrmvllvvavfivcwtphihyika 304
QY 239 VHIIVCYTLMILRLKSVRLLSGSREKDNLRITKLVLVVAVFIICWPIHIFILVEA 298
Db 305 litipettfgtvswhficialgytnscnlpnvlyafldenfkrcfrefcipcsttiequnst 364
QY 299 LGSTSHSTAALSSYFCIALGTYNSNLNPLYLAFLDENFKRCFRDCEPILKMMERQOSTN 358
Db 365 rvrgntrehpstantv 380
QY 359 RVR-NIVQDPASMRDV 373

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RESULT 9
ID R71964 standard; Protein; 398 AA.
AC R71964;
DT 20-OCT-1995 (first entry)
DE Rat mu opioid receptor.
KW Mu opioid receptor; MOR-1; gene therapy; diagnostic.
OS Rattus sp.
PN W09507983-A.
PD 23-MAR-1995.
PF 13-SEP-1994; U10358.
PR 13-SEP-1993; US-120601.
PA (INDV) UNIV INDIANA FOUND.
PI Yu L;
DR WPI: 95-131351/17.
DR N-PSDB; Q89222.
PT New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.
PS Disclosure; Page 190-194; 266pp; English.
CC A 365 bp fragment of the mouse delta opioid receptor was used to
CC screen a rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in Q89222, encoding a
CC mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in
CC transfected CHO cells.
SQ Sequence 398 AA;

Query Match	59.0%;	Score 1674;	DB 13;	Length 398;
Best Local Similarity	65.8%;	Pred. No. 8.35e-145;		
Matches	208;	Conservative	54;	Mismatches 50;
			Indels	4;
			Gaps	4;

[illegible]

QY	119	YLMNSWPEGDVLCRIYISIDYNNMFTSIFLEWMSYDRYIAVCHPVALDERTPCLKAKII	178
Db	168	nycnwllssaiglpymfmattkkyrg-s-ldcrltfshptw-ywenllkicvfilafajmp	244
QY	179	NICIMWLLASSVGISAIYVGIKVREDVDVIECSIQEPDDEYSWMDLFMKICVFAFVIP	238
Db	245	lllitvcyglmllrlksvrmlsgskedrnllrltrmvlvavavfiwcpibhiyvilika	304
QY	239	VLTIIVCYTMILRLKKSVALLSGSRREKDRNLRLRIKVLVAVAFIICWPIPHIPIILVEA	298
Db	305	litiipettfgtvswhficalgytunclnpviyafidenfkrcfrefcipientsttequnst	364
QY	299	LGSTSHSTAALSSYFCIALGYTNSSLNPVLYALFDENFKRCFRDCCPIKHMENQSTN	358
Db	365	rvtqrutrehpstantv	380
QY	359	RVR-NTVQDPASMRDV	373

RESULT	ID	Accession	Protein	AA
AC	R76780	standard	Protein	400 AA.
DT	11-DEC-1995	(first entry)		
DE	Human mu opiate receptor.			
KW	Mu opiate receptor; hMOR; opiate agonist; opiate antagonist; drug abuse; analgesic.			
OS	Homo sapiens.			
FH	Key	Location/Qualifiers		
FT	Modified_site	9		
FT	/label= Glycosylation			
FT	/note= "N-linked glycosylation site"			
FT	Modified_site	11		
FT	/label= Glycosylation			
FT	/note= "N-linked glycosylation site"			
FT	Modified_site	32		
FT	/label= Glycosylation			
FT	/note= "N-linked glycosylation site"			
FT	Modified_site	40		
FT	/label= Glycosylation			
FT	/note= "N-linked glycosylation site"			
FT	Modified_site	48		
FT	/label= Glycosylation			
FT	/note= "N-linked glycosylation"			
FT	Domain	68..87		
FT	/label= Transmembrane_domain			
FT	Domain	107..125		
FT	/label= Transmembrane_domain			
FT	Domain	144..165		
FT	/label= Transmembrane_domain			
FT	Domain	188..208		
FT	/label= Transmembrane_domain			
FT	Domain	236..256		
FT	/label= Transmembrane_domain			
FT	Domain	284..304		
FT	/label= Transmembrane_domain			
FT	Domain	322..341		
FT	/label= Transmembrane_domain			
PN	W09520667-A1.			
PD	03-AUG-1995.			
PF	30-JAN-1995; U01144.			
PR	28-JAN-1994; US-188275.			
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.			
PA	(USSH) US SEC DEPT HEALTH.			
PI	Johnson PS, Persico AM, Uhl G, Wang J;			
DR	WPI; 95-275452/36.			
DR	N-PSDB; Q93102.			
PT	New DNA encoding human mu opiate receptor - used esp. for screening			
PT	cpds. for activity as opiate agonists or antagonists			
PS	Claim 1; Page 25-26; 49pp; English.			
CC	hMOR cDNA was obt'd. from a human cerebral cortical cDNA library			
CC	screened with fragments of a rat mu opiate receptor. Expression			
CC	of hMOR1 in COS cells revealed high affinity recognition of the mu			

QY 117 AVYLMNSWPFQGVLCIKIVISIDYNNMTSIFLTMSVDRYIAVCHPYKALDFRTPLKAK 176
Db 167 lnicicwlasgvgvpmwamvtqprdga-vv-cmlqfisp--swywdtvcikicvflfaf 222
QY 177 IINICIMWLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSW-WDLEFMKICVFAF 235
Db 223 vvpililtvcygmllrlrsvrllsgskedrsllritrmvllvvgafovawapihifvi 282
QY 236 VIPVLIITVCYTLMLRLKSVRLLSGSRKEDRNLRITKLVVAVAFIICWTPIHIFIL 295
Db 283 wtlvdinrrdplvvaalhlclalgyanslnpvyafldenfkrcfrqlcrtpcgrqep 342
QY 296 VEALGSTSHSTA-ALSSYYFCIALGYTNSLNPLYAFLDENFKRCFRDPCFPKRMER 354
Db 343 gslrrprga 351
QY 355 QSTNRVRNT 363

RESULT 13
ID R67670 standard; Protein; 372 AA.
AC R67670;
DE Mouse delta opioid receptor (first entry)
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe.
OS Mus musculus.
PN W09428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR N-PSDB; Q75927
PT polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PI screening assays for useful drug substances.
PS Claim 5; Page 215-221; 300pp; English.
CC The amino acid sequence of the novel mouse delta opioid receptor MOR1.
CC The corresponding gene was isolated from a mouse brain cDNA library using
CC a fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRIF) receptor
CC subtypes STR1, STR2 and STR3. The 1.3 kb EcoRI-SacI fragment from the
CC mouse delta opioid receptor clone, lambda msl-2, was subcloned into the
CC CMV promoter-based expression vector pCMV-6c. The resultant construct
CC pCMV-msl-2 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete,
CC truncated or chimaeric opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 372 AA;

Query Match 56.3%; Score 1597; DB 12; Length 372;
Best Local Similarity 66.7%; Pred. No. 1.94e-137;
Matches 206; Conservative 51; Mismatches 46; Indels 6; Gaps 5;
Db 47 alalaitalysavcavglgnvlfmfgivrytklktatniyifnaladalatstlpfqs 106
QY 57 AIPVITAVYSVVFVGLVGNLSLVMFVIRYTKMKTATNIIYIFNALDALVTTMPFQS 116
Db 107 akylmetwpgellckavlsidyymftsiftlmsvdrvriavchpykaldfrtpakak 166
QY 117 AVYLMNSWPFQGVLCIKIVISIDYNNMTSIFLTMSVDRYIAVCHPYKALDFRTPLKAK 176
Db 167 lnicicwlasgvgvpmwamvtqprdga-vv-cmlqfisp--swywdtvcikicvflfaf 222

QY 177 IINICIMWLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSW-WDLEFMKICVFAF 235
Db 223 vvpililtvcygmllrlrsvrllsgskedrsllritrmvllvvgafovawapihifvi 282
QY 236 VIPVLIITVCYTLMLRLKSVRLLSGSRKEDRNLRITKLVVAVAFIICWTPIHIFIL 295
Db 283 wtlvdinrrdplvvaalhlclalgyanslnpvyafldenfkrcfrqlcrtpcgrqep 342
QY 296 VEALGSTSHSTA-ALSSYYFCIALGYTNSLNPLYAFLDENFKRCFRDPCFPKRMER 354
Db 343 gslrrprga 351
QY 355 QSTNRVRNT 363

RESULT 14
ID R66503 standard; Protein; 371 AA.
AC R66503;
DE Murine delta opioid receptor.
KW delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;
KW drug addiction; neurological disorder; psychiatric; disorder;
KW cardiovascular disorder.
OS Mus musculus.
PN FR2697850-A.
PD 13-MAY-1994.
PF 10-NOV-1992; 013526.
PR 10-NOV-1992; FR-013526.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B;
DR WPI; 94-178255/22.
DR N-PSDB; Q66656.
PT New nucleic acid encoding opioid receptor - and related
PT polypeptide, antisense nucleic acid, probes, recombinant cells
PT and ligands, useful in diagnosis and treatment of e.g.
PT neurological disorders
PS Claim 8; Page 19-20; 29pp; French.
CC A cDNA bank constructed from hybridoma NG108-15, was used to
CC transfect COS-1 cells. The cells were tested for ability to bind
CC tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or
CC absence of the opioid antagonist naloxone. Clone K56 was isolated
CC from a positive colony and found to contain a 2216bp insert. This
CC cDNA encodes a delta opioid (enkephalin) receptor with apparent
CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
SQ Sequence 371 AA;

Query Match 52.8%; Score 1499; DB 10; Length 371;
Best Local Similarity 64.9%; Pred. No. 4.50e-128;
Matches 200; Conservative 52; Mismatches 51; Indels 5; Gaps 5;
Db 47 alalaitalysavcavglgnvlfmfgivrytklktatniyifnaladalatstlpfqs 106
QY 57 AIPVITAVYSVVFVGLVGNLSLVMFVIRYTKMKTATNIIYIFNALDALVTTMPFQS 116
Db 107 akylmetwpgellckavlsidyymftsiftlmsvdrvriavchpykaldfrtpakak 166
QY 117 AVYLMNSWPFQGVLCIKIVISIDYNNMTSIFLTMSVDRYIAVCHPYKALDFRTPLKAK 176
Db 167 lnicicwlasgvgvpmwamvt-pgmwgyacs-sspv-qlv1-dvtvcikicvflfafv 222
QY 177 IINICIMWLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEYSW-WDLEFMKICVFAFV 236
Db 223 vvpililtvcygmllrlrsvrllsgskedrsllritrmvllvvgafovawapihifvi 282
QY 237 IPVLIITVCYTLMLRLKSVRLLSGSRKEDRNLRITKLVVAVAFIICWTPIHIFILV 296
Db 283 wtlvdinrrdplvvaalhlclalgyanslnpvyafldenfkrcfrqlcrtpcgrqep 342
QY 297 EALGSTSHSTA-ALSSYYFCIALGYTNSLNPLYAFLDENFKRCFRDPCFPKRMERQ 355
Db 343 slrrprga 350

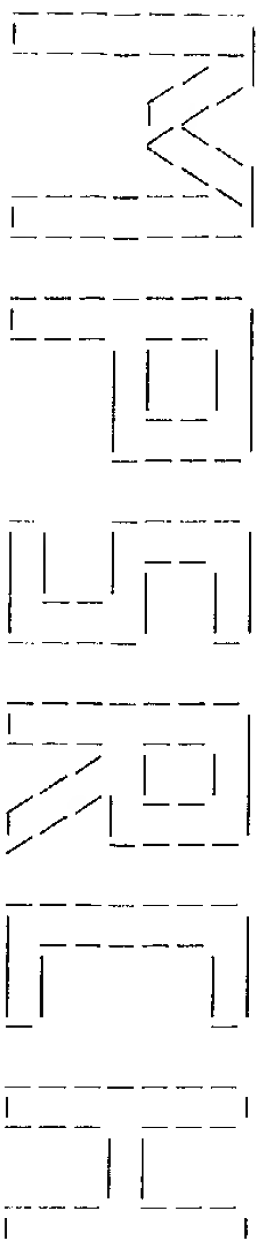
QY 356 STNRVRNT 363

RESULT 15
ID R71968 standard; protein; 367 AA.
AC R71968;
DT 20-OCT-1995 (first entry)
DE Rat opiod receptor.
KW Opiod receptor; gene therapy; diagnostic.
OS Rattus sp.
PN W09507983-A.
PD 23-MAR-1995.
PF 13-SEP-1994; U10358.
PR 13-SEP-1993; US-120601.
PA (INDV) UNIV INDIANA FOUND.
PI Yu L;
DR WPI; 95-131351/17.
DR N-PSDB; Q89233.
PT New nucleic acid encoding new human mu opiod receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.
PS Example 9; Page 218-222; 266pp; English.
CC The cDNA given in Q89233 was isolated from a rat brain library by
CC low stringency hybridization with rat mu opiod receptor cDNA
CC (Q89222). The clone encoded a 367-amino acid protein (R71968)
CC that showed high homology with mu, kappa and delta opiod receptors
CC but lacked affinity for their ligands, suggesting it to be
CC a novel member of the opiod receptor family.
SQ Sequence 367 AA;

Query Match 51.9%; Score 1473; DB 13; Length 367;
Best Local Similarity 59.3%; Pred. No. 1.37e-125;
Matches 188; Conservative 63; Mismatches 61; Indels 5; Gaps 5;

Db 40 safplglkvltivglylavcigllgnclvmvylrrhtkmtatniyifnladtlvll 99
QY 51 SAHSPALPVITATAVSVVEVGLVGNLSLVMFVITRYTKMTATNIYIFNLADALVTT 110
Db 100 tlpfgtdillgfwpfgnalcvtiaidymfstftltamsvdryvaichpiraldvr 159
QY 111 TMPFQSAVYLMNSWPRGDLCKIVISIDYNNMFTSTFTLTMSVDRYIAVCHPYKALDFR 170
Db 160 tsskagavnvaialasvgyvpvaimgsaqv-edee-ieclveipaqdy-wgpyfa-ic 215
QY 171 FPLKAKIINICIMLIASSVGISAIVLGGTKVREDVDVIECSLQFPD-DEYSWMDLFMKIC 229
Db 216 iflfsfipvlisvcslmirrlrgvrlslgsrekdnrlrritrlvllvvavfvgcwtp 275
QY 230 VFVFAFVIPVLIIVCYTIMLRKLSVRLSGSRKRDNLRRITKLVLVVAVFIIICWTP 289
Db 276 vqvfvlvqglgyvpgsetavailrfctalgynvscnlpilyafldenfkacfkccass 335
QY 290 IHIFILVEALGSTSHSTALSSYFCIALGYTNSSLNPVLYAFLDENFKRCFRDQCFPIK 349
Db 336 lhremqvsdrvrsiakd 352
QY 350 MRMEROSTNRRVRNTVQD 366

Search completed: Thu Apr 16 13:36:10 1998
Job time : 93 secs.



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Mpserch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 16 13:33:04 1998; Maspar time 19.37 Seconds
Tabular output not generated. 840.647 Million cell updates/sec

Title: >US-08-292-694A-2
Description: (1-380) from US08292694A.pep
Perfect Score: 2839
Sequence: 1 MESPIQIFRGDGPFTCSPSA.....RNTVQDPASMDYGVGMKNKPV 380

Scoring table: PAM 150
Gap 11

Searched: 195121 seqs, 42852602 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir55
1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 40.199; Variance 186.150; scale 0.216

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2829	99.6	380	2	S36143	A/Accession: S36143.	1.16e-243
2	2816	99.2	380	2	JC2434	A/Accession: JC2434.	1.85e-242
3	2747	96.8	380	2	JC2338	TOIG of: jc2338 check	4.52e-236
4	2746	96.7	380	2	I57005	TOIG of: i57005 check	5.59e-236
5	2610	91.9	380	2	A55259	TOIG of: a55259 check	2.16e-223
6	2350	82.8	310	2	MESPIQIFRG	This is a DE line.	2.34e-199
7	1680	59.2	392	2	S65693	TOIG of: s65693 check	1.23e-137
8	1678	59.1	398	2	A57510	A/Status: nucleic acid	1.87e-137
9	1677	59.1	400	2	I56553	A/Accession: I56553.	2.31e-137
10	1674	59.0	398	2	I56517	TOIG of: i56517 check	4.35e-137
11	1659	58.4	398	2	I56504	TOIG of: i56504 check	1.04e-135
12	1612	56.8	372	2	I38657	A/Accession: I38657.	2.13e-131
13	1610	56.7	372	2	S34592	TOIG of: s34592 check	3.25e-131
14	1597	56.3	372	2	B48227	TOIG of: b48227 check	5.06e-130
15	1473	51.9	367	2	I56520	A/Accession: I52654.	1.16e-118
16	1471	51.8	367	2	JC2421	A/Accession: JC2421.	1.77e-118
17	1470	51.8	367	2	I49022	A/Title: Cloning and	2.18e-118
18	1465	51.6	370	2	S43087	TOIG of: s43087 check	6.26e-118
19	980	34.5	391	2	C41795	A/Accession: C41795.	8.85e-74
20	978	34.4	391	2	A39297	TOIG of: a39297 check	1.34e-73
21	976	34.4	391	2	A41795	F;95-120/Domain: trans	2.04e-73
22	968	34.1	388	2	JN0605	F;84-109/Domain: trans	1.08e-72
23	963	33.9	384	2	A47249	TOIG of: a47249 check	3.04e-72

24	954	33.6	384	2	JC4629	TOIG of: jc4629 check	1.98e-71
25	936	33.0	369	2	JC2083	F;77-105/Domain: trans	8.34e-70
26	927	32.7	369	2	A45291	TOIG of: a45291 check	5.41e-69
27	922	32.5	369	2	D41795	A/Accession: I56236.	1.53e-68
28	912	32.1	369	2	B41795	F;80-105/Domain: trans	1.22e-67
29	909	32.0	346	2	S29248	TOIG of: s29248 check	2.27e-67
30	850	29.9	363	2	I38974	A/Cross-references: EM	4.64e-62
31	819	28.8	363	2	I57955	A/Accession: I57955.	2.83e-59
32	819	28.8	364	2	JN0763	A/Accession: JN0763.	2.83e-59
33	815	28.7	418	2	A46226	A/Accession: S32501.	6.46e-59
34	792	27.9	328	2	I38973	A/Cross-references: EM	7.45e-57
35	788	27.8	363	2	I57940	A/Cross-references: GB	1.70e-56
36	734	25.9	428	2	S30508	A/Cross-references: EM	1.15e-51
37	732	25.8	428	2	A44021	TOIG of: a44021 check	1.73e-51
38	639	22.5	359	2	S44425	TOIG of: s44425 check	3.24e-43
39	629	22.2	359	2	JC1104	A/Title: Molecular clo	2.49e-42
40	623	21.9	355	2	A45177	TOIG of: a45177 check	8.45e-42
41	617	21.7	359	2	A48857	TOIG of: a48857 check	2.87e-41
42	616	21.7	359	2	S15403	TOIG of: s15403 check	3.51e-41
43	615	21.7	359	2	A42656	TOIG of: a42656 check	4.31e-41
44	614	21.6	349	2	G01765	TOIG of: g01765 check	5.28e-41
45	614	21.6	349	2	I59336	TOIG of: i59336 check	5.28e-41

ALIGNMENTS

RESULT	ID	1	STANDARD;	PRT;	380 AA.
XX	XX	S36143	xxxxxx		
DT	DT	01-JAN-1900			
XX	XX				
DE	DE	A/Accession: S36143.			
CC	CC	A/Accession: S36143			
CC	CC	A/Status: preliminary			
CC	CC	A/Molecule type: mRNA			
CC	CC	A/Residues: 1-380 <NIS>			
CC	CC	R;Chen, Y.; Mestek, A.; Liu, J.; Yu, L.			
CC	CC	Biochem. J. 295, 625-628, 1993			
CC	CC	A/Title: Molecular cloning of a rat kappa opioid receptor reveals sequence simi			
CC	CC	A/Reference number: S38825			
CC	CC	A/Accession: S38825			
CC	CC	A/Status: preliminary			
CC	CC	A/Molecule type: mRNA			
CC	CC	A/Residues: 1-380 <CHE>			
CC	CC	A/Cross-references: GB:L22001; NID:g409236; PID:g409237			
CC	CC	R;Minami, M.; Toya, T.; Katano, Y.; Maekawa, K.; Nakamura, S.; Onogi, T.; Kaneko			
CC	CC	FEBS Lett. 329, 291-295, 1993			
CC	CC	A/Title: Cloning and expression of a cDNA for the rat kappa-opioid receptor.			
CC	CC	A/Reference number: S36102			
CC	CC	A/Accession: S36102			
CC	CC	A/Molecule type: mRNA			
CC	CC	A/Residues: 1-41, 'L', 43-380 <MIN>			
CC	CC	R;Li, S.; Zhu, J.; Chen, C.; Chen, Y.W.; Deriel, J.K.; Ashby, B.; Liu-Chen, L.Y			
CC	CC	Biochem. J. 295, 629-633, 1993			
CC	CC	A/Title: Molecular cloning and expression of a rat kappa opioid receptor.			
CC	CC	A/Reference number: S39015			
CC	CC	A/Accession: S39015			
CC	CC	A/Molecule type: mRNA			
CC	CC	A/Residues: 1-344, 'Y', 346-380 <LIS>			
CC	CC	R;Meng, F.; Xie, G.			
CC	CC	Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958, 1993			
CC	CC	A/Title: Cloning and pharmacological characterization of a rat kappa opioid rec			
CC	CC	A/Reference number: A48789; MUID:94052210			
CC	CC	A/Accession: A48789			
CC	CC	A/Status: preliminary; translated from GB/EMBL/DBJ			
CC	CC	A/Molecule type: mRNA			
CC	CC	A/Residues: 1-380 <RES>			
CC	CC	A/Cross-references: EMBL:U00442; NID:g403486; PID:g403487			
CC	CC	C;Keywords: G protein-coupled receptor; transmembrane protein			
CC	CC	SEQUENCE 380 AA; 42688 MW; 808499 CN;			

Query Match		99.6%;	Score 2829;	DB 2;	Length 380;
Best Local Similarity		98.9%;	Pred. No. 1.16e-243;		
Matches		376;	Conservative	3;	Mismatches 1; Indels 0; Gaps 0;
Db	1	MESPIQIFRGE	PPTCAPSACLLPNSSSWF	PNMAESDSNGSVGSEDOQLES	PAHISPAIPV 60
QY	1	MESPIQIFRGD	PPTCSPSACLLPNSSSWF	PNMAESDSNGSVGSEDOQLES	PAHISPAIPV 60
Db	61	ITTA	VSVFVVGVLGNSLVMFV	IIIRYTKMKTATNIYIFNLALADALV	TTMPQSAVYL 120
QY	61	ITTA	VSVFVVGVLGNSLVMFV	IIIRYTKMKTATNIYIFNLALADALV	TTMPQSAVYL 120
Db	121	MNSW	PFGDVLCKIVISIDYNNMFTS	IFTLTMSVDRIA	VCHPVKALDFRTP
QY	121	MNSW	PFGDVLCKIVISIDYNNMFTS	IFTLTMSVDRIA	VCHPVKALDFRTP
Db	181	CIMW	LASSVGISAIVLG	TKVREDVDVIECSLQFPDDEYS	WMDLFMKICVYFAFV
QY	181	CIMW	LASSVGISAIVLG	TKVREDVDVIECSLQFPDDEYS	WMDLFMKICVYFAFV
Db	241	IIIV	CYTLMILRLKSVRL	LSGSRKDRNLRLRI	TKIVVAVFIICWTP
QY	241	IIIV	CYTLMILRLKSVRL	LSGSRKDRNLRLRI	TKIVVAVFIICWTP
Db	301	STSH	STAALSSYYFCIALGY	TNSSLNPVLYAF	LDENFKRCFRCFPIK
QY	301	STSH	STAALSSYYFCIALGY	TNSSLNPVLYAF	LDENFKRCFRCFPIK
Db	361	RNTV	QDPASMRDVG	GMNKPV 380	
QY	361	RNTV	QDPASMRDVG	GMNKPV 380	
RESULT 2 STANDARD; PRT; 380 AA.					
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XX	xxxxxx				
DT	01-JAN-1900				
DE	A:Accession: JC2434.				
CC	A:Accession: JC2434				
CC	A:Molecule type: mRNA				
CC	A:Residues: 1-380 <NIS>				
CC	A:Cross-references: DDBJ:D31663				
CC	C:Genetics:				
CC	A:Map position: 1A2-3				
CC	A:Introns: 86/2; 204/1				
CC	C:Keywords: receptor				
SQ	SEQUENCE 380 AA; 42630 MW; 803251 CN;				
Query Match 99.2%; Score 2816; DB 2; Length 380;					
Best Local Similarity 99.5%; Pred. No. 1.85e-242;					
Matches 378; Conservative 0; Mismatches 2; Indels 0; Gaps 0;					
Db	1	MESPIQIFRGD	PPTCSPSACLLPNSSSWF	PNMAESDSNGSVGSEDOQLES	PAHISPAIPV 60
QY	1	MESPIQIFRGD	PPTCSPSACLLPNSSSWF	PNMAESDSNGSVGSEDOQLES	PAHISPAIPV 60
Db	61	ITTA	VSVFVVGVLGNSLVMFV	IIIRYTKMKTATNIYIFNLALADALV	TTMPQSAVYL 120
QY	61	ITTA	VSVFVVGVLGNSLVMFV	IIIRYTKMKTATNIYIFNLALADALV	TTMPQSAVYL 120
Db	121	MNSW	PFGDVLCKIVISIDYNNMFTS	IFTLTMSVDRIA	VCHPVKALDFRTP
QY	121	MNSW	PFGDVLCKIVISIDYNNMFTS	IFTLTMSVDRIA	VCHPVKALDFRTP
Db	181	CIMW	LASSVGISAIVLG	TKVREDVDVIECSLQFPDDEYS	WMDLFMKICVYFAFV
QY	181	CIMW	LASSVGISAIVLG	TKVREDVDVIECSLQFPDDEYS	WMDLFMKICVYFAFV

Db	241	IIIVCYTLMILRLKSVRL	LSGSRKDRNLRLRI	TKIVVAVFIICWTP	PIHFIIVEALG	300
QY	241	IIIVCYTLMILRLKSVRL	LSGSRKDRNLRLRI	TKIVVAVFIICWTP	PIHFIIVEALG	300
Db	301	STSHSTAALSSYYFCIALG	TNSSLNPVLYAF	LDENFKRCFRD	CFPIKRMERQSTNRV	360
QY	301	STSHSTAALSSYYFCIALG	TNSSLNPVLYAF	LDENFKRCFRD	CFPIKRMERQSTNRV	360
Db	361	RNTVQDPASMRDVG	GMNKPV	380		
QY	361	RNTVQDPASMRDVG	GMNKPV	380		
RESULT 3 STANDARD; PRT; 380 AA.						
XX	ID	JC2338				
XX	AC	xxxxxx				
XX	DT	01-JAN-1900				
DE	TOIG of: jc2338	check: 8304	from: 1	to: 380.		
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CC	>P1:JC2338					
CC	kappa opioid receptor - human					
CC	C:Species: Homo sapiens (man)					
CC	C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 10-Sep-1997					
CC	C:Accession: JC2338; A55354					
CC	R:Mansson, E.; Bare, L.; Yang, D.					
CC	Biochem. Biophys. Res. Commun. 202, 1431-1437, 1994					
CC	A:Title: Isolation of a human kappa opioid receptor cDNA from placenta.					
CC	A:Reference number: JC2338					
CC	A:Accession: JC2338					
CC	A:Molecule type: mRNA					
CC	A:Residues: 1-380 <MAN>					
CC	A:Experimental source: placenta					
CC	R:Wang, J.B.; Johnson, P.S.; Wu, J.M.; Wang, W.F.; Uhl, G.R.					
CC	J. Biol. Chem. 269, 25966-25969, 1994					
CC	A:Title: Human kappa opiate receptor second extracellular loop elevates dynorphin					
CC	A:Reference number: A55354					
CC	A:Accession: A55354					
CC	A>Status: preliminary					
CC	A:Molecule type: mRNA					
CC	A:Residues: 136-279 <MAN>					
CC	A:Cross-references: GB:L36130; NID:g598184; PID:g598185					
CC	C:Comment: This receptor preferentially binds to dynorphins.					
CC	C:Keywords: G protein-coupled receptor; receptor; transmembrane protein					
CC	F:60-85/Domain: transmembrane #status predicted <TM1>					
CC	F:95-114/Domain: transmembrane #status predicted <TM2>					
CC	F:133-154/Domain: transmembrane #status predicted <TM3>					
CC	F:177-199/Domain: transmembrane #status predicted <TM4>					
CC	F:228-251/Domain: transmembrane #status predicted <TM5>					
CC	F:275-296/Domain: transmembrane #status predicted <TM6>					
CC	F:311-333/Domain: transmembrane #status predicted <TM7>					
SQ	SEQUENCE 380 AA; 42659 MW; 802911 CN;					
Query Match 96.8%; Score 2747; DB 2; Length 380;						
Best Local Similarity 93.9%; Pred. No. 4.52e-236;						
Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;						
Db	1	MESPIQIFRGE	PPTCAPSACLPN	SSSWFPGWAEPDS	NGSAGSEDAQLEPAHISPAIPV	60
QY	1	MESPIQIFRGD	PPTCSPSACLLP	NSSSWFPNMAESDS	NGSVGSEDOQLES	PAHISPAIPV 60
Db	61	ITTA	VSVFVVGVLGNSL	VMFVITIRYTKMKT	ATNTIYIFNLALADALV	TTMPFQSTVYL 120
QY	61	ITTA	VSVFVVGVLGNSL	VMFVITIRYTKMKT	ATNTIYIFNLALADALV	TTMPQSAVYL 120
Db	121	MNSW	PFGDVLCKIVISID	YNNMFTSIFTLTMS	VDRIA	VCHPVKALDFRTP
QY	121	MNSW	PFGDVLCKIVISID	YNNMFTSIFTLTMS	VDRIA	VCHPVKALDFRTP
Db	181	CIMW	LASSVGISAIVLG	TKVREDVDVIECSL	QFPDDEYS	WMDLFMKICVYFAFV
QY	181	CIMW	LASSVGISAIVLG	TKVREDVDVIECSL	QFPDDEYS	WMDLFMKICVYFAFV

Db 181 C1WLSSVGSIAVLGGIKVREDVDVIECSLQFPDDYSWWDLEMKICVFIFAFAVIPVL 240
QY 181 C1WLSSVGSIAVLGGIKVREDVDVIECSLQFPDDYSWWDLEMKICVFIFAFAVIPVL 240
Db 241 IIVCYTILMLRLKSVRLLSGSRKDRNLRIIRLVVVAFAVVCWPIHIFILVEALG 300
QY 241 IIVCYTILMLRLKSVRLLSGSRKDRNLRIIRLVVVAFAVVCWPIHIFILVEALG 300
Db 301 STSHSTAALSSYYFCIALGYTNSSLNPILYAFLDENFKRCFRDCEPILKMEROSTNRV 360
QY 301 STSHSTAALSSYYFCIALGYTNSSLNPILYAFLDENFKRCFRDCEPILKMEROSTNRV 360
Db 361 RNTVQDPAYLRDIDGMNKPV 380
QY 361 RNTVQDPASMRDVGGMNKPV 380
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ID I57005
AC xxxxxx
XX 01-JAN-1900
DT TOIG of: I57005 check: 8302 from: 1 to: 380.
XX TOIG of: I57005 check: 8302 from: 1 to: 380
CC >P1:I57005
CC opioicd receptor kappa-1 - human
CC C/Species: Homo sapiens (man)
CC C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Aug-1997
CC C/Accession: I57005
CC R/Zhu, J.; Chen, C.; Xue, J.
CC Life Sci. 56, 201-207, 1995
CC A/Title: Cloning of a human .kappa. opioicd receptor from the brain.
CC A/Reference number: I57005
CC A/Accession: I57005
CC A/Status: preliminary; translated from GB/EMBL/DBJ
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <RES>
CC A/Cross-references: GB:L37362; NID:g722617; PID:g722618
CC C/Genetics:
CC A/Gene: GDB:OPR1: KOR
CC A/Cross-references: GDB:132651; OMIM:165196
CC A/Map position: 8q11.2-8q11.2
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SQ
Query Match 96.7%; Score 2746; DB 2; Length 380;
Best Local Similarity 93.7%; Pred. No. 5.59e-236;
Matches 356; Conservative 18; Mismatches 6; Indels 0; Gaps 0;
Db 1 MDSPIQIFRGE2GPTCAPSACLPNNSAWFPGWAEPDSDNGSAGSEDAQLEPAHISPAIPV 60
QY 1 MESPIQIFRGDPGPTCSPSACLLPNSSSWFPMWAESDSNGSVGSEDOQLESAAHISPAIPV 60
Db 61 IITAVYSVVFVVGVLGNSLVMFVIRYTKMKTATNIIYIFNLALADALVTTMPFQSAVYL 120
QY 61 IITAVYSVVFVVGVLGNSLVMFVIRYTKMKTATNIIYIFNLALADALVTTMPFQSAVYL 120
Db 121 MNSWPFQDVLCKIYISIDYNNMFTSIFLTLMMSVDRIYAVCHPYKALDFRTPKAKIINI 180
QY 121 MNSWPFQDVLCKIYISIDYNNMFTSIFLTLMMSVDRIYAVCHPYKALDFRTPKAKIINI 180
Db 181 C1WLSSVGSIAVLGGIKVREDVDVIECSLQFPDDYSWWDLEMKICVFIFAFAVIPVL 240
QY 181 C1WLSSVGSIAVLGGIKVREDVDVIECSLQFPDDYSWWDLEMKICVFIFAFAVIPVL 240
Db 241 IIVCYTILMLRLKSVRLLSGSRKDRNLRIIRLVVVAFAVVCWPIHIFILVEALG 300
QY 241 IIVCYTILMLRLKSVRLLSGSRKDRNLRIIRLVVVAFAVVCWPIHIFILVEALG 300
Db 301 STSHSTAALSSYYFCIALGYTNSSLNPILYAFLDENFKRCFRDCEPILKMEROSTNRV 360

QY 301 STSHSTAALSSYYFCIALGYTNSSLNPILYAFLDENFKRCFRDCEPILKMEROSTNRV 360
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QY 361 RNTVQDPASMRDVGGMNKPV 380
RESULT 5 STANDARD; PRT; 380 AA.
ID A55259
AC xxxxxx
XX 01-JAN-1900
DT TOIG of: a55259 check: 7081 from: 1 to: 380.
XX TOIG of: a55259 check: 7081 from: 1 to: 380
CC >P1:A55259
CC kappa opioicd receptor - guinea pig
CC N/Alternate names: dynorphin receptor
CC C/Species: Cavia porcellus (guinea pig)
CC C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 10-Sep-1997
CC C/Accession: A55259
CC R/Xie, G.; Meng, F.; Mansour, A.; Thompson, R.C.; Hoversten, M.T.; Goldstein, A
CC Proc. Natl. Acad. Sci. U.S.A. 91, 3779-3783, 1994
CC A/Title: Primary structure and functional expression of a guinea pig kappa opio
CC A/Reference number: A55259
CC A/Accession: A55259
CC A/Status: preliminary
CC A/Molecule type: mRNA
CC A/Residues: 1-380 <XIE>
CC A/Cross-references: GB:U04092; NID:g476106; PID:g476107
CC C/Keywords: transmembrane protein
CC A/SEQUENCE 380 AA; 42736 MW; 800736 CN;
SQ
Query Match 91.9%; Score 2610; DB 2; Length 380;
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Matches 338; Conservative 21; Mismatches 5; Indels 0; Gaps 0;
Db 17 ARNACLLPNGSAMLPGWAEPDSDNGSAGSEDOQLEPAHISPAIPVITAVYSVVFVGLVG 76
QY 17 SPSACLLPNSSSWFPMWAESDSNGSVGSEDOQLESAAHISPAIPVITAVYSVVFVGLVG 76
Db 77 NSLVMFVIRYTKMKTATNIIYIFNLALADALVTTMPFQSTVYLMNSWPFQDVLCKIVIS 136
QY 77 NSLVMFVIRYTKMKTATNIIYIFNLALADALVTTMPFQSAVYLMNSWPFQDVLCKIVIS 136
Db 137 IDYNNMFTSIFLTLMMSVDRIYAVCHPYKALDFRTPKAKIINIC1WLSSVGSIAIIL 196
QY 137 IDYNNMFTSIFLTLMMSVDRIYAVCHPYKALDFRTPKAKIINIC1WLSSVGSIAIIL 196
Db 197 GGTKVREDVDVIECSLQFPDDYSWWDLEMKICVFIFAFAVIPVLIIVCYTILMLRLKSV 256
QY 197 GGTKVREDVDVIECSLQFPDDYSWWDLEMKICVFIFAFAVIPVLIIVCYTILMLRLKSV 256
Db 257 RLLSGSRKDRNLRIIRLVVVAFAVVCWPIHIFILVEALGSTSHSTAALSSYYFCI 316
QY 257 RLLSGSRKDRNLRIIRLVVVAFAVVCWPIHIFILVEALGSTSHSTAALSSYYFCI 316
Db 317 ALGYTNSSLNPILYAFLDENFKRCFRDCEPILKMEROSTNRVNTVQDPASMRDVGGM 376
QY 317 ALGYTNSSLNPILYAFLDENFKRCFRDCEPILKMEROSTNRVNTVQDPASMRDVGGM 376
Db 377 NKPV 380
QY 377 NKPV 380
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RESULT	ID	156553	STANDARD;	PRT;	400 AA.
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XX	DT	01-JAN-1900			
XX	DE				
XX					
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CC		R:Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.R			
CC		submitted to GenBank, August 1994			
CC		A:Reference number: A38991			
CC		A:Accession: A38991			
CC		A:Status: translated from GB/EMBL/DBJ			
CC		A:Molecule type: mRNA			
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CC		R:Wang, J.B.; Johnson, P.S.; Persico, A.M.; Hawkins, A.L.; Griffin, C.A.; Uhl, G.R			
CC		FEBS Lett. 338, 217-222, 1994			
CC		A:Title: Human mu opiate receptor. cDNA and genomic clones, pharmacologic characte			
CC		A:Reference number: S41075			
CC		A:Accession: S41075			
CC		A:Status: nucleic acid sequence not shown			
CC		A:Molecule type: mRNA			
CC		A:Residues: 1-50, 'N', 52-400 <WA2>			
CC		R:Bare, L.A.; Mansson, E.; Yang, D.			
CC		FEBS Lett. 354, 213-216, 1994			
CC		A:Title: Expression of two variants of the human mu opioid receptor mRNA in SK-N-S			
CC		A:Reference number: S51215			
CC		A:Accession: S51215			
CC		A:Status: preliminary			
CC		A:Molecule type: mRNA			
CC		A:Residues: 387-400 <BAR>			
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CC		A:Gene: GDB:OPRMI			
CC		A:Cross-references: GDB:137216; OMIM:600018			
CC		A:Map position: 6q24-6q25			
CC		C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein			
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CC		F:107-132/Domain: transmembrane #status predicted <TMM2>			
CC		F:144-165/Domain: transmembrane #status predicted <TMM3>			
CC		F:188-208/Domain: transmembrane #status predicted <TMM4>			
CC		F:236-257/Domain: transmembrane #status predicted <TMM5>			
CC		F:283-304/Domain: transmembrane #status predicted <TMM6>			
CC		F:323-342/Domain: transmembrane #status predicted <TMM7>			
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DB		Query Match	59.1%;	Score 1677;	DB 2; Length 400;
DB		Best Local Similarity	66.6%;	Pred. No. 2.31e-137;	
DB		Matches 207;	Conservative 52;	Mismatches 49;	Indels 3; Gaps 3;
DB		70	ATTMALYSIVCVGLFENFLVMYVIIVRYTKMKATATNIYIFNLALADALATSTLPFSYN	129	
DB		59	PVIITAVYSVFVGLVGNLSVMFEVITRTKMTATNIIYIFNLALADALVTTTFPQSAY	118	
DB		130	YLMGTWPFGTILCKIVISIDYNNMFTSIFLLCTMSYDRYIAVCHPVKALDFRTPRNAKII	189	
DB		119	YIMNSWPFGLCKIVISIDYNNMFTSIFLLIMSVDRYIAVCHPVKALDFRTPRNAKII	178	
DB		190	NVCNWLISSAIGLPVMEATTKYRG-S-IDCITLFFSHPTW-YWENLLKICVFIFAFIMP	246	
DB		179	NICIMWLASSVGSIAIVGGTKVREDVDVIECSIQFPDDEYSWMDLFMKICVFVFAFVIP	238	
DB		247	VIIITVCGIMTLRLKSVRMLSGSKEKDRNLRRITRMVLYVAVFIVCWTPIHIVLIKA	306	

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QY 239 VLIIVCYTLMILRLKSVPLLSGSRREKDRNLRLRTKVLVWVAVFIICWPIPIHILVEA 298
Db 307 LVIPETTFQGVSWHFCIALGYTNSCLNPVLVAFIDENFKRCFREFCIPITSSNIEQNST 366
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QY 299 LGSTSHSTAALSSYYFCIALGYTNSLNPVLVAFIDENFKRCFRDFCFPIKRMERQSTN 358
      | : | : | : |
Db 367 RIRQNRDHPG 377
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QY 359 RYENTVQDPAS 369

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AC xxxxxx
XX
DT 01-JAN-1900
XX
DE TOIG of: I56517 check: 8374 from: 1 to: 398.
XX
CC TOIG of: I56517 check: 8374 from: 1 to: 398
CC
CC >P1;I56517
CC mu-opioid receptor - rat
CC C/Species: Rattus norvegicus (Norway rat)
CC C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Mar-1997
CC C/Accession: I56517; I57951; A49680; I52314; S34593; A48799; I58154
CC R/Burrow, J.R.; Zhang, G.; Bouvier, C.; Saez, C.; Ronnekleiv, O.K.; Kelly, M.T.
CC J. Neurochem. 64, 14-24, 1995
CC A/Title: Characterization and distribution of a cloned rat mu-opioid receptor.
CC A/Reference number: I56517; MUID:95096825
CC A/Accession: I56517
CC A/Status: preliminary; translated from GB/EMBL/DDBJ
CC A/Molecule type: mRNA
CC A/Residues: 1-398 <RES>
CC A/Cross-references: EMBL:U02083; NID:g403573; PID:g403574
CC R/Chen, Y.; Mestek, A.; Liu, J.; Hurley, J.A.; Yu, L.
CC Mol. Pharmacol. 44, 8-12, 1993
CC A/Title: Molecular cloning and functional expression of a mu-opioid receptor fr
CC A/Reference number: I57951; MUID:93341493
CC A/Accession: I57951
CC A/Status: preliminary; translated from GB/EMBL/DDBJ
CC A/Molecule type: mRNA
CC A/Residues: 1-398 <RES>
CC A/Cross-references: GB:U13069; NID:g348250; PID:g348251
CC R/Eppler, C.M.; Hulmes, J.D.; Wang, J.B.; Johnson, B.; Corbett, M.; Luthin, D.R
CC J. Biol. Chem. 268, 26447-26451, 1993
CC A/Title: Purification and partial amino acid sequence of a mu opioid receptor f
CC A/Reference number: A49680; MUID:94075333
CC A/Accession: A49680
CC A/Status: preliminary
CC A/Molecule type: protein
CC A/Residues: 272-291 <EPP>
CC A/Experimental source: brain membranes
CC A/Note: sequence extracted from NCBI backbone (NCBIP:140841)
CC R/Sedgl, M.; Roy, S.; Ramakrishnan, S.; Elde, R.; Loh, H.H.
CC Biochem. Biophys. Res. Commun. 209, 563-574, 1995
CC A/Title: Complementary DNA cloning of a mu-opioid receptor from rat peritoneal
CC A/Reference number: I52314; MUID:95251654
CC A/Accession: I52314
CC A/Status: preliminary
CC A/Molecule type: mRNA
CC A/Residues: 101-340 <SED>
CC A/Cross-references: GB:S77863; NID:g998526
CC A/Experimental source: Sprague Dawley, peritoneal macrophages
CC R/Fukuda, K.; Kato, S.; Mori, K.; Nishi, M.; Takeshima, H.
CC FEBS Lett. 327, 311-314, 1993
CC A/Title: Primary structures and expression from cDNAs of rat opioid receptor de
CC A/Reference number: S34592
CC A/Accession: S34593
CC A/Molecule type: mRNA
CC A/Residues: 1-244, 'V', 246-398 <FUK>
CC R/Wang, J.

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CC      Proc. Natl. Acad. Sci. U.S.A. 90, 10230-10234, 1993
CC      A/Title: Mu opiate receptor: cDNA cloning and expression.
CC      A/Reference number: A48799; MUID:94052137
CC      A/Accession: A48799
CC      A/Status: preliminary; translated from GB/EMBL/DBJ
CC      A/Molecule type: mRNA
CC      A/Residues: 1-244,'V',246-398 <WAN>
CC      A/Cross-references: GB:L20684; NID:g409149; PID:g409150
CC      R/Thompson, R.C.; Mansour, A.; Akil, H.; Watson, S.J.
CC      Neuron 11, 903-913, 1993
CC      A/Title: Cloning and pharmacological characterization of a rat mu opiod receptor.
CC      A/Reference number: 158154; MUID:94059560
CC      A/Accession: 158154
CC      A/Status: preliminary; translated from GB/EMBL/DBJ
CC      A/Molecule type: mRNA
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CC      A/Gene: MUR1
CC      C/Keywords: G protein-coupled receptor; transmembrane protein
CC      SQUENCE 398 AA; 44508 MW; 870781 CN;

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Best Local Similarity 65.8%; Pred. No. 4.35e-137;
Matches 208; Conservative 54; Mismatches 50; Indels 4; Gaps 4;

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QY      59 PVITTAIVSVFVGLVGNLSVMFVIRYTKMTATNITYFNALADALVTTTTPQSAV 118

Db      128 YLMTWPEFTILCKIVISIDYNNMFTSIFTLCTMSVDRYAVCHPVKALDFRTPRNATV 187
QY      119 YLMSWPFQDYLCKIVISIDYNNMFTSIFTLTMSVDRYAVCHPVKALDFRTPKAKII 178

Db      188 NYCNWILSSAIGLPVMEFATTKYRQG-S-IDCTLTFESHPTW-YWENLTKICVFIFAFIMP 244
QY      179 NICTWLLASSVGSISAVLGTFKVEDVDVIECSLQFPDDEXSWWDLFMKICVFVFAFVLP 238

Db      245 ILITVTCYGLMILRLKSVRLSGSKEKDRNLRITRMVLYVAVFIVCWTPIHIVYIIKA 304
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Db      305 LITPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPITSSTIEQNST 364
QY      299 LGSTSHSTALSSYFICIALGYTNSCLNPVLYAFLDENFKRCFREFCIPIKRMEROSTN 358

Db      365 RVRONTREHPSTANTV 380
QY      359 RVR-NTVQDPASMRDV 373

RESULT 11
ID      156504 STANDARD; PRT; 398 AA.
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AC      xxxxxx
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DT      01-JAN-1900
XX
DE      TOIG of: 156504 check: 8604 from: 1 to: 398.
XX
CC      TOIG of: 156504 check: 8604 from: 1 to: 398
CC
CC      >P1:156504
CC      mu opiod receptor - rat
CC      C/Species: Rattus norvegicus (Norway rat)
CC      C/Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-Jul-1996
CC      C/Accession: 156504
CC      R/Zastawny, R.L.; George, S.R.; Nguyen, T.; Cheng, R.; Tsatsos, J.; Briones-Urbina
CC      J. Neurochem. 62, 2099-2105, 1994
CC      A/Title: Cloning, characterization, and distribution of a mu-opiod receptor in ra
CC      A/Reference number: 156504; MUID:94246380
CC      A/Accession: 156504
CC      A/Status: preliminary; translated from GB/EMBL/DBJ
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CC      A/Molecule type: mRNA
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CC      SQUENCE 398 AA; 44403 MW; 871809 CN;

Query Match          58.4%; Score 1659; DB 2; Length 398;
Best Local Similarity 65.8%; Pred. No. 1.04e-135;
Matches 208; Conservative 53; Mismatches 51; Indels 4; Gaps 4;

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QY      59 PVITTAIVSVFVGLVGNLSVMFVIRYTKMTATNITYFNALADALVTTTTPQSAV 118

Db      128 YLMTWPEFTILCKIVISIDYNNMFTSIFTLCTMSVDRYAVCHPVKALDFRTPRNATV 187
QY      119 YLMSWPFQDYLCKIVISIDYNNMFTSIFTLTMSVDRYAVCHPVKALDFRTPKAKII 178

Db      188 NYCNWILSSAIGLPVMEFATTKYRQG-S-IDCTLTFESHPTW-YWENLTKICVGLFAFIMP 244
QY      179 NICTWLLASSVGSISAVLGTFKVEDVDVIECSLQFPDDEXSWWDLFMKICVFVFAFVLP 238

Db      245 VLIITVCYGLMILRLKSVRLSGSKEKDRNLRITRMVLYVAVFIVCWTPIHIVYIIKA 304
QY      239 VLIITVCYTLMLRLKSVRLSGSREKDRNLRITKLVVAVVAFIICWTPIHIFIVEA 298

Db      305 LITPETTFQTVSWHFCIALGYTNSCLNPVLYAFLDENFKRCFREFCIPITSSTIEQNST 364
QY      299 LGSTSHSTALSSYFICIALGYTNSCLNPVLYAFLDENFKRCFREFCIPIKRMEROSTN 358

Db      365 RVRONTREHPSTANTV 380
QY      359 RVR-NTVQDPASMRDV 373
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RESULT 12
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AC      xxxxxx
XX
DT      01-JAN-1900
XX
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CC      A/Accession: 138657
CC      A/Status: preliminary; translated from GB/EMBL/DBJ
CC      A/Molecule type: mRNA
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CC      SQUENCE 372 AA; 40368 MW; 725194 CN;

Query Match          56.8%; Score 1612; DB 2; Length 372;
Best Local Similarity 63.1%; Pred. No. 2.13e-131;
Matches 217; Conservative 60; Mismatches 58; Indels 9; Gaps 8;

Db      15 LEANASDAYPS-A-CPSAGANASGPPGARSAS-SIALATAITALYSACVAGLGNVLYM 71
QY      22 LIPNSSSWFPNMAESDSNGSVGEDQLESAAHISPAIPVITTAIVSVFVGLVGNLSVM 81

Db      72 FGIIVRYTKMTATNITYFNALADALATSTLPQSAKYLIMETWPFGEILLCKAVLSIDYNN 131
QY      82 FVIRYTKMTATNITYFNALADALVTTTTPQSAVYIMNSWPFQDYLCKIVISIDYNN 141

Db      132 MFTSIFTLTMSVDRYAVCHPVKALDFRTPAKAKLINICIWVLASGVGPIMMAVTRP 191
QY      142 MFTSIFTLTMSVDRYAVCHPVKALDFRTPKAKLINICIWLLASSVGSISAVLGSTKV 201

Db      192 RDGA-VV-CMLQFPSP--SWYWDVTYTKICVFELFAVVPILITVTCYGLMLRLSVRLS 247
QY      202 REDVDVIECSLQFPDDEXSW-WDLFMKICVFVFAFVLPVLIITVCYTLMLRLKSVRLS 260

Db      248 GSKEKDRSLRITRMVLYVGAFFVWCAPIHIFIVYTWLVLDIDRDPVLYAALHCLIALG 307
QY      261 GSREKDRNLRITKLVVAVVAFIICWTPIHIFIVEALGSTSHSTA-ALSSYFICIALG 319
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Db 283 VWTIVDINRRDPLVVAALHICIALGYANSSLNPLVAFIDENFKRCFROLCRTPCGRQEP 342
QY 296 VEALGSTSHSTA-ALSSYYFCIALGYTNSSLNPLVAFIDENFKRCFRODFCFPIKRMER 354
Db 343 GSLRRPRQA 351
QY 355 QSTNRVRNT 363

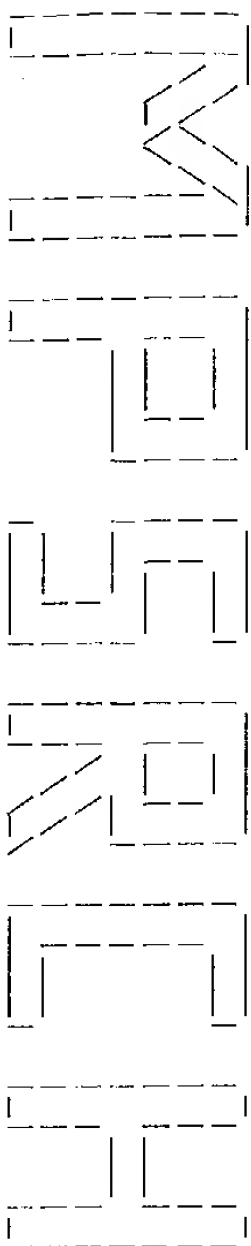
RESULT 15
ID 156520 STANDARD; PRT; 367 AA.
XX 156520
AC xxxxxx
XX 01-JAN-1900
DT 01-JAN-1900
XX
DE A:Accession: I52654.

CC A:Accession: I52654
CC A:Status: preliminary; translated from GB/EMBL/DDBJ
CC A:Molecule type: mRNA
CC A:Residues: 1-367 <RE2>
CC A:Cross-references: GB:I29419; NID:g510718; PID:g510719
CC C:Keywords: G protein-coupled receptor; transmembrane protein
SQ SEQUENCE 367 AA; 40523 MW; 720655 CN;

Query Match 51.9%; Score 1473; DB 2; Length 367;
Best Local Similarity 59.38; Pred. No. 1.16e-118;
Matches 188; Conservative 63; Mismatches 61; Indels 5; Gaps 5;

Db 40 SAFLPLGLKVTIVGLVLAVCIGLLGNCGLVMYVILRHTKMTATNIYIFNLALADTLVLL 99
QY 51 SAHISPAIPVITTAIVSVVVGVLGNSLVMFVILRITKMTATNIYIFNLALADLVTT 110
Db 100 TLPEQGTDLILGFEPFGNALCKTVIAIDYYNMFTSTFTLTAMSVDRYVAICHPIRALDVR 159
QY 111 TMPEQSAVYILMNSWPGDVLCKIVISIDYYNMFTSIFTLTMSVDRIYAVCHPVKALDER 170
Db 160 TSSKAQAVNVAIMALASVGVPAIMGSAQV-EDDE-IECLVEIPAPQDY-WGPVFA-IC 215
QY 171 TPLKAKIINICIMWLASSVGSIAIVLGGTKREDVDVIECSLQFPD-DEYSWMDLFMKIC 229
Db 216 IFLSFIIIPVLIISVCSIMIRRLRGVRLSGSREKDRNLRLRITRLVLYVVAVFVGWTP 275
QY 230 VEVFAFVIVPVLIIYCYTLMILRLKSVRLSGSREKDRNLRLRITKLVLYVVAVFIICWTP 289
Db 276 VQVFVLVQGLGVQPGSEFTAVAILRFTALGYVNSCLNPILYAFIDENFKACFRKFCASS 335
QY 290 IHFILVEALGSTSHSTAALSSYYFCIALGYTNSSLNPLVYAFIDENFKRCFRDQFPPIK 349
Db 336 LIREMQVSDRVRSIAKD 352
QY 350 IRMERQSTNRVRNTVQD 366

Search completed: Thu Apr 16 13:34:17 1998
Job time : 73 secs.



(TM)

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Msrch_p protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 16 13:30:34 1998; Maspar time 10.94 seconds
871.365 Million cell updates/sec
Tabular output not generated.

Title: >US-08-292-694A-2
Description: (1-380) from US08292694A.pep
Perfect Score: 2839
Sequence: 1 MESPIQIFRGDGPITCPSA.....RNTVQDPASMRDVGGMKPV 380

Scoring table: PAM 150
Gap 11

Searched: 69112 seqs, 25083644 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swiss1

Statistics: Mean 50.098; Variance 102.197; scale 0.490

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	2839	100.0	380	1	OPRK_MOUSE	KAPPA-TYPE OPIOID RECE	0.00e+00
2	2829	99.6	380	1	OPRK_RAT	KAPPA-TYPE OPIOID RECE	0.00e+00
3	2747	96.8	380	1	OPRK_HUMAN	KAPPA-TYPE OPIOID RECE	0.00e+00
4	2610	91.9	380	1	OPRK_CAVPO	KAPPA-TYPE OPIOID RECE	0.00e+00
5	1678	59.1	398	1	OPRM_MOUSE	MU-TYPE OPIOID RECEPTO	0.00e+00
6	1676	59.0	398	1	OPRM_RAT	MU-TYPE OPIOID RECEPTO	0.00e+00
7	1675	59.0	400	1	OPRM_HUMAN	MU-TYPE OPIOID RECEPTO	0.00e+00
8	1672	58.9	401	1	OPRM_PIG	MU-TYPE OPIOID RECEPTO	0.00e+00
9	1610	56.7	372	1	OPRD_RAT	DELTA-TYPE OPIOID RECE	1.46e-293
10	1608	56.6	372	1	OPRD_HUMAN	DELTA-TYPE OPIOID RECE	3.79e-293
11	1597	56.3	372	1	OPRD_MOUSE	DELTA-TYPE OPIOID RECE	7.09e-291
12	1473	51.9	367	1	OPRX_RAT	NOCICEPTIN RECEPTOR (O	2.65e-265
13	1471	51.8	367	1	OPRX_MOUSE	NOCICEPTIN RECEPTOR (O	6.84e-265
14	1465	51.6	370	1	OPRX_HUMAN	NOCICEPTIN RECEPTOR (O	1.18e-263
15	1459	51.4	370	1	OPRX_PIG	NOCICEPTIN RECEPTOR (O	5.98e-260
16	1447	51.0	370	1	OPRX_CAVPO	NOCICEPTIN RECEPTOR (O	3.25e-224
17	1273	44.8	228	1	OPRD_PIG	DELTA-TYPE OPIOID RECE	1.65e-164
18	980	34.5	391	1	SSR1_MOUSE	SOMATOSTATIN RECEPTOR	4.20e-164
19	978	34.4	391	1	SSR1_RAT	SOMATOSTATIN RECEPTOR	4.07e-163
20	976	34.4	391	1	SSR1_HUMAN	SOMATOSTATIN RECEPTOR	4.44e-162
21	968	34.1	388	1	SSR4_HUMAN	SOMATOSTATIN RECEPTOR	4.56e-161
22	963	33.9	384	1	SSR4_RAT	SOMATOSTATIN RECEPTOR	3.01e-159
23	954	33.6	384	1	SSR4_MOUSE	SOMATOSTATIN RECEPTOR	

24	938	33.0	368	1	SSR2_BOVIN	SOMATOSTATIN RECEPTOR	5.16e-156
25	936	33.0	369	1	SSR2_PIG	SOMATOSTATIN RECEPTOR	1.31e-155
26	927	32.7	369	1	SSR2_RAT	SOMATOSTATIN RECEPTOR	8.59e-154
27	922	32.5	369	1	SSR2_MOUSE	SOMATOSTATIN RECEPTOR	8.78e-153
28	912	32.1	369	1	SSR2_HUMAN	SOMATOSTATIN RECEPTOR	9.14e-151
29	850	29.9	333	1	GPR8_HUMAN	PROBABLE G PROTEIN-COU	2.77e-138
30	819	28.8	363	1	SSR5_HUMAN	SOMATOSTATIN RECEPTOR	4.60e-132
31	815	28.7	418	1	SSR3_HUMAN	SOMATOSTATIN RECEPTOR	2.91e-131
32	812	28.6	363	1	SSR5_MOUSE	SOMATOSTATIN RECEPTOR	1.16e-130
33	792	27.9	328	1	GPR7_HUMAN	PROBABLE G PROTEIN-COU	1.17e-126
34	788	27.8	363	1	SSR5_RAT	SOMATOSTATIN RECEPTOR	7.39e-126
35	734	25.9	428	1	SSR3_RAT	SOMATOSTATIN RECEPTOR	4.37e-115
36	732	25.8	428	1	SSR3_MOUSE	SOMATOSTATIN RECEPTOR	1.09e-114
37	639	22.5	359	1	AG2R_CANFA	TYPE-1 ANGIOTENSIN II	2.83e-96
38	629	22.2	359	1	AG2R_HUMAN	TYPE-1A ANGIOTENSIN II	2.63e-94
39	626	22.1	359	1	AG2R_PIG	TYPE-1 ANGIOTENSIN II	1.02e-93
40	623	21.9	355	1	CKR1_HUMAN	C-C CHEMOKINE RECEPTOR	3.98e-93
41	617	21.7	359	1	AG2R_RABIT	TYPE-1 ANGIOTENSIN II	6.00e-92
42	616	21.7	359	1	AG2R_BOVIN	TYPE-1 ANGIOTENSIN II	9.43e-92
43	615	21.7	359	1	AG2S_RAT	TYPE-1B ANGIOTENSIN II	1.48e-91
44	614	21.6	349	1	GALR_HUMAN	GALANIN RECEPTOR (GALL	2.33e-91
45	610	21.5	359	1	AG2S_MOUSE	TYPE-1B ANGIOTENSIN II	1.42e-90

ALIGNMENTS

RESULT ID	1	OPRK_MOUSE	STANDARD;	PRT;	380 AA.
AC	P33534;				
DT	01-FEB-1994 (REL. 28, CREATED)				
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	KAPPA-TYPE OPIOID RECEPTOR (KOR-1) (MSL-1).				
GN	OPRK1.				
OS	MUS MUSCULUS (MOUSE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BRAIN;				
RX	MEDLINE; 93342064.				
RA	YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,				
RA	BELL G.I.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 95100967.				
RA	NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI I.;				
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 95251663.				
RA	LIU H.C., LU S., AUGUSTIN L.B., FELSHEIM R.F., CHEN H.C.,				
RA	LOH H.H., WEI L.N.;				
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 209:639-647(1995).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE; 96084989.				
RA	BELKOWSKI S.M., ZHU J., LIU-CHEN L.Y., EISENSTEIN T.K.,				
RA	ADLER M.W., ROGERS T.J.;				
RL	J. NEUROIMMUNOL. 62:113-117(1995).				
CC	-I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM				
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR				
CC	FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF				
CC	AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.				
CC	-I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-I- TISSUE SPECIFICITY: BRAIN (NEOCORTECX, HIPPOCAMPUS, AMYGALA,				
CC	MEDIAL HABENTULA, HYPOTHALAMUS, LOCUS CERULEUS, AND PARABRACHIAL				
CC	NUCLEUS).				
CC	-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL; L11065; G348249; -.				
DR	EMBL; D31665; G808876; -.				
DR	EMBL; D31663; G808876; JOINED.				

DR EMBL; D31664; G808876; JOINED.
DR EMBL; S77872; G998532; -.
DR EMBL; S77868; G998532; JOINED.
DR EMBL; S77869; G998532; JOINED.
DR EMBL; S81111; E257489; -.
DR PIR; A48227; A48227.
DR GCRDB; GCR_0635; -.
DR MGD; MGT:97439; OPRK1.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
FT CONFLICT 211 211 S -> L (IN REF. 2 AND 3).
FT CONFLICT 231 231 F -> V (IN REF. 2 AND 3).
SQ SEQUENCE 380 AA; 42652 MW; C6F33212 CRC32;

Query Match 100.0%; Score 2839; DB 1; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MESPIQIFRGDPPTCSBACLLPNSSSWFPMWAESDNGSVGSEDQQLSAHISPAIPV 60
QY 1 MESPIQIFRGDPPTCSBACLLPNSSSWFPMWAESDNGSVGSEDQQLSAHISPAIPV 60
Db 61 IITAVYSVFVVGVLGNSIVMEVIRYTKMKTATNITYFNALADALVTTPMQSAVYL 120
QY 61 IITAVYSVFVVGVLGNSIVMEVIRYTKMKTATNITYFNALADALVTTPMQSAVYL 120
Db 121 MNSWPFQDVLCKIVISIDYYNMFSTIFLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180
QY 121 MNSWPFQDVLCKIVISIDYYNMFSTIFLTMSVDRIYAVCHPVKALDFRTPLKAKIINI 180
Db 181 CIWLLASSVGISAIVLGKTKREDVDYIECSLQFPDDEYSWMDLFMKICVEFAFVIVPL 240
QY 181 CIWLLASSVGISAIVLGKTKREDVDYIECSLQFPDDEYSWMDLFMKICVEFAFVIVPL 240
Db 241 IITVCTLMILRLKSVRLISGSKREKDRNLRLRITKLVVVAVFIICWTPIHIFLIVEALG 300
QY 241 IITVCTLMILRLKSVRLISGSKREKDRNLRLRITKLVVVAVFIICWTPIHIFLIVEALG 300
Db 301 STSHSTAALSSYFCIALGYTNSSLNPLYAFLDENEKRCFRDCEFPDKMRMERQSTNRV 360
QY 301 STSHSTAALSSYFCIALGYTNSSLNPLYAFLDENEKRCFRDCEFPDKMRMERQSTNRV 360
Db 361 RNTVQDPASMRDVGGMKNKPV 380
QY 361 RNTVQDPASMRDVGGMKNKPV 380

RESULT 2
ID OPRK RAT STANDARD; PRT; 380 AA.
AC P34975;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)

DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN OPRK1 OR KOR-D.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94059008.
RA CHEN Y., MESTEK A., LIU J., YU L.;
RL BIOCHEM. J. 295:625-628(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93374033.
RA MINAMI M., TOYA T., KATAO Y., MAEKAWA K., NAKAMURA S., ONOGI T.,
RA KANEKO S., SATOH M.;
RL FEBS LETT. 329:291-295(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 94059009.
RA LI S., ZHU J., CHEN C., CHEN Y.-W., DERIEL J.K., ASHBY B.,
RA LIU-CHEN L.-Y.;
RL BIOCHEM. J. 295:629-633(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RX MEDLINE; 94052210.
RA MENG F., XIE G.-X., THOMPSON R.C., MANSOUR A., GOLDSTEIN A.,
RA WATSON S.J., AKIL H.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:9954-9958(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=BRAIN;
RX MEDLINE; 93380575.
RA NISHI M., TAKESHIMA H., FUKUDA K., KATO S., MORI K.;
RL FEBS LETT. 330:77-80(1993).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE; 95204422.
RA YAKOVLEV A.G., KRUEGER K.E., FADEN A.I.;
RL J. BIOL. CHEM. 270:6421-6424(1995).
CC -I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L22001; G409237; -.
DR EMBL; D16829; G404116; -.
DR EMBL; L22536; G425189; -.
DR EMBL; U00442; G403487; -.
DR EMBL; D16534; G415310; -.
DR EMBL; U17995; G727260; -.
DR EMBL; U17993; G727260; JOINED.
DR EMBL; U17994; G727260; JOINED.
DR PIR; S36143; S36143.
DR PIR; S38825; S38825.
DR GCRDB; GCR_0636; -.
DR GCRDB; GCR_0724; -.
DR GCRDB; GCR_0790; -.
DR GCRDB; GCR_0804; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
FT CONFLICT 42 42 V -> L (IN REF. 2).
FT CONFLICT 345 345 C -> Y (IN REF. 3).
SQ SEQUENCE 380 AA; 42688 MW; EE858A46 CRC32;

Query Match 99.6%; Score 2829; DB 1; Length 380;
Best Local Similarity 98.9%; Pred. No. 0.00e+00;
Matches 376; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 1 MESPIQIFRGEPTCAPSACLLPNSSWFPNWAESDSNGSVGSEDQOLEPAHISPAIPV 60
QY 1 MESPIQIFRGEPTCAPSACLLPNSSWFPNWAESDSNGSVGSEDQOLESAHISPAIPV 60
Db 61 IITAVYSVFEVVGGLVNSLVMFVLIIRYTKMKTATNTIYIFNLALADALVTTTTFQSAVYL 120
QY 61 IITAVYSVFEVVGGLVNSLVMFVLIIRYTKMKTATNTIYIFNLALADALVTTTTFQSAVYL 120
Db 121 MNSWPFEGDVLCKIVISIDYNNMFTSIFLLTMMSVDRIYAVCHPVKALDFRTPLKAKIINI 180
QY 121 MNSWPFEGDVLCKIVISIDYNNMFTSIFLLTMMSVDRIYAVCHPVKALDFRTPLKAKIINI 180
Db 181 CIWLLASSVGISAIVLGKTKVREDVDVIECSLQFPDDEYSWMDLFMKICVFVFAFVIVPVL 240
QY 181 CIWLLASSVGISAIVLGKTKVREDVDVIECSLQFPDDEYSWMDLFMKICVFVFAFVIVPVL 240
Db 241 IITVCYTIMILRLKSVRLSGSREKDRNLRRITKVLVYVAVFIICWTPIHIFILVEALG 300
QY 241 IITVCYTIMILRLKSVRLSGSREKDRNLRRITKVLVYVAVFIICWTPIHIFILVEALG 300
Db 301 STSHSTALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDCEFPKMRMEROSTNRV 360
QY 301 STSHSTALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDCEFPKMRMEROSTNRV 360
Db 361 RNTVQDPASMRDVGGMNKPV 380
QY 361 RNTVQDPASMRDVGGMNKPV 380

RESULT 3
ID OPRK HUMAN STANDARD; PRT; 380 AA.
AC P41145;
DT 01-FEB-1995 (REL. 31, CREATED)
DT 01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE KAPPA-TYPE OPIOID RECEPTOR (KOR-1).
GN OPRK1 OR OPRK.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 94338360.
RA MANSSON E., BARE L.A., YANG D.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 202:1431-1437(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE; 95350200.
RA SIMONIN F., GAVERIAUS-RUFF C., BEFORT K., LANNES B., MICHELETTI G.,
RA MATTEI M.-G., CHARON G., BLOCH B., KIEFFER B.;
RL PROC. NATL. ACAD. SCI. U.S.A. 92:7006-7010(1995).

RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 95174504.
RA ZHU J., CHEN C., XUE J.C., KUNAPULI S., DERIEL J.K., LIU-CHEN L.-Y.;
RL LIFE SCI. 56:201-207(1995).
CC -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF
AUTONOMIC AND ENDOCRINE FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U11053; G532060; -.
DR EMBL; U17298; G596070; -.
DR EMBL; U37362; G722618; -.
DR PIR; JC2338; JC2338.
DR MIM; 165196; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 58 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 59 85 1 (POTENTIAL).
FT DOMAIN 86 95 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 96 117 2 (POTENTIAL).
FT DOMAIN 118 132 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 133 154 3 (POTENTIAL).
FT DOMAIN 155 173 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 174 196 4 (POTENTIAL).
FT DOMAIN 197 222 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 223 247 5 (POTENTIAL).
FT DOMAIN 248 275 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 276 299 6 (POTENTIAL).
FT DOMAIN 300 311 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 312 333 7 (POTENTIAL).
FT DOMAIN 334 380 CYTOPLASMIC (POTENTIAL).
FT DISULFID 131 210 BY SIMILARITY.
FT LIPID 345 345 PALMITATE (POTENTIAL).
FT CARBOHYD 25 25 POTENTIAL.
FT CARBOHYD 39 39 POTENTIAL.
SQ SEQUENCE 380 AA; 42659 MW; 1980629E CRC32;

Query Match 96.8%; Score 2747; DB 1; Length 380;
Best Local Similarity 93.9%; Pred. No. 0.00e+00;
Matches 357; Conservative 17; Mismatches 6; Indels 0; Gaps 0;

Db 1 MESPIQIFRGEPTCAPSACLLPNSSWFPNWAESDSNGSVGSEDQOLEPAHISPAIPV 60
QY 1 MESPIQIFRGEPTCAPSACLLPNSSWFPNWAESDSNGSVGSEDQOLESAHISPAIPV 60
Db 61 IITAVYSVFEVVGGLVNSLVMFVLIIRYTKMKTATNTIYIFNLALADALVTTTTFQSAVYL 120
QY 61 IITAVYSVFEVVGGLVNSLVMFVLIIRYTKMKTATNTIYIFNLALADALVTTTTFQSAVYL 120
Db 121 MNSWPFEGDVLCKIVISIDYNNMFTSIFLLTMMSVDRIYAVCHPVKALDFRTPLKAKIINI 180
QY 121 MNSWPFEGDVLCKIVISIDYNNMFTSIFLLTMMSVDRIYAVCHPVKALDFRTPLKAKIINI 180
Db 181 CIWLLASSVGISAIVLGKTKVREDVDVIECSLQFPDDEYSWMDLFMKICVFVFAFVIVPVL 240
QY 181 CIWLLASSVGISAIVLGKTKVREDVDVIECSLQFPDDEYSWMDLFMKICVFVFAFVIVPVL 240
Db 241 IITVCYTIMILRLKSVRLSGSREKDRNLRRITKVLVYVAVFIICWTPIHIFILVEALG 300
QY 241 IITVCYTIMILRLKSVRLSGSREKDRNLRRITKVLVYVAVFIICWTPIHIFILVEALG 300
Db 301 STSHSTALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDCEFPKMRMEROSTNRV 360
QY 301 STSHSTALSSYYFCIALGYTNSSLNPVLYAFLDENFKRCFRDCEFPKMRMEROSTNRV 360
Db 361 RNTVQDPAYLRDIDGMNKPV 380
QY 361 RNTVQDPASMRDVGGMNKPV 380

RESULT	ID	OPRK_CAVPO	STANDARD;	PRT;	380 AA.
AC	P41144;				
DT	01-FEB-1995 (REL. 31, CREATED)				
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	KAPPA-TYPE OPIOID RECEPTOR (KOR-1).				
GN	OPRK1.				
OS	CAVIA PORCELLUS (GUINEA PIG).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-HARTLEY; TISSUE-BRAIN;				
RX	MEDLINE; 94224825.				
RA	XIE G.X., MENG F., MANSOUR A., THOMPSON R.C., HOVERSTEN M.T.,				
RA	GOLDSTEIN A., WATSON S.J., AKIL H.;				
RL	PROC. NATL. ACAD. SCI. U.S.A. 91:3779-3783(1994).				
CC	-1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM				
CC	ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR				
CC	FOR DYNORPHINS. MAY PLAY A ROLE IN AROUSAL AND REGULATION OF				
CC	AUTONOMIC AND NEUROENDOCRINE FUNCTIONS.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.				
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
DR	EMBL; U04092; G476107; -.				
DR	GCRL; GCR_0991; -.				
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.				
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;				
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.				
FT	DOMAIN	1	58	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	59	85	1 (POTENTIAL).	
FT	DOMAIN	86	95	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	96	117	2 (POTENTIAL).	
FT	DOMAIN	118	132	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	133	154	3 (POTENTIAL).	
FT	DOMAIN	155	173	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	174	196	4 (POTENTIAL).	
FT	DOMAIN	197	222	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	223	247	5 (POTENTIAL).	
FT	DOMAIN	248	275	CYTOPLASMIC (POTENTIAL).	
FT	TRANSMEM	276	299	6 (POTENTIAL).	
FT	DOMAIN	300	311	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	312	333	7 (POTENTIAL).	
FT	DOMAIN	334	380	CYTOPLASMIC (POTENTIAL).	
FT	DISULFID	131	210	BY SIMILARITY.	
FT	LIPID	345	345	PALMITATE (POTENTIAL).	
FT	CARBOHYD	25	25	POTENTIAL.	
FT	CARBOHYD	39	39	POTENTIAL.	
FT	SEQUENCE	380 AA;	42736 MW;	F9F34C4C CRC32;	
Query Match		91.9%;	Score 2610;	DB 1;	Length 380;
Best Local Similarity		92.9%;	Pred. No. 0.00e+00;		
Matches	338;	Conservative	21;	Mismatches	5; Indels 0; Gaps 0;
Db	17 ARNACLLPNGSAWLPGWAEPDNGSAGPQDEQLPEPAHISPAIPVIITAVYSVVEVGLVG				76
QY	17 SPSACLLPNSSSWEPNWAESDSNGSVGSEDDQLSAHISPAIPVIITAVYSVVEVGLVG				76
Db	77 NSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMMPEQSTVYLMNSWPFEGDVLCKIYIS				136
QY	77 NSLVMFVIIRYTKMKTATNIYIFNLALADALVTTTMMPEQSAVYLMNSWPFEGDVLCKIYIS				136
Db	137 IDYNNMETSIFTLTMMSVDRYIAVCHPVKALDFRTPKAKLINICIMWLLSSVGISAITL				196
QY	137 IDYNNMETSIFTLTMMSVDRYIAVCHPVKALDFRTPKAKLINICIMWLLSSVGISAIVL				196
Db	197 GGTQVREDVDIIECSLQFPDDYSWMDLFMKICVFVFAFVLPVLIITVCYTLMILREKSV				256
QY	197 GGTQVREDVDIIECSLQFPDDDEYSWMDLFMKICVFVFAFVLPVLIITVCYTLMILREKSV				256
Db	257 RLLSGSREKDRNLRRITRLVLVVAVFIICWTPIHIFILVEALGSTSHSTAALSSYYFCI				316

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Db      317  ALGYTNSLNPLIYAFLDENEKRCFRDPCFPKRMEROSTSVYNTVDPAYMYNDGV 376
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      317  ALGYTNSLNPLVYAFLDENEKRCFRDPCFPKRMEROSTSVYNTVDPAYMYNDGV 376
Db      377  NKPV 380
      ||||
QY      377  NKPV 380

RESULT      5
ID  OPRM_MOUSE      STANDARD;      PR1;      398 AA.
AC  P42866; Q60768;
DT  01-NOV-1995 (REL. 32, CREATED)
DT  01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT  01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE  MU-TYPE OPIOID RECEPTOR (MOR-1).
OS  OPRM1 OR OPRM OR MOR.
OS  MUS MUSCULUS (MOUSE).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUKHERIA; RODENTIA.
RN  [1]
RC  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6; TISSUE=LIVER;
RX  MEDLINE; 94377496.
RA  MIN B.H., AUGUSTIN L.B., FELSHEIM R.F., FUCHS J.A., LOH H.H.;
RL  PROC. NATL. ACAD. SCI. U.S.A. 91:9081-9085(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=BRAIN;
RX  MEDLINE; 95377399.
RA  ROSSI G.C., PAN Y.X., BROWN G.P., PASTERNAK G.W.;
RL  FEBS LETT. 369:192-196(1995).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/C; TISSUE=BRAIN;
RX  MEDLINE; 95318184.
RA  KAUFMAN D.L., KEITH D.E., ANTON B., TIAN J., MAGENDO K.,
RA  NEWMAN D., TRAN T., LEE D.S., WEN C., XIA Y., LUSIS A.J.,
RA  EVANS C.J.;
RL  J. BIOL. CHEM. 270:15877-15883(1995).
CC  -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC  ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC  FOR BETA-ENDORPHIN.
CC  -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR  EMBL; U10561; G565069; -.
DR  EMBL; U10558; G565069; JOINED.
DR  EMBL; U10559; G565069; JOINED.
DR  EMBL; U10560; G565069; JOINED.
DR  EMBL; U26915; G1055231; -.
DR  EMBL; U19380; G885865; -.
DR  MGD: MGI:97441; OPRM.
KW  PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW  G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW  PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT  DOMAIN      1      64      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM      65      94      1 (POTENTIAL).
FT  DOMAIN      95      103      CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM     104      121      2 (POTENTIAL).
FT  DOMAIN     122      143      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM     144      163      3 (POTENTIAL).
FT  DOMAIN     164      193      CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM     194      209      4 (POTENTIAL).
FT  DOMAIN     210      234      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM     235      257      5 (POTENTIAL).
FT  DOMAIN     258      280      CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM     281      303      6 (POTENTIAL).
FT  DOMAIN     304      311      EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM     312      328      7 (POTENTIAL).
FT  DOMAIN     329      398      CYTOPLASMIC (POTENTIAL).

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FT DISULFID 140 217 BY SIMILARITY.
FT LIPID 351 351 PALMITATE (POTENTIAL).
FT CARBOHYD 9 9 POTENTIAL.
FT CARBOHYD 31 31 POTENTIAL.
FT CARBOHYD 38 38 POTENTIAL.
FT CARBOHYD 46 46 POTENTIAL.
FT CONFLICT 22 22 C -> W (IN REF. 3).
SQ SEQUENCE 398 AA; 44421 MW; C0211489 CRC32;

Query Match 59.1%; Score 1678; DB 1; Length 398;
Best Local Similarity 65.8%; Pred. No. 0.00e+00;
Matches 208; Conservative 55; Mismatches 49; Indels 4; Gaps 4;

Db 68 AITMALYSIVCVGLFGNFLVMYIVRYTKMKTATNIIYFNLAADALATSTLPQSVN 127
QY 59 PVITAVSVFVGLVGNLSLVMFVITRYTKMKTATNIIYFNLAADALVTTTTPFQSAV 118
Db 128 YLMGTWPEGNILCKIVISIDYNNMETSIFTLCTMSVDRIYAVCHPYKALDERTPRNAKIV 187
QY 119 YLMNSWPEGDYLOKIVISIDYNNMETSIFTLCTMSVDRIYAVCHPYKALDERTPLKAKII 178
Db 188 NVCNWLSSAIGLPVFMATTKYRQG-S-IDCTLTFSHPTW-YWENLTKICVFETFTMP 244
QY 179 NICIWLLASSVGSIAIVLGTQVREDVYIECSLQFPDDEYSWMDLKMICVEFAFVIP 238
Db 245 VLIITVCGMLRLRLKSVRLSGSKERDNLRTIRMYLVVAVFIYCWTPIHIYIKA 304
QY 239 VLIITVCGTLMILRLKSVRLSGSKERDNLRTIKLVVAVFIICWTPIHIFILVEA 298
Db 305 LITIPETPQTVSWHFCIALGYTNSCLNPLYAFLDENFKRCFERFCIPTSTIEQNSA 364
QY 299 LGSISHSTAALSSYYFCIALGYTNSCLNPLYAFLDENFKRCFCRPFPIKRMERQSTIN 358
Db 365 RIRQNTREHPSTANTV 380
QY 359 RVR-NTVQDPASMRDV 373

RESULT 6
ID OPRM_RAT STANDARD; PRT; 398 AA.
AC P33535; Q64064; Q62846;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DI 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1) (OPIOID RECEPTOR B) (MUOR1).
GN OPRM1 OR MOR-B.
OS RATTUS NORVEGICUS (RAT).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN 11]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 93351652.
RA FUKUDA K., KATO S., MORI K., NISHI M., TAKESHIMA H.;
RL FEBS LETT. 327:311-314(1993).
RN 12]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94052137.
RA WANG J.-B., IMAI Y., EPLER M.C., GREGOR P., SPIVAK C., UHL G.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 90:10230-10234(1993).
RN 13]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 93341493.
RA CHEN Y., MESTEK A., LIU J., HURLEY J.A., YU L.;
RL MOL. PHARMACOL. 44:8-12(1993).
RN 14]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
RA BUNZOW J.R., GRANDY D.K., KELLY M.;
RL SUBMITTED (SEP-1993) TO EMBL/GENBANK/DBJ DATA BANKS.
RN 15]
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RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=OLFACTORY BULB;
RX MEDLINE; 94059560.
RA THOMPSON R.C., MANSOUR A., AKIL H., WATSON S.J.;
RL NEURON 11:903-913(1993).
RN 16]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94246380.
RA ZASTAWNY R.L., GEORGE S.R., NGUYEN T., CHENG R., TSATSOS J.,
RA BRIONES-URBINA R., O'DOWD B.F.;
RL J. NEUROCHEM. 62:2099-2105(1994).
RN 17]
RP SEQUENCE OF 356-391 FROM N.A.
RX MEDLINE; 95172221.
RA ZIMPRICH A., SIMON T., HOLTF V.;
RL FEBS LETT. 359:142-146(1995).
CC -I- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDORPHIN.
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -I- TISSUE SPECIFICITY: BRAIN. IS EXPRESSED IN THE CEREBRAL CORTEX,
CC CAUDATE PUTAMEN, NUCLEUS ACCUMBENS, SEPTAL NUCLEI, THALAMUS,
CC HIPPOCAMPUS, AND HABENULA. NOT DETECTED IN CEREBELLUM.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC EMBL; D16349; G391867; -.
CC EMBL; L20684; G409150; -.
CC EMBL; L13069; G348251; -.
CC EMBL; U02083; G403574; -.
CC EMBL; L22455; G437672; -.
CC EMBL; U35424; G1017732; -.
CC EMBL; S75669; G861432; -.
CC PIR; S34593; S34593.
CC GCRDB; GCR_0633; -.
CC GCRDB; GCR_0637; -.
CC GCRDB; GCR_0639; -.
CC GCRDB; GCR_0640; -.
CC GCRDB; GCR_0864; -.
CC PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
CC G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
CC PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
CC DOMAIN 1 64 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 65 94 1 (POTENTIAL).
CC DOMAIN 95 103 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 104 121 2 (POTENTIAL).
CC DOMAIN 122 143 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 144 163 3 (POTENTIAL).
CC DOMAIN 164 193 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 194 209 4 (POTENTIAL).
CC DOMAIN 210 234 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 235 257 5 (POTENTIAL).
CC DOMAIN 258 280 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 281 303 6 (POTENTIAL).
CC DOMAIN 304 311 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 312 328 7 (POTENTIAL).
CC DOMAIN 329 398 CYTOPLASMIC (POTENTIAL).
CC DISULFID 140 217 BY SIMILARITY.
CC LIPID 351 351 PALMITATE (POTENTIAL).
CC CARBOHYD 9 9 POTENTIAL.
CC CARBOHYD 31 31 POTENTIAL.
CC CARBOHYD 38 38 POTENTIAL.
CC CARBOHYD 46 46 POTENTIAL.
CC CONFLICT 237 237 F -> G (IN REF. 6).
CC CONFLICT 245 245 V -> I (IN REF. 3 AND 4).
CC CONFLICT 387 391 LENIE -> KIVLE (IN REF. 7).
SQ SEQUENCE 398 AA; 44494 MW; 2C21013D CRC32;

Query Match 59.0%; Score 1676; DB 1; Length 398;
Best Local Similarity 66.1%; Pred. No. 0.00e+00;
Matches 209; Conservative 53; Mismatches 50; Indels 4; Gaps 4;

Db 68 AITMALYSIVCVGLFGNFLVMYIVRYTKMKTATNIIYFNLAADALATSTLPQSVN 127
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QY      59 PVIIITAVYSVVEVVGVLGNSLVMEVVIIRYTKMKIATNIIYFNALADALVTTTMRQSAV 118
Db      128 YLMGTWPFGTILCKIVISIDYYNMFISIFTLCTMSVDRIYAVCHPVKALDFRTPRNAKIV 187
QY      119 YLMNSWPFEGDVLCKIVISIDYYNMFISIFTLTMSVDRIYAVCHPVKALDFRTPLAKIIT 178
Db      188 NVCNWILSSAIGLPVMEATTKYRG-S-IDCTLFESHPTW-YWENLTKICVFIFAFIMP 244
QY      179 NICIWLASSVGISAVLGGTKVREDVDVIECSIQFPDDEXSWWDLFMKICVFVFAFVIP 238
Db      245 VLIITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVWVAVFIVCWTPIHIVLIKA 304
QY      239 VLIITVCYTIMILRLKSVRLSGSREKDRNLRRITKLVVWVAVFIIICWTPIHIFILVEA 298
Db      305 LTIIPETTFQTVSWHFCIALGYTNSCLNPVLYAFIDENFKRCFREFCIPTSSTIEQONST 364
QY      299 LGTSHSTALSSYYFCIALGYTNSSLNPVLYAFIDENFKRCFRDPCFPDKMRMEROSTN 358
Db      365 RVRONTREHPSTANTV 380
QY      359 RVR-NTVQDPASMRDV 373
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RESULT 7
ID OPRM_HUMAN STANDARD; PRT; 400 AA.
AC P35372;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1 OR MOR1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE; 94139928.
RA WANG J.-B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,
RA UHL G.R.;
RL FEBS LETT. 338:217-222(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA MESTER A. JR., HURLEY J.H., BYE L.S., CAMPBELL A., TIAN M.,
RA CHEN Y., YU L.;
RL SUBMITTED (XXX-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDORPHIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L25119; G452073; -.
DR EMBL; L29301; G459832; -.
DR GCRDB; GCR_0885; -.
DR GCRDB; GCR_0966; -.
DR MM: 600018; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 66 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 67 96 1 (POTENTIAL).
FT DOMAIN 97 105 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 106 123 2 (POTENTIAL).
FT DOMAIN 124 145 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 146 165 3 (POTENTIAL).
FT DOMAIN 166 195 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 196 211 4 (POTENTIAL).
FT DOMAIN 212 236 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 237 259 5 (POTENTIAL).
FT DOMAIN 260 282 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 283 305 6 (POTENTIAL).
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FT DOMAIN 306 313 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 314 330 7 (POTENTIAL).
FT DOMAIN 331 400 CYTOPLASMIC (POTENTIAL).
FT DISULFID 142 219 BY SIMILARITY.
FT LIPID 353 353 PALMITATE (POTENTIAL).
FT CARBOHYD 9 9 POTENTIAL.
FT CARBOHYD 12 12 POTENTIAL.
FT CARBOHYD 33 33 POTENTIAL.
FT CARBOHYD 40 40 POTENTIAL.
FT CARBOHYD 48 48 POTENTIAL.
FT CONFLICT 51 51 N -> D (IN REF. 2).
FT CONFLICT 234 234 V -> L (IN REF. 2).
SQ SEQUENCE 400 AA; 44764 MW; 3F40D610 CRC32;
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Query Match 59.0%; Score 1675; DB 1; length 400;
Best local Similarity 66.6%; Pred. No. 0.00e+00;
Matches 207; Conservative 52; Mismatches 49; Indels 3; Gaps 3;

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Db      70 AITMALYSIVCVGLFNGFLVMYVIVRYTKMKIATNIIYFNALADALATSTLPEQSVN 129
QY      59 PVIIITAVYSVVEVVGVLGNSLVMEVVIIRYTKMKIATNIIYFNALADALVTTTMRQSAV 118
Db      130 YLMGTWPFGTILCKIVISIDYYNMFISIFTLCTMSVDRIYAVCHPVKALDFRTPRNAKII 189
QY      119 YLMNSWPFEGDVLCKIVISIDYYNMFISIFTLTMSVDRIYAVCHPVKALDFRTPLAKIIT 178
Db      190 NVCNWILSSAIGLPVMEATTKYRG-S-IDCTLFESHPTW-YWENLTKICVFIFAFIMP 246
QY      179 NICIWLASSVGISAVLGGTKVREDVDVIECSIQFPDDEXSWWDLFMKICVFVFAFVIP 238
Db      247 VLIITVCYGLMILRLKSVRLSGSKEKDRNLRRITRMVLVWVAVFIVCWTPIHIVLIKA 306
QY      239 VLIITVCYTIMILRLKSVRLSGSREKDRNLRRITKLVVWVAVFIIICWTPIHIFILVEA 298
Db      307 LTIIPETTFQTVSWHFCIALGYTNSCLNPVLYAFIDENFKRCFREFCIPTSSTIEQONST 365
QY      299 LGTSHSTALSSYYFCIALGYTNSSLNPVLYAFIDENFKRCFRDPCFPDKMRMEROSTN 358
Db      367 RIRONTRDHPS 377
QY      359 RVRNTVQDPAS 369
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RESULT 8
ID OPRM_PIG STANDARD; PRT; 401 AA.
AC Q95247;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE MU-TYPE OPIOID RECEPTOR (MOR-1).
GN OPRM1.
OS SUS SCROFA (PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; ARTIODACTYLIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX;
RA PAMPUCH M.P., OSINSKI M.A., BROWN D.R., MURTAUGH M.P.;
RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. RECEPTOR
CC FOR BETA-ENDORPHIN.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; L38645; G1553057; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 67 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 68 97 1 (POTENTIAL).
FT DOMAIN 98 106 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 107 124 2 (POTENTIAL).
FT DOMAIN 125 146 EXTRACELLULAR (POTENTIAL).
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RP SEQUENCE FROM N.A.
RC TISSUE=CEREBRAL CORTEX, AND STRIATUM;
RA MEDLINE; 94260835.
RX KNAPP R.J., MALATYNSKA E., FANG L., LI X., BABIN E., NGUYEN M.,
RA SANTORO G., VARGA E.V., HRUBEY V.J., ROESKE W.R., YAMAMURA H.I.;
RL LIFE SCI. 54:463-469(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95107267.
RA SIMONIN F., BEFORT K., GAVERIAUX-RUFF C., MATTHES H., NAPPET V.,
RA LANNES B., MICHELETTI G., KIEFER B.;
RA MOL. PHARMACOL. 46:1015-1021(1994).
CC -!- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
CC ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
CC STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; U07882; G497314; -.
DR EMBL; U10504; E162517; -.
DR MTM; 165195; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT DOMAIN 1 45 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 46 75 1 (POTENTIAL).
FT DOMAIN 76 84 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 85 102 2 (POTENTIAL).
FT DOMAIN 103 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 144 3 (POTENTIAL).
FT DOMAIN 145 174 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 175 190 4 (POTENTIAL).
FT DOMAIN 191 215 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 216 238 5 (POTENTIAL).
FT DOMAIN 239 261 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 262 284 6 (POTENTIAL).
FT DOMAIN 285 293 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 294 310 7 (POTENTIAL).
FT DOMAIN 311 372 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 18 18 POTENTIAL.
FT CARBOHYD 33 33 BY SIMILARITY.
FT DISULFID 121 198 PALMITATE (POTENTIAL).
FT LIPID 333 333 F -> C (IN REF. 2).
FT CONFLICT 27 27 PG -> AR (IN REF. 2).
FT CONFLICT 40 41 PG -> A (IN REF. 2).
FT CONFLICT 348 348 P -> A (IN REF. 2).
FT CONFLICT 370 370 R -> A (IN REF. 2).
SQ SEQUENCE 372 AA; 40450 MW; CFF92985 CRC32;

Query Match 56.6%; Score 1608; DB 1; Length 372;
Best Local Similarity 65.38; Pred. No. 3.79e-293;
Matches 213; Conservative 56; Mismatches 48; Indels 9; Gaps 8;

Db 15 LFANASDAYPS-A-FPSAGANASGPPGSGAS-SLALATATATATLAYSACVAGLLGNVLM 71
22 LLPSSSWFPPNWAESDSNGSVGSEDDQLESAAHISPAIPVITAVYSVFVVGVLGNSLVM 81
Db 72 FGIIVRYTKMTATINITYFNLLADALATSTLPFQSAKIMETWPFGECLKAVLSIDYYN 131
82 FVLIIRYTKMTATINITYFNLLADALATVTTMPFQSAVYIMNSWPFQDLCKIVISIDYYN 141
Db 132 MFTSIFLLTMSVDRIYAVCHPVKALDFRTPAKALINICIVWLASGVGPIMMAVTRP 191
142 MFTSIFLLTMSVDRIYAVCHPVKALDFRTPEKAKINICIVWLASSVGSATVLGTKV 201
Db 192 RDGA-VV-CMLQPPS--SWYWDVTVKICVFLFAFVVDILITTCYGLMLRLRSVRLS 247
202 REDVDVIECSLQFPDEXSW-WDLFMKICVFVFAFVLYLLIIVCYTLMILRLKSVRLS 260
Db 248 GSKKEDRSLRITRWLVVGAFFVVCWAPIHIFVLYWLLVDIDRRDPLVVAALHCTALG 307
QY 261 GSREKDRNLRRITKLVVAVVFIICWTPIHIFILVEALGSTSHSTA-ALSSYYFCIALG 319
Db 308 YANSLNPVLYAFDENFKRCFRQLC 333

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QY      320 YTNSSSLNPVLYAFLEDFENFKRCFRDFC 345

RESULT 11
ID      OPBD.MOUSE      STANDARD;      PRT;      372 AA.
AC      P32300;
DT      01-OCT-1993 (REL. 27, CREATED)
DT      01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
DT      01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE      DELTA-TYPE OPIOID RECEPTOR (DOR-1) (K56) (MSL-2).
      OPRD1.
OS      MUS MUSCULUS (MOUSE).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
      OC      EUTHERIA; RODENTIA.
      [1]
      RN      RP      SEQUENCE FROM N.A.
      RX      MEDLINE; 93101664.
      RA      KIEFFER B.L., BEFORE K., GAVERIAUX-ROUE C., HIRTH C.G.;
      RL      PROC. NATL. ACAD. SCI. U.S.A. 89:12048-12052(1992).
      [2]
      RN      RP      SEQUENCE FROM N.A.
      RX      MEDLINE; 93110361.
      RA      EVANS C.J., KEITH D.E. JR., MORRISON H., MAGENDZO K., EDWARDS R.H.;
      RL      SCIENCE 258:1952-1955(1992).
      [3]
      RN      RP      SEQUENCE FROM N.A.
      RC      TISSUE=BRAIN;
      RX      MEDLINE; 93342064.
      RA      YASUDA K., RAYNOR K., KONG H., BREDER C.D., TAKEDA J., REISINE T.,
      RL      BELF G.I.;
      RL      PROC. NATL. ACAD. SCI. U.S.A. 90:6736-6740(1993).
      [4]
      RN      RP      SEQUENCE FROM N.A.
      RA      KEITH D.E. JR., ANTON B., EVANS C.J.;
      RL      PROC. WEST. PHARMACOL. SOC. 36:299-306(1993).
      [5]
      RN      RP      SEQUENCE OF 8-372 FROM N.A.
      RX      MEDLINE; 94022364.
      RA      BZDEGA T., CHIN H., KIM K., JUNG H.H., KOZAK C.A., KLEE W.A.;
      RL      PROC. NATL. ACAD. SCI. U.S.A. 90:9305-9309(1993).
      [6]
      RN      RP      3D-STRUCTURE MODELLING.
      RX      MEDLINE; 97001837.
      RA      ALKORTA I., LOEW G.H.;
      RL      PROTEIN ENG. 9:573-583(1996).
      CC      -1- FUNCTION: INHIBITS NEUROTRANSMITTER RELEASE BY REDUCING CALCIUM
      CC      ION CURRENTS AND INCREASING POTASSIUM ION CONDUCTANCE. HIGHLY
      CC      STEREOSELECTIVE. RECEPTOR FOR ENKEPHALINS.
      CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
      CC      -1- TISSUE SPECIFICITY: BRAIN, WITH HIGH CONCENTRATIONS IN THE BASAL
      CC      GANGLIA AND LIMBIC REGIONS.
      CC      -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
      DR      EMBL; L06322; G192943; -.
      DR      EMBL; L07271; -: NOT_ANNOTATED_CDS.
      DR      EMBL; L11064; G348247; -.
      DR      EMBL; S65335; G442326; -.
      DR      EMBL; S66181; G435782; -.
      DR      PIR; S37807; S37807.
      DR      PIR; B48227; B48227.
      DR      GCRDB; GCR_0229; -.
      DR      GCRDB; GCR_0493; -.
      DR      GCRDB; GCR_0634; -.
      DR      GCRDB; GCR_0842; -.
      DR      MGI; MGI:97438; OPRD1.
      DR      PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
      KW      G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
      KW      PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
      ET      DOMAIN      1      45      EXTRACELLULAR (POTENTIAL).
      ET      TRANSMEM      46      75      1 (POTENTIAL).
      ET      DOMAIN      76      84      CYTOPLASMIC (POTENTIAL).
      ET      TRANSMEM      85      102      2 (POTENTIAL).
      ET      DOMAIN      103      124      EXTRACELLULAR (POTENTIAL).

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FT	CONFLICT	246		246	S -> P (IN REF. 2).	
FT	CONFLICT	348		348	S -> T (IN REF. 3).	
SQ	SEQUENCE	367 AA;	40523 MW;	7FD40CCC CRC32;		
 Query Match						
	Best Local Similarity	59.9%;	Score 1473;	DB 1;	length 367;	
	Matches	188;	Conservative	63;	Mismatches 61;	Indels 5; Gaps 5;
Db	40	SAFLPLGLKVTIVGLYLAVCIGGLLGNCLVMYVILRHTKMKATNIIYFNLALADTLVL	99			
QY	51	SAHISPAIPVIITAAVSVEFVGVLGNSLVMFEVIIIRTEKMKTATNIYIFNLALADALT	110			
Db	100	TLPFGDTDLGLFWPFGNALCKTVIAIDYYNMETSTFTLRAMSVDRYVAICHPIRALDVR	159			
QY	111	TMPEQSAYVLMNSWPFGEVLDCKIVISIDYYNMETSIFTLEMSVDRIYAVCHPVKALDFR	170			
Db	160	TSSKAQAVNAIWAALASVGVPAVIMGSAQV-EDEE-IECLEVELPAPODY-WGPVFA-IC	215			
QY	171	TPLKAKIITNICIMWLASSVGSIAIVLGTKVREDVDVIECSLQEPD-DEYSWMDLFEMKIC	229			
Db	216	IFLFSFIIPVLIISVCYSMLTRRLRGVKRLLSGRREKDRNLRRITRLVLYVVAVFVGCTP	275			
QY	230	VFEFAFVIPVLIITVCIYTLMLIRLKS VKRLLSGRREKDRNLRRITKLVLVVAVFIICTWP	289			
Db	276	VQVFVLVOGLGVQPGETAVALIRFCIALGYVNSCLNPILIYAFLDENFKACFRKFCASS	335			
QY	290	IHFIFLVEALGSTSHSTAALSYFFICIALGYTNSLNPLVLYAFLEDENFKRCFRDFCFPIK	349			
Db	336	LHREMÖVSDRVRSIAKD	352			
QY	350	MMERQSTNRVNNTVQD	366			

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RESULT 13
ID OPRL_MOUSE STANDARD; PRT; 367 AA.
AC P35377; Q60645;
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID
DE RECEPTOR) (KOR-3) (ORGC) (K3 OPIATE RECEPTOR).
OS OPRL1 OR OPRL OR OOR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6N; TISSUE=BRAIN;
RA YASUDA K., JONES E., REISINE T., BELL G.I.;
RL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95100967.
RA NISHI M., TAKESHIMA H., MORI M., NAKAGAWARA K.I., TAKEUCHI T.;
RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:1353-1357(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA MATTHEWS H.W.D.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A.
RA PAN Y.X., XU J., PASTERNAK G.W.;
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95327076.
RA PAN Y.X., CHENG J., XU J., ROSSI G., JACOBSON E., RYAN-MORO J.,
RA BROOKS A.I., DEAN G.E., STANDIFER K.M., PASTERNAK G.W.;
RL MOL. PHARMACOL. 47:1180-1188(1995).
RN [6]
RP SEQUENCE OF 1-357 FROM N.A.
RC STRAIN=BALE/C; TISSUE=SPLEEN;

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RA	HALFORD W.P., GEBHARDT B.M., CARR D.J.J.;
RL	SUBMITTED (AUG-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC	-1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN EQ.
CC	HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,
CC	INCLUDING INSTINCTIVE BEHAVIOURS AND EMOTIONS. THE ACTIVITY OF
CC	THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLIL
CC	CYCLASE.
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR	EMBL; U04952; G440880; -.
DR	EMBL; D31667; G808874; -.
DR	EMBL; D31666; G808874; JOINED.
DR	EMBL; X91813; G1008982; -.
DR	EMBL; U32932; G1464791; -.
DR	EMBL; U32928; G1464791; JOINED.
DR	EMBL; U32930; G1464791; JOINED.
DR	EMBL; U09421; G551485; -.
DR	EMBL; U14165; G540093; -.
DR	GCRDB; GCR_0891; -.
DR	MGI; MGI:97440; OPR1.
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.
FT	DOMAIN 1 47 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 48 74 1 (POTENTIAL).
FT	DOMAIN 75 84 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 85 106 2 (POTENTIAL).
FT	DOMAIN 107 121 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 122 143 3 (POTENTIAL).
FT	DOMAIN 144 162 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 163 185 4 (POTENTIAL).
FT	DOMAIN 186 208 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 209 233 5 (POTENTIAL).
FT	DOMAIN 234 261 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 262 285 6 (POTENTIAL).
FT	DOMAIN 286 297 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 298 319 7 (POTENTIAL).
FT	DOMAIN 320 366 CYTOPLASMIC (POTENTIAL).
FT	DISULFID 120 197 BY SIMILARITY.
FT	LIPID 331 331 PALMITATE (POTENTIAL).
FT	CARBOHYD 21 21 POTENTIAL.
FT	CARBOHYD 26 26 POTENTIAL.
FT	CARBOHYD 36 36 POTENTIAL.
FT	CONFLICT 348 349 SI -> TV (IN REF. 2).
SO	SEQUENCE 367 AA; 40491 MW; 3F472156 CRC32;

Query Match	51.8%;	Score 1471;	DB 1;	length 367;
Best Local Similarity	59.3%;	Pred. No. 6.84e-265;		
Matches 188;	Conservative	63;	Mismatches 61;	Indels 5;
				Gaps 5;
Db 40	SAFLPLGLKVTIVGLYLAIVCGIGLLGNCLVMYVILRHTKMKTATNIYIFNLALADTLVLL	99		
QY 51	SAHISPATPVITITAVYSVVEFVGLVGNLSVMFVIIIRYTKMKTATNIYIFNLALADALVTT	110		
Db 100	TLEPQGTDLILGFWPFGNALCKTVIAIDYNNMFTSTFTLTAMSVDRYVAICHPIRALDVR	159		
QY 111	TMPFQSAVYILMNSWPFEGDVLCKTVISIDYNNMFTSIFTLTMSVDYRIAVCHPVKALDFR	170		
Db 160	TSSKAQAVNVAITWALASVGVGPVAIMGSAQV-EDEE-TECLVETPAQODY-WGPVFA-IC	215		
QY 171	TEPKAKIINICIMLLASSVGISALVLGGTKVREDVDVIECSIQPFD-DEYSWMDLFMKIC	229		
Db 216	TELESFILPVLLISVCYSMLMRRLRGVRLLLSGSREKDRNLRRTRKLVLVVAVFVGCTWP	275		
QY 230	VEYFAFVIPVLLIITVCYITLMILRLKSVRLLLSGSREKDRNLRRTRKLVLVVAVFIICWTP	289		
Db 276	VQYFVVLVQGLGVQPGSETAVAILRECTALGYVNSCLNPILYAFITDENKCAQFRKFCASA	335		
QY 290	IHTFTLVEALGSTSHSTALSSYIFCIALGYTNSSLNPVLYAFILDENKRCFRDFCFPIK	349		
Db 336	IHRNQVSDRVRSIAKD	352		
QY 350	MRMERQSTNRVRNTVQD	366		

RESULT	14			
ID	OPRX_HUMAN	STANDARD;	PRI;	370 AA.
AC	P41146;			
DT	01-FEB-1995 (REL. 31, CREATED)			
DT	01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	NOCEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID RECEPTOR) (KOR-3).			
DE	RECEPTOR (KOR-3).			
GN	ORP1 OR ORL1 OR OOR.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; EUTHERIA; PRIMATES.			
OC	[1]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=BRAIN STEM;			
RC	MEDLINE; 94185768.			
RX	MOLLEREAU C., PARMENTIER M., MAILLEUX P., BUTOUR J.L., MOISAND C., CHALON P., CAPUT D., VASSART G., MEUNIER C.;			
RA	FEBS LETT. 341:33-38(1994).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	LEE P.H., ZHU J., LIU-CHEN L., CHANG K.;			
RA	SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
RL	-1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.			
CC	HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS, INCLUDING INSTINCTIVE BEHAVIOURS AND EMOTIONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLYL CYCLASE.			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL; X77130; G471317; -.			
DR	EMBL; U30185; G1144297; -.			
DR	PIR; S43087; S43087.			
DR	GCRDB; GCR_0987; -.			
DR	PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.			
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.			
KW	DOMAIN	1	50	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	51	77	1 (POTENTIAL).
FT	DOMAIN	78	87	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	88	109	2 (POTENTIAL).
FT	DOMAIN	110	124	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	125	146	3 (POTENTIAL).
FT	DOMAIN	147	165	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	166	188	4 (POTENTIAL).
FT	DOMAIN	189	211	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	212	236	5 (POTENTIAL).
FT	DOMAIN	237	264	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	265	288	6 (POTENTIAL).
FT	DOMAIN	289	300	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	301	322	7 (POTENTIAL).
FT	DOMAIN	323	370	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	123	200	BY SIMILARITY.
FT	LIPID	334	334	PALMITATE (POTENTIAL).
FT	CARBOHYD	21	21	POTENTIAL.
FT	CARBOHYD	28	28	POTENTIAL.
FT	CARBOHYD	39	39	POTENTIAL.
SQ	SEQUENCE	370 AA;	40693 MW;	BE3C3E8F CRC32;
Query Match				
Best Local Similarity		51.6%;	Score 1465;	DB 1; length 370;
Matches		186;	Conservative	65;
			Mismatches	63;
			Indels	5;
			Gaps	5;
Db	43	GAFPLPLGLKVIIVGLYLAVCYGGLLGNCLVMYVILRHRTKMKATNIIYIFNLALADTVLL	102	
QY	51	SAHISPAIPVITIAVYSVFVGLVGNLSVMFVIIRYTKMTATNIIYIFNLALADALVT	110	
Db	103	TLPFGQTDILLGLFWPEGNALCKTVIAIDYNNMTSTFTLANSVDRYVAICHPIRALDVR	162	
QY	111	TMFQSAVYVLMNSWPEGDYCKIVISIDYNNMTSIFTLNMSVDRYIAVCHPVKALDFR	170	

[illegible]

RESULT	15			
ID	OPRX_PIG	STANDARD;	PRT;	370 AA.
AC	P79292;			
DT	01-NOV-1997 (REL. 35, CREATED)			
DT	01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)			
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)			
DE	NOCICEPTIN RECEPTOR (ORPHANIN FQ RECEPTOR) (KAPPA-TYPE 3 OPIOID RECEPTOR) (KOR-3) (ORGC) (K3 OPIATE RECEPTOR).			
GN	OPRL.			
OS	SUS SCROFA (PIG).			
OC	EUMAROTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; ARTIODACTYLA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=CEREBRAL CORTEX;			
RA	OSINSKI M.A., PAMPUSCH M.S., BROWN D.R., MURTAUGH M.P.;			
RL	SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.			
CC	-1- FUNCTION: RECEPTOR FOR THE NEUROPEPTIDE NOCICEPTIN/ORPHANIN FQ.			
CC	HAS A POTENTIAL ROLE IN MODULATING A NUMBER OF BRAIN FUNCTIONS,			
CC	INCLUDING INSTINCTIVE BEHAVIOURS AND EMOTIONS. THE ACTIVITY OF			
CC	THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH INHIBITS ADENYLAT			
CC	CYLASE (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
DR	EMBL; U72758; G1763257; -.			
KW	PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.			
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN;			
KW	PHOSPHORYLATION; LIPOPROTEIN; PALMITATE.			
FT	DOMAIN	1	50	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	51	77	1 (POTENTIAL).
FT	DOMAIN	78	87	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	88	109	2 (POTENTIAL).
FT	DOMAIN	110	124	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	125	146	3 (POTENTIAL).
FT	DOMAIN	147	165	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	166	188	4 (POTENTIAL).
FT	DOMAIN	189	211	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	212	236	5 (POTENTIAL).
FT	DOMAIN	237	264	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	265	288	6 (POTENTIAL).
FT	DOMAIN	289	300	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	301	322	7 (POTENTIAL).
FT	DOMAIN	323	370	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	123	200	BY SIMILARITY.
FT	LIPID	334	334	PALMITATE (POTENTIAL).
FT	CARBOHYD	21	21	POTENTIAL.
FT	CARBOHYD	28	28	POTENTIAL.
FT	CARBOHYD	39	39	POTENTIAL.
SO	SEQUENCE	370 AA;	40610 MW;	E1050DAC CRC32;
Query Match				
Best Local Similarity		51.48;	Score 1459;	DB 1; Length 370;
Matches 188; Conservative		58.98;	Pred. No. 2.02e-262;	
		62;	Mismatches 64;	Indels 5; Gaps 5;
Db	43 GAFLPLGLKVTVGLYLAACVGGLLGCLVMYVILRHFKMKKTATNIYIFNLALADTAVLL	102		
:	: : : : : : : :			

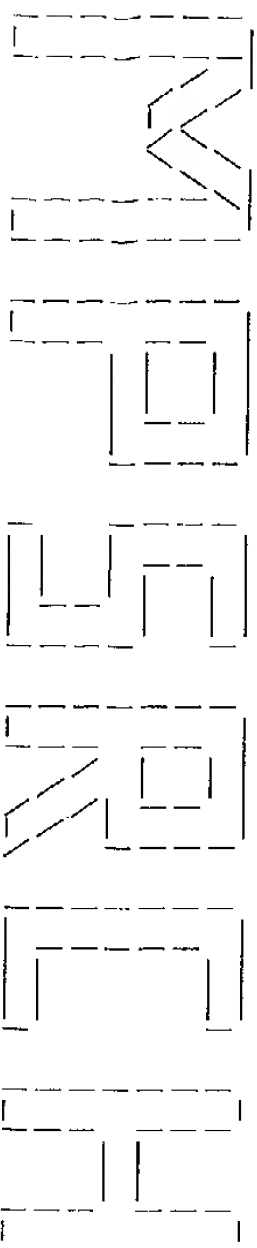
Tue Apr 21 08:03:58 1998

US-08-292-694A-2.rsp

Page 12

QY	51	SAHISPAIPVITTAIVSVVEVVGIVGNSLWMEVLIIRYTKMKTAANNIYFENLALADALVYT	110
Db	103	TLEFGTDLVLGFWPFGNALCAVIAIDYNNMETSATLLTAMSVDRVVAICHPIRALDVR	162
QY	111	TMPEFQSAVYILMNSWPFEGDVLCKIVISIDYNNMETSIFLLIMSVDRYLAVCHPVKALDER	170
Db	163	TSSKAQAVNVAIWALASIVGVPAVIMGSAQV-EDDE-IECLVEIPAPQDY-WGPVFA-VC	218
QY	171	TPLKAKIINICIMWLASSVGISALVIGITKVREDVDVIECSTQFPD-DEYSWMDLFMKIC	229
Db	219	IELEFVIPVLIISVCYSILMVRIRGVRLLSGSREKDRNLRLITRLVLVVAVFGCWT	278
QY	230	VEFEAFVIPVLIIVCYTLMILRLKSVRLLSGSREKDRNLRLITKVLVVAVFITICWTP	289
Db	279	VOVEVLVQGLGVQPGSETAVAVLEPCTALGVVNSCLNPILYAFLEDNENKACFRKCCAPT	338
QY	290	IHIFILVEALGSTSHSTALSSYFCIALGYTNSLNPVLVYAFLEDNENKRCFRDCCPIK	349
Db	339	RRREMQVSDRVRSIAKDVA	357
QY	350	MMMERQSTNRVRNTVQDPA	368

Search completed: Thu Apr 16 13:31:11 1998
Job time : 37 secs.



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(TM)

Msrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 16 13:31:30 1998; MasPar time 19.25 Seconds
831.466 Million cell updates/sec
Tabular output not generated.

Title: >US-08-292-694A-2
Description: (1-380) from US08292694A.pep
Perfect Score: 2839
Sequence: 1 MESPIQIFRGDPGPTCPSA.....RNTVQDPASMRDVGGMKRPV 380

Scoring table: PAM 150
Gap 11

Searched: 140555 seqs, 42109429 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl5
1:sp_fungi 2:sp_human 3:sp_invertebrate 4:sp_mammal
5:sp_mhc 6:sp_organelle 7:sp_phage 8:sp_plant
9:sp_bacteria 10:sp_rodent 11:sp_virus 12:sp_vestebate
13:sp_unclassified

Statistics: Mean 48.552; Variance 120.533; scale 0.403

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1680	59.2	392	2	Q12930	MT OPIOID RECEPTOR VAR	1.87e-253
2	1652	58.2	383	12	O42324	MT-OPIOID RECEPTOR.	1.08e-248
3	1650	58.1	401	4	P79350	MT OPIOID RECEPTOR.	2.37e-248
4	1339	47.2	240	10	Q64120	MT-OPIOID RECEPTOR MOR	1.26e-195
5	860	30.3	117	10	Q60733	KAPPA OPIOID RECEPTOR	2.17e-115
6	662	23.3	119	10	Q64206	DELTA OPIOID RECEPTOR/	7.46e-83
7	635	22.4	98	10	P97266	MT-OPIOID RECEPTOR (FR	1.83e-78
8	615	21.7	372	10	O08726	GALANIN RECEPTOR TYPE	3.19e-75
9	609	21.5	359	12	P79785	ANGIOTENSIN II RECEPT	2.98e-74
10	605	21.3	359	10	O35210	ANGIOTENSIN II RECEPT	1.32e-73
11	594	20.9	354	10	O35313	CCRS5.	7.92e-72
12	587	20.7	352	4	O02746	CHEMOKINE RECEPTOR CCR	1.07e-70
13	585	20.6	354	10	P97405	BETA CHEMOKINE RECEPT	2.24e-70
14	585	20.6	354	10	P97308	C-C CHEMOKINE RECEPT	2.24e-70
15	586	20.6	362	12	O91383	ANGIOTENSIN II RECEPT	1.55e-70
16	580	20.4	352	2	O14705	CCRS5 RECEPTOR (FRAGMEN	1.43e-69
17	579	20.4	354	10	O35891	CC CHEMOKINE RECEPTOR-	2.08e-69
18	576	20.3	352	2	O14692	CCRS5 RECEPTOR (FRAGMEN	6.32e-69
19	576	20.3	352	2	O14697	CCRS5 RECEPTOR (FRAGMEN	6.32e-69
20	576	20.3	352	4	O18770	CCRS5 RECEPTOR (FRAGMEN	6.32e-69

21	575	20.3	352	2	O14702	CCRS5 RECEPTOR (FRAGMEN	9.16e-69
22	575	20.3	352	2	O14699	CCRS5 RECEPTOR (FRAGMEN	9.16e-69
23	575	20.3	352	2	O14704	CCRS5 RECEPTOR (FRAGMEN	9.16e-69
24	575	20.3	352	2	O14700	CCRS5 RECEPTOR (FRAGMEN	9.16e-69
25	575	20.3	352	2	O15538	CCRS5 RECEPTOR (FRAGMEN	9.16e-69
26	575	20.3	352	2	O14701	CCRS5 RECEPTOR (FRAGMEN	9.16e-69
27	575	20.3	352	2	O14707	CCRS5 RECEPTOR (FRAGMEN	9.16e-69
28	573	20.2	352	2	O14695	CCRS5 RECEPTOR (FRAGMEN	1.92e-68
29	573	20.2	352	4	O02778	CC CHEMOKINE RECEPTOR	1.92e-68
30	572	20.1	352	2	O14706	CCRS5 RECEPTOR (FRAGMEN	2.78e-68
31	569	20.0	352	2	O14696	CCRS5 RECEPTOR (FRAGMEN	8.46e-68
32	567	20.0	352	2	O14693	CCRS5 RECEPTOR (FRAGMEN	1.77e-67
33	569	20.0	383	11	O89609	G PROTEIN-COUPLED RECE	8.46e-68
34	565	19.9	352	2	O14703	CCRS5 RECEPTOR (FRAGMEN	3.72e-67
35	564	19.9	352	4	O18772	CCRS5 RECEPTOR (FRAGMEN	5.39e-67
36	563	19.8	352	4	O18771	CCRS5 RECEPTOR (FRAGMEN	7.80e-67
37	562	19.8	352	2	O14698	CCRS5 RECEPTOR (FRAGMEN	1.13e-66
38	558	19.7	352	2	O14708	CCRS5 RECEPTOR (FRAGMEN	4.96e-66
39	537	18.9	289	12	O42179	COSMID 48D10, COMPLETE	1.15e-62
40	535	18.8	360	4	O18793	CHEMOKINE RECEPTOR.	2.41e-62
41	532	18.7	353	12	P79960	MESENCHYME-ASSOCIATED	7.26e-62
42	519	18.3	344	2	O15133	PURINERGIC RECEPTOR P2	8.64e-60
43	515	18.1	333	2	O14694	CCRS5 RECEPTOR (FRAGMEN	3.75e-59
44	514	18.1	361	10	O35811	G-PROTEIN COUPLED RECE	5.42e-59
45	505	17.8	678	3	Q94736	TACHYKININ-LIKE RECEPT	1.47e-57

ALIGNMENTS

RESULT	ID	PRELIMINARY;	PRT;	392 AA.
AC	Q12930;			
DI	01-NOV-1996 (TREMBLREL. 01, CREATED)			
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)			
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)			
DE	MT OPIOID RECEPTOR VARIANT.			
GN	MOR1.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=BRAIN;			
RX	MEDLINE; 95046336.			
RA	BARE L.A., MANSSON E., YANG D.;			
RL	FEBS LETT. 354:213-216(1994).			
RN	[2]			
RP	SEQUENCE OF 1-388 FROM N.A.			
RC	TISSUE=BRAIN;			
RX	MEDLINE; 94139928.			
RA	WANG J.B., JOHNSON P.S., PERSICO A.M., HAWKINS A.L., GRIFFIN C.A.,			
RA	UHL G.R.;			
RL	FEBS LETT. 338:217-222(1994).			
DR	EMBL; U12569; G607912; -			
DR	PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.			
FT	VARIANT 40 40 D -> N (IN REF. 2).			
FT	VARIANT 51 51 D -> N (IN REF. 2).			
FT	VARIANT 207 207 I -> M (IN REF. 2).			
FT	VARIANT 234 234 L -> V (IN REF. 2).			
SO	SEQUENCE 392 AA; 43939 MW; 3359DDB4 CRC32;			

Query Match 59.2%; Score 1680; DB 2; Length 392;
Best Local Similarity 65.0%; Pred. No. 1.87e-253;
Matches 210; Conservative 53; Mismatches 56; Indels 4; Gaps 4;

Db	70	ATTMALYSIVCVGIGFNFLVMYVIVRYTKMKRTATNIIYFNALADATATLPFQSVN	129
Qy	59	PVITAVYSVEFVGVGNSLVMFVIIRYTKMTATNIIYFNALADATATLPFQSAV	118
Db	130	YLMGTWPFGLTICKIVISIDYNNMFTSIFCTMSVDRIYAVCHPVKALDERIPRNAKII	189
Qy	119	YLMNSWPFGLVCKIVISIDYNNMFTSIFCTMSVDRIYAVCHPVKALDERIPRNAKII	178

[illegible]

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DT      01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE      MU OPIOID RECEPTOR.
OS      BOS TAURUS (BOVINE).
OC      EUTHERIA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; ARTIODACTYLA.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=STRIATUM;
RA      SIMON E.J., VILLEM S., ANDRIA M., ONOPRISHVILI I., HILLER J.M.;
RL      SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDJ DATA BANKS.
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR      EMBL; U89677; GI881731; -.
DR      PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW      G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SQ      SEQUENCE   401 AA;  45045 MW;  5673B9B8 CRC32;

Query Match                      58.1%; Score 1650; DB 4; Length 401;
Best Local Similarity    65.9%; Pred. No. 2,37e-248;
Matches     205; Conservative    54; Mismatches 49; Indels    3; Gaps    3;

Db      71 AIIIMALYSIVCVGLFGNFLVMYVIYRTKMKTAIINXIIFNLADALATSLPQSYN 130
QY      59 PYITAVYSVFVGVGLGNSLVMEVLIRTKMTAIIINXIIFNLADALATSLPQSAV 118
        ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      131 YLMGTWPEFTILCKIIVISIDYYNMFTSTLTCTMSVDRYIAVCHPVKALDLTPRNAKIT 190
QY      119 YLMNSWPFEGDYLCKIIVISIDYYNMFTSIPTLLTMSVDRIYAVCHPVKALDFRPLAKIT 178
        ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      191 NICNWILLSAIGLPVMEATIKYRG-S-IDSTTFESHPTW-YWENLIKICVFIFAIMP 247
QY      179 NICIWLLASSVGISAIVLGITKVEDVATECSLQFPDEYSWMDLFMKICEVEFAFVIP 238
        ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      248 IIITTCYGLMILRLKSVRMLSGSKEKDRLRRITRVLVVVAVFIWCWPPIHIVAIKA 307
QY      239 VLIITVCYTMLTRLKSVRLLSGREKDRNLFRITKLVLVVAVFIIICWPIHIFIVEA 298
        :||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      308 LITIPETFQTQVSWHFICIALGYTNSCLNPVLYAFLDENEKRCRFECIPTSSIEQNST 367
QY      299 LGSIHSHTAALLSYFFICIALGYTNSCLNPVLYAFLDENEKRCRFECIPKMRMERQSTN 358
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      368 RIRONTRDHP 378
QY      359 RVNNTVQDPAS 369
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT      4
ID      Q64120 PRELIMINARY; PRI; 240 AA.
AC      Q64120;
DT      01-NOV-1996 (TREMBLREL. 01, CREATED)
DT      01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT      01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE      MU-OPIOID RECEPTOR MOR (FRAGMENT).
OS      RATUUS NORVEGICUS (RAT).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; RODENTIA.
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 95251654.
RA      SEDOT M., ROY S., RAMAKRISHNAN S., ELDE R., LOH H.H.;
RL      BIOCHEM. BIOPHYS. RES. COMMUN. 209:563-574(1995).
CC      -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR      EMBL; S77863; EI199500; -.
DR      PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW      G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT      NON_TER      1
SQ      SEQUENCE   240 AA;  27408 MW;  D3C58BBF CRC32;

Query Match                      47.2%; Score 1339; DB 10; Length 240;
Best Local Similarity    68.3%; Pred. No. 1.26e-195;
Matches     166; Conservative    39; Mismatches 35; Indels    3; Gaps    3;

Db      1 TATNIYFNIALDALATSLPFSQSVNYLMGTWPEFTILCKIIVISIDYYNMFTSIPTLCT 60
        |||||||||||||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

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QY	92	TAINIYIENLALADALVTTTMEPQSAVILMNSWPEGDVLCKIVISIDYYNFTSITLLM	151
Db	61	MSVDRYIAVCHPVKALDFERTPRNAKIYVNCNMTLSSAIGLPVMEFATIKYRQ-S-IDCT	118
QY	152	MSVDRYIAVCHPVKALDFERTPLKAKITINICIMWLLASSVGISAIVLGGIKYREDVDVIECS	211
Db	119	LTFESHPTW-YWENLKKICVFIEAFIMPILITVQYGLMILRLKSVRMLSGSKEDRNLRL	177
QY	212	LOFPDDEYSWMDLFMKICVFIEFAFVAPVPLIITVQYTIMILRLKSVRMLSGSKEDRNLRL	271
Db	178	ITRMVLVVAVEIVCWTPIHILYVILKALITIPETTFQTVSWHFCIALGYNSCLNPVLYA	237
QY	272	ITKVLVVAVEIICWTPIHIFILVEALGSTHSTAALSSYFCIALGYNSCLNPVLYA	331
Db	238	FLD 240	
QY	332	FLD 334	

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RESULT      5
ID          Q60733          PRELIMINARY;      PRT;      117 AA.
AC          Q60733;
DT          01-NOV-1996 (TREMBLREL. 01, CREATED)
DT          01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DT          01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE          KAPPA OPIOID RECEPTOR (FRAGMENT).
GN          OPRK1.
OS          MUS MUSCULUS (MOUSE).
OC          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC          EUTHERIA; RODENTIA.
RN          11]
RP          SEQUENCE FROM N.A.
RA          GRANDY D.K.;
RL          SUBMITTED (DEC-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC          -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR          EMBL: U16998; G595937; -.
DR          PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW          G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT          NON_TER      1
FT          NON_TER      1
FT          NON_TER      1
SQ          SEQUENCE      117 AA;      13071 MW;      FCCCF68E1 CRC32;

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Query Match          30.3%; Score 860; DB 10; Length 117;
Best Local Similarity 98.3%; Pred. No. 2.17e-115;
Matches 115; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 YIKMKTAINIYIFENLTPLADALVTTTMPFQSAVYILNMSWPDGLCKIVISIGYYNMFTSI 60
    |||||
QY 87 YIKMKTAINIYIFENLTALADALVTTTMPFQSAVYILNMSWPDGLCKIVISIDYYNMFTSI 146
    |||||

Db 61 FTLTMSVDORYIAVCHPYKALDERTPLKAKIINICIMTLASSVGISAIVLGGTKVRE 117
    |||||
QY 147 FTLTMSVDORYIAVCHPYKALDERTPLKAKIINICIMTLASSVGISAIVLGGTKVRE 203
    |||||

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ID	RESULT	6	PRELIMINARY;	PRT;	119 AA.
AC	Q64206;				
DT	01-NOV-1996 (TREMBLERL. 01, CREATED)				
DT	01-NOV-1996 (TREMBLERL. 01, LAST SEQUENCE UPDATE)				
DT	01-NOV-1996 (TREMBLERL. 01, LAST ANNOTATION UPDATE)				
DE	DELTA OPIOID RECEPTOR/DOR (FRAGMENT).				
OS	MUS MUSCULUS (MOUSE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	ROY S., SEDQI M., RAMAKRISHNAN S., BARKE R.A., LOH H.H.;				
RL	CELL. IMMUNOL. 169:271-277 (1995).				
DR	EMBL; S81965; E257239; -.				
FT	NON TER	1			
SO	SEQUENCE	119 AA;	13380 MW;	DFC85C30	CRC32;

	Query Match	23.38;	Score 662;	DB 10;	Length 119;	
	Best Local Similarity	69.9%;	Pred. No. 7,46e-83;			
	Matches	86;	Conservative	17;	Mismatches 15;	Indels 5;
					Gaps	4;
Db	1	IFTLTMSVDRIYAVCHPYKALDERTPAKAKLINCICWVLASGVGPIMVMAYTQPRDGA	60			
QY	146	IFTLTMSVDRIYAVCHPYKALDERTPLKAKIINICIWLLASSVGSISATVLTGTRKVEDV	205			
Db	61	-LY-CMLQFSP--SWKWDVTYKICVFLFAFVVPILITTCYGLMLRLRSVRLSGSKE	116			
		:::				
QY	206	DYTFCSLQFPDDEYSW-WDLFMKICVFVEAFVPIVLIITVCYTLMLRLKSVRLSGSKE	264			
Db	117	KDR	119			
QY	265	KDR	267			

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RESULT 7
ID P97266 PRELIMINARY; PRT; 98 AA.
AC P97266;
DT 01-MAY-1997 (TREMBLER, 03, CREATED)
DT 01-MAY-1997 (TREMBLER, 03, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLER, 05, LAST ANNOTATION UPDATE)
DE MU-OP10ID RECEPTOR (FRAGMENT).
OS CAVIA PORCELLUS (GUINEA PIG).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA RONNEKLEIV O.K., BOSCH M.A., CUNNINGHAM M.J., WAGNER E.J.,
RA GRANDY D.K., KELLY M.J.;
RL SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: U67928; G1763013; -.
DR PROSITE; PS00237; G-PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
FT NON_TER 1 1
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11161 MW; 28F749E6 CRC32;

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Query Match          22.4%; Score 635; DB 10; Length 98;
Best Local Similarity 81.6%; Pred. No. 1.83e-78;
Matches      80; Conservative    8; Mismatches 10; Indels   0; Gaps   0;
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RESULT      8
ID      008726      PRELIMINARY;      PRT;      372 AA.
AC      008726;
DT      01-JUL-1997 (TREMBLREL. 04, CREATED)
DT      01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT      01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE      GALANIN RECEPTOR TYPE 2.
GN      GALR2.
OS      RATIUS NORVEGICUS (RAT).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; RODENTIA.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=HYPOTHALAMUS;
RA      HOWARD A.D., TAN C., SHIAO L.L., PALYHA O.C., MCKEE K.K.,
RA      WEINBERG D.H., FEIGNER S.D., CASCIERI M.A., SMITH R.G., PLOEG L.H.T.,
RA      SULLIVAN K.A.;
RL      SUBMITTED (MAY-1997) TO EMBL/GENEBANK/DBJ DATA BANKS.
RN      [2]
RP      SEQUENCE FROM N.A.

```


RA SMITH K.E., FORRAY C., WALKER M.W., JONES K.A., TAMM J.A., BARD J.,
RA BRANCHER T.A., LINEMEYER D.L., GERALD C.,
RN J. BIOL. CHEM. 272:24612-24616(1997).
RP [3]
RP SEQUENCE FROM N.A.
RA SMITH K.E., FORRAY C., WALKER M., JONES K.A., TAMM J.A., BARD J.,
RA BRANCHER T.A., LINEMEYER D.L., GERALD C.,
RN SUBMITTED (JUN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [4]
RP SEQUENCE FROM N.A.
RA WANG S., HASHEMI T., HE C., STRADER C., BAYNE M.,
RL MOL. PHARMACOL. 52:337-343(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA PATHI Z., CUNNINGHAM A.M., IBEN L.G., BATTAGLINO P.B., WARD S.A.,
RA NICHOL K.A., PINE K.A., WANG J., GOLDSTEIN M.E., TISMAA T.P.,
RA ANTAL ZIMANYI I.,
RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; U94322; G2055417; -.
DR EMBL; AF010318; G2440011; -.
DR EMBL; Y15248; E1168194; -.
DR EMBL; AF008548; G2245685; -.
SQ SEQUENCE 372 AA; 40675 MW; 86ED0A8A CRC32;

Query Match	21.7%;	Score 615;	DB 10;	Length 372;
Best Local Similarity	29.5%;	Pred. No. 3.19e-75;		
Matches	97;	Conservative 110;	Mismatches 109;	Indels 13;
				Gaps 11;

[illegible]

RESULT	9		
ID	P79785	PRELIMINARY;	PRT; 359 AA.
AC	P79785;		
DT	01-MAY-1997 (TREMBLREL. 03, CREATED)		
DT	01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)		
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)		
DE	ANGIOTENSIN II RECEPTOR.		
OS	GALLUS GALLUS (CHICKEN).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;		
CC	GALLIFORMES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	KEMPF H., LE MOULLEC J.M., CORVOL P., GASC J.M.;		
RL	FEBS LETT. 399:198-202(1996).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
DR	EMBL: U76704; G1763532; -.		
DR	PROSITE: PS00237; G_PROTEIN_RECEPTOR; 1.		
KW	G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.		
SO	SEQUENCE 359 AA; 41220 MW; 476B3461 CRC32;		

Query Match	21.5%;	Score 609;	DB 12;	Length 359;
Best Local Similarity	34.8%;	Pred. No. 2.98e-74;		
Matches 101; Conservative		82; Mismatches 94;	Indels 13;	Gaps 12;

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Db      29 IMPTVYVSIHFIIIGIFGNSLVVIVVICYMKLKTVASIFLNLALADLCFLITLPL-WAAY 87
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      60 VITAVYSVVFVVGVLVGNLSVMFVITIKTKMKTATNIIYIFNLALADALVTTTMMFQSAVY 119

Db      88 TAMEYQWPEGNCLOCLASAGISFNELASVFLTCLSIDRYLAIVHPVKSRIKRTMFAVAV 147
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      120 L-MN-SWPEGVLCRKIVISIDYXNMFTSFTLTMSVDRYIAVCHPVKALDFRTPLKAKI 177

Db      148 TCIVIVILAGVASLPVLIHRNIEFAENMNTVCGFRYDNNNTLIR-VGLGLSKNLLGFLI 206
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      178 INICIVILASSVGISALVLGSTKVRDEVDVIECSIQPDDEYSWMDLEMKICVFVFAVVI 237

Db      207 PFLIIITSYTLMKILKKAYQIQ--RNKERN-DIIFKMIVALVEFFEFSSWIPHQVFTFLD 263
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      238 PVLIIIVCYTLMILRLKSVRLLSGSRDRNLRLRITKVLVVAVAVIICWTPIHIF-IL- 295

Db      264 VLIQLHVITDCKITDIVDTAMPFTTICIAVENNCLNPFYVVFEGKNEKKYF 313
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY      296 V-EAL-GSTS-HSTAALSSYY-FCIALGTYTNSSLNPVLVYAFLEDFENKRCF 341

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RESULT 10
ID 035210 PRELIMINARY; PRT; 359 AA.
AC 035210;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE ANGIOTENSIN II RECEPTOR.
GN GRAT1.
OS MERIONES UNGUICULATUS (MONGOLIAN JIRD).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MONGOLIAN GERBIL;
RA MORITZ R., JOHREN O., HIMENO A., SHIBATA S., HAUSER W.,
RA SAAVEDRA J.M.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: AF011903; G2293554; -.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.
KW G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SQ SEQUENCE 359 AA; 40779 MW; B3033953 CRC32;

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Query Match	21.3%;	Score 605;	DB 10;	Length 359;
Best Local Similarity	35.5%;	Pred. No. 1.32e-73;		
Matches 103;	Conservative	78;	Mismatches 96;	Indels 13;
				Gaps 11;

Dø	29	VMPDLXSIEFVVGIFGNSLVIVIVFYFMKLTIVASVFLLNLALADLCFTLLPY-WAVY	87
QY	60	VITAVYSVFVGVGLVGNLSVMFEVIIRYTKMKTATNIYIENLALADALAYTTTMEPQSAVY	119
Dø	88	TAMEYRMPFGNHLCKIASAGISEFNLYASVELLTCLSIDRYLAIVHPMKSRLERTMLVAKY	147
QY	120	L-MN-SWPEFDVLCKIAVISIDYYNMFTSIFTLTMSVDRIYAWCHPVKALDERTPCLKAKI	177
Dø	148	TCVVIMWLAGLASLPVAVIHNRVYFIENNSTVCAPHY-ESQNSTLPVGLTEKNILGFME	206
QY	178	INICWMCLASSVGISAIVLGTRVEDVYLIESLOQEPDDEYSWMDLFMKJVEFEAFVI	237
Dø	207	PFLILTSYTLIWKKALK--KAYEIQKNPRN-DDIERIIMAVLFFEFESWIPEHQIFTELDD	263
QY	238	PVLIIIVCYTLMILRLKSVRLLSGSRERKDNRIRTKLVVVAAVFIIICWPPIHIF-IL-	295
Dø	264	VLIQLGYIRDCKIADVVDTAMPITICTIAYFNNCINPLFYGFGLGKKFKKYF	313
QY	296	V-EALGSTSHST-AALSSYFCIAL-GTYNSSLNPLVYAFLDENETKRCE	341

RESULT	11		
ID	035313	PRELIMINARY;	PRT; 354 AA.
AC	035313;		
DT	01-JAN-1998	(TREMBLREL. 05, CREATED)	
DT	01-JAN-1998	(TREMBLREL. 05, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998	(TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE	CCR5.		
OS	MUS MUSCULUS (MOUSE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; RODENTIA.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=129;		
RX	MEDLINE; 97404635.		
RA	DORANZ B.J., LU Z.H., RUCKER J., ZHANG T.Y., SHARRON M., CEN Y.H.,		
RA	WANG Z.X., GUO H.H., DU J.G., ACCAVITTI M.A., DOMS R.W., PEIPER S.C.;		
RL	J. VIROL. 71:6305-6314(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=129;		
RA	PEIPER S.C., LU Z.-H.;		
RL	SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.		
DR	EMBL; AF019772; G2431976; -.		
SO	SEQUENCE 354 AA; 40862 MW; 76A5D450 CRC32;		

Query Match	20.98;	Score 594;	DB 10;	Length 354;
Best Local Similarity	30.28;	Pred. No. 7.92e-72;		
Matches	91;	Conservative 94;	Mismatches 100;	Indels 16;
				Gaps 13;

Db	23	QKINVKQIAAQLPPLYSLVEIFGEVGNMVFLLISCKRKISYTDIYLLNLAISDLLFL	82
QY	50	ESAHISPAIPVILITAVSYVEFVGLVGNLSLMEFVILIRYTKKTAIINIIYENLALADALVT	109
Db	83	LILPF-WAHYAANEMTEGNIMCKVFETGVYHIGYFGGIFILLITIDRYLAIVHAEFALKV	141
QY	110	TTMPFQSAVYLIMSMPFGDVLCKIVISIDYYNMETSIFILLTMSVDRYIAVCHPVKALDF	169
Db	142	RTVIEGVITSVVTWVAVAFASLPEIIFTRSQ-KEGFHTT-CSPHPHTQYHFWKSFQTLK	199
QY	170	RTPLKAKIINICIMLLASSVGISAIVLGGTKVREDVDVIECSLQFPDDEXSWWDLFMKIC	229
Db	200	MWILSLILPLVMILCYSGILH--T-LFCRNEKKRH-RAV-RLIFAIMIVYFLFWTP	252
QY	230	VFEFAFVIVPLILITVCTYILMLRLKRSVRLLSGSRKEDBNLRITKVLVWVAVFIIOWTP	289
Db	253	YNIVLLLTTEQEEFFGLNCCSSNRDLQAMQATELTGKTHGCLNPVIYAFVGEKFRSYLSV	312
QY	290	IHI-FILV--EAL-G-STSHSTAALS-SYFICIALGYTNSSLNPVLYAFILDENFMKRCFRD	343
Db	313	F 313	
QY	344	F 344	

RESULT	12		
ID	002746	PRELIMINARY;	PRT; 352 AA.
AC	002746;		
DT	01-JUL-1997	(TREMBLREL. 04, CREATED)	
DT	01-JUL-1997	(TREMBLREL. 04, LAST SEQUENCE UPDATE)	
DT	01-JUL-1997	(TREMBLREL. 04, LAST ANNOTATION UPDATE)	
DE	CHEMOKINE RECEPTOR CCR5.		
OS	MACACA MULATTA (RHEMUS MACAQUE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; PRIMATES.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	HAUER D.A., MARCULIES B.J., CLEMENTS J.E.;		
RL	SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.		
DR	EMBL; U96762; G2088633; -.		
SQ	SEQUENCE	352 AA; 40507 MW; 70CC04AD CRC32;	

Query Match 20.78; Score 587; DB 4; Length 352;

Best Local Similarity	29.2%;	Pred. No. 1.07e-70;
Matches	88;	Conservative 99; Mismatches 98; Indels 16; Gaps 14;
Db	21	QKINWQIARLLPPLYSLVFEFGVGNILVLLINCKRLKSMIDIYLLNLAIISDLFL 80
QY	50	ESAHISPAIPVITAVSYSVFVGLVGNLSVMFVIRYTKMKATNTIYIFNLALADALVT 109
Db	81	LTYPF-WAHYAAQWDFGNTMCOLLTGLYFIGFSGIEFFILLTIDRYLAIVHAVFALKA 139
QY	110	TTMPEQSAVYLLMNSWPEFGDYLCRKIVISIDYNNMFTSIFTLTMMASVDRIYAVCHPVKALDE 169
Db	140	RYTFEGVTSVITWVAVAFASLPDGIIFTRSQ-REGLIHT-CSSHEPYSQYQFWKNFQTLK 197
QY	170	RFPFLKAKIINICIMWLASSVGTSAIVLGGTKVREDVDVIECSLQFPDDEYSWMDLFMKIC 229
Db	198	MYILGLVLPBLVMVICYG-SIL--KT--LLRCRNEKKRH-RAV-RLIFTIIVYFLFWAP 250
QY	230	VVFVAFVIPVLIIVCYTLMILRLKSVRLLSGSRREKDRNLRLITKVLVWVAVFIICWTP 289
Db	251	YNIVLLNLTFOEFFGLNNCCSSNRLDQAMQVTEFLGMTHCCANPPIIYAFVGEKEFRNYLLV 310
QY	290	IHT-FIL-V-EAL-G-STHSITALS-SYFICIALGYTNSLNPVLYAFLDENFKRCFRD 343
Db	311	F 311
QY	344	F 344

RESULT	13		
ID	P97405	PRELIMINARY;	PRT; 354 AA.
AC	P97405;		
DT	01-MAY-1997 (TREMBLREL. 03, CREATED)		
DT	01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)		
DT	01-MAY-1997 (TREMBLREL. 03, LAST ANNOTATION UPDATE)		
DE	BETA CHEMOKINE RECEPTOR.		
GN	CKR5.		
OS	MUS MUSCULUS (MOUSE).		
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
OC	EUTHERIA; RODENTIA.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=129/OLA;		
RA	KUZIEL W.A., BECK M.A., DAWSON T.C., MAEDA N.;		
RL	SUBMITTED (DEC 1996) TO EMBL/GENBANK/DBJ DATA BANKS.		
DR	EMBL; U68565; G1698716; -		
SO	SEQUENCE 354 AA; 40889 MW; B52D4BD7 CRC32;		

Query Match	20.6%;	Score 585;	DB 10;	Length 354;
Best Local	Similarity	30.2%;	Pred. No. 2.24e-70;	
Matches	91; Conservative	93;	Mismatches 101;	Indels 16;
				Gaps 13;

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Db      23 QKINVKQIAAQLLPPLYSIVFIEFGVGNMVFLLISCKKLKSVTDIYLLNLAIISDLFL 82
        :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
QY      50 ESAHSPAIPVIITAVSYVEVVGVLGNSLVMFVILIRYTKMKATNIYEENLALADALVT 109
        :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :

Db      83 LTLPE-WAHYAANEMIFCNIMCKVFETGVYHIGYEGGIPELLITIDRYLAIVHAVEALKV 141
        :   :   :   |   |   |   :   :   :   :   :   :   :   :   :   :   :
QY     110 TLMPEQSAVYLMSNMPGVDVLCIKIVISIDYNNMTSIFTLLMSVDRIYAVCHPVKALDF 169
        :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :

Db     142 RIVNEGVITSVLTWVAAYEASLPEIIFTRSQ-KEGFHVP-CSPHEPHTQYYFWKSEQTLK 199
        ||   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
QY     170 RTPLKAKIINICIWLASVGISAIYLGSTKVREDVDVTECSLQFPDDEYSWMDLEFKIC 229
        :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :

Db     200 MYILSLILPLLVMITCYS-GILH--T-LFCRNEKKRE-RAV-RLIFAIMIVYLEWTWP 252
        :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
QY     230 VEFVAFVIPVLLIIVCYTIMLRKLSVRLLSGSREKDRMRRTKLVLVVAAVFIICTWP 289
        :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :

Db     253 YNIVALLTTFOEFFGLNCCSSNRILDQAMQATEITLGMTHCINPVIYAFVGEKFRSYLSV 312
        :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
QY     290 IHI-FIIV--EAL-G-SISHSTAALS-SYFFICIALGTNSSLNPLYAFLDENEKRCERD 343

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CY          344 F 344

RESULT      14
ID          P97308      PRELIMINARY;      PRT;      354 AA.
AC          P97308;
DT          01-MAY-1997 (TREMBLREL. 03, CREATED)
DT          01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT          01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)
DE          C-C CHEMOKINE RECEPTOR 5.
GN          CCR5.
OS          MUS MUSCULUS (MOUTSE).
OC          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC          EUTHERIA; RODENTIA.
RN          [11]
RP          SEQUENCE FROM N.A.
RA          GUO B., KUNO K., HARADA A., MATSUSHIMA K.;
RL          SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN          [12]
RP          SEQUENCE FROM N.A.
RA          STRAIN=C57 BLACK/6; TISSUE=LIVER, KIDNEY AND SPLEEN;
RC          KUHMANN S.E., PLATT E.J., KOZAK S.L., KABAT D.;
RL          J. VIROL. 71:8642-8656(1997).
RN          [13]
RP          SEQUENCE FROM N.A.
RC          STRAIN=C57 BLACK/6; TISSUE=LIVER, KIDNEY AND SPLEEN;
RC          KUHMANN S.E., PLATT E.J., KABAT D.;
RL          SUBMITTED (SEP-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR          EMBL; D83648; G1777330; -.
DR          EMBL; AF022990; G2444487; -.
SQ          SEQUENCE 354 AA; 40785 MW; 78210143 CRC32;

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Query Match	20.6%;	Score 585;	DB 10;	Length 354;
Best Local Similarity	30.0%;	Pred. No. 2.24e-70;		
Matches	92;	Conservative	93;	Mismatches 105; Indels 17; Gaps

Db	23	QKINVKQIAQOLLPLYSLVFEGVGNMVFLLISCKKIKSVTDIYLLNLALISDLFL	82
	:	:	:
QY	50	ESAHISPAIPVIITAVYSVVEVGLVGNLSVMFVILRYTKKKTATNTIYIFNLALADALVT	109
Db	83	LTLPE-WAHYAANEWFEGNIMCKVFETGLYHIGYFGGIFILLITIDRYLAIVHAFALKV	141
	:	:	:
QY	110	TTMPFGSAVXLMNSWPFEGDVLCKIVTSIDYNNMFTSIFLTMMSSVDRYIAVCHPYKALDF	169
Db	142	RTVNFGVITNSVTWAVAVFASLPELIFTRSQ-KEGFHYT-CSPHEPHTQYHFWKSPQLK	199
	:	:	:
QY	170	RTPLKAKIINICIMLLASSVGISALVIGTKVREDVDVIECSQFPDDEYSWMDLFMKIC	229
Db	200	MVILSLLEPLVMVICYS-GILH--T--LFRCRNEKKRH-RAY-RLIFAIMYFLFWTP	252
	:	:	:
QY	230	VVFVAFVLPVLIITVCTYLTMLIRLKSVRLLSGSREKDRNLRIITKLVLVVAVFETICWTP	289
Db	253	YNIVLLTTFQEEFFGLNCCSSNRDLQAMQATETLGMTHCCINPVITYAFVGEKERSTLSV	312
	:	:	:
QY	290	IHI-FTLV--EAL-G-STSHSTAALS-SYFICIALGYTNSSLNPVLYAFLDENFKRCFRD	343
Db	313	F-FRKHM 318	
	:	:	:
QY	344	FCFPIKM 350	

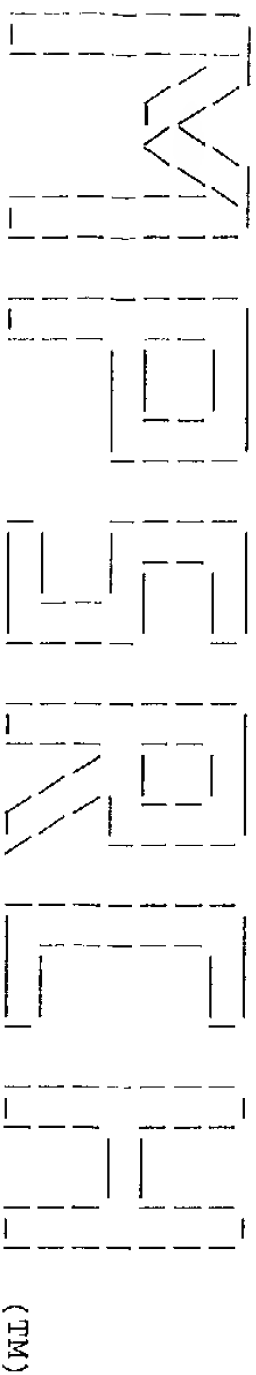
RESULT	15	
ID	Q91383	PRELIMINARY; PRT; 362 AA.
AC	Q91383;	
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)	
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE	ANGIOGENSIN II RECEPTOR {CLONE XAT}.	
OS	XENOPUS LAEVIS (AFRICAN CLAWED FROG).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AMPHIBIA; ANURA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	NISHIMATSU S., KOYASU N., SUGAYA T., OHNISHI J., YAMAGISHI T.,	

RA MURAKAMI K., MIYAZAKI H.,
RL BLOCHM. BIOPHYS. ACTA 1218:401-407 (1994).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
DR EMBL: S73388; E136505; -.
KW PROSITE; PS00237; G-PROTEIN RECEPTOR; 1.
DR G-PROTEIN COUPLED RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN.
SQ SEQUENCE 362 AA; 41267 MW; 9704F695 CRC32;

Query Match	20.6%;	Score 586;	DB 12;	Length 362;
Best Local Similarity	33.1%;	Pred. No. 1.55e-70;		
Matches	100;	Conservative	80;	Mismatches 105;
			Indels	17;
			Gaps	14;

[illegible]

Search completed: Thu Apr 16 13:32:44 1998
Job time : 74 secs.



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(TM)

MPrch_n n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Tue Apr 21 00:03:11 1998; Maspar time 1242.52 Seconds
1341.823 Million cell updates/sec
Tabular output not generated.

Title: >US-08-292-694A-1
Description: (1-1410) from US08292694A.seq
Perfect Score: 1410
N.A. Sequence: 1 GCGCACCCTTGCTGATGCCAA.....AACCCAGATTCACTGCAG 1410
Comp: CGCGTGGACGACTAGGGTT.....TTGGGCTAATGTGACGTC

Scoring table: TABLE jmetric
Gap 60

Mmatch STD : Dbase 0; Query 0
Searched: 354530 seqs, 591221332 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database: emb153
1:em_in 2:em_or 3:em_om 4:em_ov 5:em_pi 6:em_htg
7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
13:em_pat
Database: genbank105
14:gb_ro 15:gb_om 16:gb_ov 17:gb_in 18:gb_pi 19:gb_ba
20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
26:gb_htg

Statistics: Mean 9.323; Variance 3.013; scale 3.094

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description	Pred. No.
1	1410	100.0	1410	14	MUSKAPOPRE		Mouse kappa opioid rec	0.00e+00
2	1208	85.7	1288	14	S81111		kappa-opioid receptor	0.00e+00
3	617	43.8	1185	14	S77868S3		kappa opioid receptor	0.00e+00
4	526	37.3	638	14	MUSMORGD3		Mouse MORGD gene for k	0.00e+00
5	354	25.1	488	14	MUSMORGD2		Mouse MORGD gene for k	0.00e+00
6	354	25.1	1109	14	S77868S2		kappa opioid receptor	0.00e+00
7	275	19.5	432	14	MMU16998		Mus musculus kappa opi	0.00e+00
8	273	19.4	423	14	MUSMORGD1		Mouse MORGD gene for k	0.00e+00
9	273	19.4	2074	14	S77868S1		kappa opioid receptor	0.00e+00
10	229	16.2	1273	14	RATRORD		Rat mRNA for opioid re	1.90e-252
11	229	16.2	1358	14	RATXOR1A		Rat kappa opioid recep	1.90e-252
12	229	16.2	2094	14	RATXOR1B		Rattus norvegicus kapp	1.90e-252
13	229	16.2	2481	25	E08874		cDNA coding rat kappa-	1.90e-252
14	229	16.2	2481	14	RATROK		Rattus norvegicus mRNA	1.90e-252

15	198	14.0	4742	14	RNU00442		Rattus norvegicus kapp	1.50e-212
16	160	11.3	658	14	RNKOR2		Rattus norvegicus kapp	4.61e-164
17	68	4.8	4048	14	RNKOR3		Rattus norvegicus kapp	9.30e-51
18	17	4.6	1733	14	CPU04092		Cavia porcellus Hartle	2.86e-47
19	38	2.7	1757	14	RNKOR1		Rattus norvegicus kapp	1.97e-17
20	32	2.3	1142	25	A48343		Sequence 1 from Patent	2.02e-11
21	29	2.1	1461	14	RATSR		Rat somatostatin recep	1.45e-08
22	22	2.1	1699	14	RATSON		Rattus norvegicus mRNA	1.45e-08
23	29	2.1	3615	14	RNGPCRNA		R.norvegicus mRNA for	1.45e-08
24	28	2.0	2858	14	CPU04369		Cavia porcellus Hartle	1.23e-07
25	25	1.8	356	14	MMKOR3S06		Mus musculus opioid re	5.93e-05
26	25	1.8	1079	14	MMU14165		Mus musculus orphan op	5.93e-05
27	25	1.8	1083	14	MUSMORGPC2		Mouse MORGC gene for o	5.93e-05
28	25	1.8	1253	14	RATOPRE		Rattus norvegicus opio	5.93e-05
29	25	1.8	1304	14	RNU05239		Rattus norvegicus opio	5.93e-05
30	25	1.8	1338	14	MMU04952		Mus musculus C57Bl/6N	5.93e-05
31	25	1.8	1452	14	RNU01913		Rattus norvegicus Spra	5.93e-05
32	25	1.8	1452	25	I62296		Sequence 3 from patent	5.93e-05
33	25	1.8	1458	16	DRAJ1596		Danio rerio mRNA for o	5.93e-05
34	25	1.8	1567	14	RATOPRECEP		Rat opioid receptor fa	5.93e-05
35	25	1.8	1817	14	RATRORC		Rat mRNA for opioid re	5.93e-05
36	25	1.8	2024	14	MMOPIRECP		M.musculus mRNA for op	5.93e-05
37	25	1.8	2354	14	RNU07871		Rattus norvegicus Spra	5.93e-05
38	25	1.8	2600	14	MMU09421		Mus musculus K3 opiate	5.93e-05
39	25	1.8	2706	14	RATXOR1A		Rattus norvegicus alte	5.93e-05
40	23	1.6	1231	16	CCMUOPI		C.commerstoni mRNA for	2.97e-03
41	23	1.6	1366	14	RNU00475		Rattus norvegicus Spra	2.97e-03
42	23	1.6	1418	14	RATRORA		Rat mRNA for rat opioi	2.97e-03
43	23	1.6	1834	14	S65335		delta opioid receptor	2.97e-03
44	23	1.6	1835	14	MUSDOPRCP		Mouse delta-opioid rec	2.97e-03
45	23	1.6	2203	14	S66181		delta opiate receptor	2.97e-03
46	23	1.6	2219	25	A38528		Sequence 1 from Patent	2.97e-03
47	23	1.6	2219	14	MUSDELTO		Mus musculus delta-opi	2.97e-03
48	23	1.6	2272	14	MUSDELOPRE		Mouse delta opioid rec	2.97e-03
49	20	1.4	36	25	A48344		Sequence 2 from Patent	7.14e-01
50	20	1.4	39	25	A48347		Sequence 5 from Patent	7.14e-01
51	20	1.4	356	14	S81965		delta opioid receptor/	7.14e-01
52	20	1.4	555	14	MMKOR3S08		Mus musculus opioid re	7.14e-01
53	20	1.4	720	14	S77863		mu-opioid receptor MOR	7.14e-01
54	20	1.4	1367	14	RNU35424		Rattus norvegicus mu o	7.14e-01
55	20	1.4	1401	14	RATMOPTOID		Rat mu opioid receptor	7.14e-01
56	20	1.4	1415	15	BTU89677		Bos taurus mu opioid r	7.14e-01
57	20	1.4	1448	14	RNU02083		Rattus norvegicus mu-o	7.14e-01
58	20	1.4	1586	14	RATMORA		Rattus norvegicus mu o	7.14e-01
59	20	1.4	1881	15	PIGMUOPR		Sus scrofa mu opioid r	7.14e-01
60	20	1.4	2135	14	RATMUOR1A		Rattus norvegicus Mu o	7.14e-01
61	20	1.4	2205	15	SSU72758		Sus scrofa orphanin FQ	7.14e-01
62	20	1.4	2397	14	RATRORB		Rat mRNA for rat opioi	7.14e-01
63	20	1.4	2402	16	CHKM3MACR		Gallus gallus M3 musca	7.14e-01
64	19	1.3	246	18	BARPOL		Equisetum arvense pol	3.93e+00
65	18	1.3	402	18	SCEMT4		S.cerevisiae EMT4 gene	2.02e+01
66	18	1.3	962	15	RABCOLA18		Rabbit alpha-1 collage	2.02e+01
67	18	1.3	1041	18	GMACLI14		Glycine max L. Merr MR	2.02e+01
68	18	1.3	1207	21	MYU87841		Monkeypox virus strain	2.02e+01
69	18	1.3	1207	21	MYU88543		Monkeypox virus tumor	2.02e+01
70	18	1.3	1316	21	MYU88142		Monkeypox virus strain	2.02e+01
71	18	1.3	1317	21	MYU87847		Monkeypox virus strain	2.02e+01
72	18	1.3	1320	21	MYU87845		Monkeypox virus strain	2.02e+01
73	19	1.3	1763	19	CU083196		Chlamydia trachomatis	3.93e+00
74	18	1.3	1832	15	HRADHS		Horse alcohol dehydrog	2.02e+01
75	18	1.3	1902	21	PWCOPOJ		Iobacco vein banding m	2.02e+01
76	19	1.3	2540	19	SSPHETGEN		Synechococcus sp. phet	2.02e+01
77	18	1.3	3096	18	AF014813		Emeritocella nidulans DN	3.93e+00
78	18	1.3	3140	18	D76430		Yeast DNA for DIS3 pro	2.02e+01
79	18	1.3	3258	15	BOVMNTNT		Bos taurus nicotinamid	2.02e+01
80	18	1.3	3711	15	BOVNAD		Bovine mitochondrial n	2.02e+01
81	18	1.3	3985	14	RNGPROCR		R.norvegicus mRNA for	2.02e+01
82	18	1.3	4148	18	SCU66834		Saccharomyces cerevisi	2.02e+01
83	18	1.3	4673	18	SCYLO021C		S.cerevisiae chromosom	2.02e+01
84	18	1.3	5135	18	ATHAR1IM15		Arabidopsis thaliana A	2.02e+01
85	18	1.3	6244	14	RNMAR1AP		R.norvegicus mRNA for	2.02e+01
86	18	1.3	7071	18	SYDEPCAA		S.vulgaris PEPC gene.	2.02e+01
87	18	1.3	8017	18	ATU76670		Arabidopsis thaliana r	2.02e+01

C	88	18	1.3	9470	19	PDU34346	Paracoccus denitrifica	2.02e+01	C	161	17	1.2	19112	21	MVIRPR	Marburg virus (Popp) N	9.55e+01
	89	18	1.3	10120	14	RATMTAP	Rattus norvegicus micr	2.02e+01	C	162	17	1.2	19116	17	DMHDGHOCD	D.melanogaster hedgcho	9.55e+01
	90	18	1.3	12787	19	MPAE000049	Mycoplasma pneumoniae	2.02e+01	C	163	17	1.2	20712	17	CEF59F4	Caenorhabditis elegans	9.55e+01
	91	18	1.3	13650	19	HPAE000582	Helicobacter pylori se	2.02e+01	C	164	17	1.2	26600	17	CEF37B1	Caenorhabditis elegans	9.55e+01
C	92	18	1.3	31889	17	CELK07C11	Caenorhabditis elegans	2.02e+01	C	165	17	1.2	27236	17	CEF32F6A	Caenorhabditis elegans	9.55e+01
	93	18	1.3	36626	17	CELC16D9	Caenorhabditis elegans	2.02e+01	C	166	17	1.2	27371	17	CELR11F4	Caenorhabditis elegans	9.55e+01
	94	18	1.3	36753	17	CELF19F10	Caenorhabditis elegans	2.02e+01	C	167	17	1.2	31434	17	CEY68A4A	Caenorhabditis elegans	9.55e+01
C	95	19	1.3	37105	17	CEC04A11	Caenorhabditis elegans	3.93e+00	C	168	17	1.2	33371	26	CEK07H11	*** SEQUENCING IN PROG	9.55e+01
	96	18	1.3	39692	17	CET22H6	Caenorhabditis elegans	2.02e+01	C	169	17	1.2	33477	17	CET07C4	Caenorhabditis elegans	9.55e+01
C	97	18	1.3	41200	18	SC8520X	S.cerevisiae chromosom	2.02e+01	C	170	17	1.2	34033	17	CELR09G11	Caenorhabditis elegans	9.55e+01
	98	18	1.3	43254	17	CELC17E7	Caenorhabditis elegans	2.02e+01	C	171	17	1.2	35357	18	SPAC13F4	S.pombe chromosome I c	9.55e+01
	99	19	1.3	95824	18	ATU90439	Arabidopsis thaliana C	3.93e+00	C	172	17	1.2	37906	17	CELT08H4	Caenorhabditis elegans	9.55e+01
C	100	18	1.3	118155	26	HS884M20	Human DNA sequence ***	2.02e+01	C	173	17	1.2	38000	17	CELF58A4	Caenorhabditis elegans	9.55e+01
	101	18	1.3	154557	26	AC002472	*** SEQUENCING IN PROG	2.02e+01	C	174	17	1.2	41397	17	CEB0285	Caenorhabditis elegans	9.55e+01
C	102	18	1.3	169546	26	AC004019	*** SEQUENCING IN PROG	3.93e+00	C	175	17	1.2	79933	17	L49403	Drosophila melanogaste	9.55e+01
	103	19	1.3	190289	21	MCU60315	Molluscum contagiosum	2.02e+01	C	176	17	1.2	80531	26	HSV460E1	Human DNA sequence ***	9.55e+01
C	104	18	1.3	231661	26	AC002470	*** SEQUENCING IN PROG	9.55e+01	C	177	17	1.2	122682	26	HS799F10	Human DNA sequence ***	9.55e+01
	105	17	1.2	21	25	A48346	Sequence 4 from Patent	9.55e+01	C	178	17	1.2	126778	26	CEY68A4	Caenorhabditis elegans	9.55e+01
	106	17	1.2	371	14	MMOR2	Mus musculus mu oploid	9.55e+01	C	179	17	1.2	129913	26	HS989H11	Caenorhabditis elegans	9.55e+01
C	107	17	1.2	539	14	MMOR3	Mus musculus mu oploid	9.55e+01	C	180	17	1.2	136254	19	ECOWW82	Human DNA sequence ***	9.55e+01
	108	17	1.2	654	16	CHKPOLITF	Gallus gallus polr-like	9.55e+01	C	181	17	1.2	137357	26	AC003003	*** SEQUENCING IN PROG	9.55e+01
C	109	17	1.2	866	15	SSU71149	Sus scrofa delta opioi	9.55e+01	C	182	17	1.2	143339	26	AC0040126	*** SEQUENCING IN PROG	9.55e+01
	110	17	1.2	883	15	BOVLFCMB	Cow (clone bovmp19) le	9.55e+01	C	183	17	1.2	160000	26	AC004057	Caenorhabditis elegans	9.55e+01
C	111	17	1.2	920	17	PMU84117	Psammecinus miliaris	9.55e+01	C	184	17	1.2	172106	26	CEY67D11	Caenorhabditis elegans	9.55e+01
	112	17	1.2	1127	19	STAREPZ	Plasmid pC223 (from St	9.55e+01	C	185	17	1.2	180000	26	AC004063	*** SEQUENCING IN PROG	9.55e+01
C	113	17	1.2	1392	14	RATPPIACS	Rat PP-1 alpha gene fo	9.55e+01	C	186	17	1.2	187816	26	CEY32F6	Caenorhabditis elegans	9.55e+01
	114	17	1.2	1404	14	S78215	protein phosphatase 1	9.55e+01	C	187	17	1.2	226018	26	HS90L6	Human DNA sequence ***	9.55e+01
	115	17	1.2	1407	14	RATPPIAA	Rat PP-1a gene for cat	9.55e+01	C	188	17	1.2	261012	26	HS343C1	Human DNA sequence ***	9.55e+01
	116	17	1.2	1610	14	MMU26915	Mus musculus mu oploid	9.55e+01	C	189	17	1.2	291821	26	CEY48E1	Caenorhabditis elegans	9.55e+01
	117	17	1.2	1796	25	I13407	Sequence 11 from paten	9.55e+01	C	190	16	1.1	31	25	I62294	G.gallus type III coll	1.63e+03
	118	17	1.2	1797	14	MUSSSTR3A	Mouse somatostatin rec	9.55e+01	C	191	15	1.1	36	25	A48820	Sequence 16 from paten	1.63e+03
	119	17	1.2	1880	19	SAPC223	Staphylococcus aureus	9.55e+01	C	192	16	1.1	54	25	A07526	Nucleotide sequence 6	4.15e+02
	120	17	1.2	1998	18	ATCHHSP60	A.thaliana mRNA for mi	9.55e+01	C	193	16	1.1	54	25	A12990	Sequence 12 from paten	4.15e+02
C	121	17	1.2	2018	14	MUSCYR61A	Mouse Cyt61 mRNA, comp	9.55e+01	C	194	15	1.1	54	16	GGC0L13	Nucleotide sequence 6	4.15e+02
	122	17	1.2	2046	21	AF005735	DNA encoding variant C	9.55e+01	C	195	15	1.1	75	23	SYNINSPN1	Sequence 1 from patent	4.15e+02
C	123	17	1.2	2061	25	E08061	Sequence 5 from patent	9.55e+01	C	196	16	1.1	90	25	E00026	Rat insulin-I gene sig	4.15e+02
	124	17	1.2	2061	25	I43345	Sequence 9 from patent	9.55e+01	C	197	16	1.1	112	21	ACBERBB2	DNA coding of insulin	4.15e+02
	125	17	1.2	2061	25	I23834	Sequence 5 from patent	9.55e+01	C	198	16	1.1	127	18	S81277	avian erythroblastosis	1.63e+03
	126	17	1.2	2061	25	I44694	Sequence 5 from patent	9.55e+01	C	199	15	1.1	128	25	A07535	19S rRNA {3' region} [1.63e+03
C	127	17	1.2	2106	18	ATU18129	Arabidopsis thaliana 5	9.55e+01	C	200	16	1.1	130	16	AF008558	Cyprinus carpio brain-	1.63e+03
	128	17	1.2	2229	14	MMU19380	Mus musculus mu oploid	9.55e+01	C	201	15	1.1	171	23	SYNHUMINA	Synthetic human insuli	4.15e+02
	129	17	1.2	2232	16	CHKPOLITG	Gallus gallus reverse	9.55e+01	C	202	16	1.1	186	25	I31100	Sequence 12 from paten	4.15e+02
C	130	17	1.2	2346	14	RNU36476	Rattus norvegicus 92-k	9.55e+01	C	203	16	1.1	186	25	I31100	M.musculus c-fes gene	4.15e+02
	131	17	1.2	2462	19	ECILVBN	E. coli 11vBN operon f	9.55e+01	C	204	16	1.1	186	14	MMCFES186	Human herpesvirus 7 DN	4.15e+02
	132	17	1.2	2477	19	ACOSLP	A.coli acetohydroxy ac	9.55e+01	C	205	15	1.1	222	18	SORDNATS2	Smyrniun olusstrum nuc	4.15e+02
C	133	17	1.2	2502	19	BACCDG	B.mecerans cyclodextri	9.55e+01	C	206	16	1.1	223	14	MUSTGLHBD	Mouse Ig rearranged he	1.63e+03
	134	17	1.2	2631	19	BMCGTM	Rattus norvegicus FTA	9.55e+01	C	207	16	1.1	223	14	MMK2MHC	Mouse K2 class I MHC g	1.63e+03
C	135	17	1.2	2720	14	AB006137	Marburg Virus genomic	9.55e+01	C	208	15	1.1	252	14	MMT14MHC	Mouse T14 class I MHC	1.63e+03
	136	17	1.2	2948	21	MAVSPA	Lactobacillus casei va	9.55e+01	C	209	15	1.1	267	14	MMQ6MHC	Mouse Q6 class I MHC g	1.63e+03
C	137	17	1.2	3261	19	LBAVALS	Drosophila melanogaste	9.55e+01	C	210	15	1.1	272	14	MMQ89MHC	Mouse Q8/9 class I MHC	4.15e+02
	138	17	1.2	3407	17	DRO20DC6Z	Drosophila melanogaste	9.55e+01	C	211	16	1.1	273	25	E00074	DNA sequence of human-	4.15e+02
C	139	17	1.2	3621	17	DML81457	p87=transporter-like p	9.55e+01	C	212	16	1.1	273	25	I00910	Sequence 2 from Patent	1.63e+03
	140	17	1.2	3753	17	DRO20DC7Z	Rattus norvegicus mRNA	9.55e+01	C	213	15	1.1	273	17	FHU10316	Fasciola hepatica clon	1.63e+03
C	141	17	1.2	3868	15	S47919	Gallus gallus reletrola	9.55e+01	C	214	15	1.1	273	17	BMOBXB5S	B. mori bombyxin B-5 (1.63e+03
	142	17	1.2	4117	14	RNAJ696	Rattus norvegicus gene f	9.55e+01	C	215	15	1.1	273	17	BMOBXB4X	B. mori bombyxin B-4 (1.63e+03
C	143	17	1.2	4558	16	GGU88211	S.pombe alpi gene.	9.55e+01	C	216	16	1.1	277	23	ARHSINS	Artificial gene for hu	4.15e+02
	144	17	1.2	4790	18	SPALP1	Bombyx mori mRNA for B	9.55e+01	C	217	15	1.1	279	15	S75109	neurokinin receptor su	1.63e+03
C	145	17	1.2	4951	17	AB007832	Sus scrofa gene encodi	9.55e+01	C	218	15	1.1	282	17	BMOBBXBJS	B. mori bombyxin B-11	4.15e+02
	146	17	1.2	5018	15	SSNAGATIT	Mouse growth factor in	9.55e+01	C	219	16	1.1	286	23	SYNINSGSA	Synthetic human proins	1.63e+03
C	147	17	1.2	5196	14	MMCYR61G	P.hybrida chsb gene fo	9.55e+01	C	220	16	1.1	290	20	POLRRISA	Parathelohania anophel	1.63e+03
	148	17	1.2	5573	18	PHCSB	Mus Musculus alphaA-cr	9.55e+01	C	221	15	1.1	301	17	DROCOPAJ1	D. melanogaster copia	1.63e+03
C	149	17	1.2	6536	14	MUSALCR01	Drosophila 68C glue ge	9.55e+01	C	222	15	1.1	304	14	MMT17MHC	Mouse T17 class I MHC	1.63e+03
	150	17	1.2	6751	17	DMSG378	Human papillomavirus t	9.55e+01	C	223	15	1.1	305	14	MMTENASCI	Rat carboxypeptidase B	4.15e+02
C	151	17	1.2	7713	21	HPV25	Squalus acanthias mult	9.55e+01	C	224	16	1.1	319	14	RATCARB02	Varanus albigularis 12	4.15e+02
	152	17	1.2	8781	16	SAUI18868	Ovis aries y chromosom	9.55e+01	C	225	16	1.1	323	16	VVAL2	MHC RT1.H alpha =major	1.63e+03
C	153	17	1.2	10063	15	CAU30306	Sequence 5 from patent	9.55e+01	C	226	15	1.1	324	14	S80390S3	cdNA encoding subunit	4.15e+02
	154	17	1.2	10564	25	I47707	Methanobacterium therm	9.55e+01	C	227	16	1.1	331	25	I22421	Monodelphis domestica	4.15e+02
C	155	17	1.2	11378	19	AE000919	Sequence 1 from Patent	9.55e+01	C	228	16	1.1	336	25	E08679	Rattus norvegicus test	1.63e+03
	156	17	1.2	11725	25	I07993	Sequence 13 from Paten	9.55e+01	C	229	16	1.1	342	15	AF007082	Ig VH [rabbits, B-lymp	4.15e+02
C	157	17	1.2	11725	25	I05479	Escherichia coli K-12	9.55e+01	C	230	15	1.1	343	14	RNCYT0BA08	Human (synthetic) insu	4.15e+02
	158	17	1.2	12697	19	ECAE000444	Methanobacterium therm	9.55e+01	C	231	16	1.1	345	15	S76746		
C	159	17	1.2	15124	19	AE000934			C	232	16	1.1	351	23	SYNINSGS		
	160	17	1.2						C	233	16	1.1					

C	234	25	E00001	DNA coding of rat pro-	4.15e+02		C	307	16	1.1	1112	19	BCU89504	Burkholderia cepacia p	4.15e+02
C	235	16	I02834	Sequence 1 from Patent	4.15e+02		C	308	16	1.1	1120	14	RATCLND2	Rat mRNA for cyclin D2	4.15e+02
C	236	16	I03587	Sequence 3 from Patent	4.15e+02		C	309	16	1.1	1125	25	T09022	Sequence 41 from patent	4.15e+02
C	237	15	PCAF003368	Penicillium chrysogenu	1.63e+03		C	310	16	1.1	1125	21	SV4STA2	Rhesus macaque polyoma	4.15e+02
C	238	15	A43569	Sequence 37 from Paten	1.63e+03		C	311	15	1.1	1146	14	MU57325	Mus musculus PS-2short	1.63e+03
C	239	16	PIHWN1A	Pituiophis melanoleucus	4.15e+02		C	312	15	1.1	1148	17	SHIRI8S2	Sarcocystis hirsuta 18	1.63e+03
C	240	15	MUSEFABA	M.musculus CC49 Fab mR	1.63e+03		C	313	16	1.1	1151	14	MMPPICG5	Mus musculus protein p	4.15e+02
C	241	16	MCXMTCTBA	M.mimus mitochondrial	4.15e+02		C	314	16	1.1	1182	21	ABO03514	Actinidia deliciosa MR	4.15e+02
C	242	16	S69384	glucagon receptor [mic	4.15e+02		C	315	15	1.1	1182	21	PYVCOAT	potato virus Y (PVY) m	4.15e+02
C	243	16	DROPRD91	D.melanogaster paired	4.15e+02		C	316	15	1.1	1183	18	ATY54561	Arabidopsis thaliana t	1.63e+03
C	244	15	PCAF003369	Penicillium citrinum m	1.63e+03		C	317	15	1.1	1198	21	REOS3NSB	Reovirus serotype 2 S3	1.63e+03
C	245	15	MUSMH37T02	G.gallus MHC class	1.63e+03		C	318	15	1.1	1206	15	RABL18RSB	Oryctolagus cuniculus	1.63e+03
C	246	15	Ggz83791	M.aureatus microsatellit	1.63e+03		C	319	15	1.1	1222	15	BYENKE	Bovine messenger RNA f	1.63e+03
C	247	16	MAOREMR	M.aureatus mRNA (440 bp	4.15e+02		C	320	15	1.1	1222	15	BOVENKEPH	S.cerevisiae SSO2 mRNA	4.15e+02
C	248	15	SZU51170	Stylochus zebra marine	1.63e+03		C	321	16	1.1	1223	18	SCSSO2A	Mus musculus glycylami	1.63e+03
C	249	16	TSU04454	Tapiroma sessile clone	4.15e+02		C	322	15	1.1	1229	14	MKGART18	R.norvegicus mRNA for	1.63e+03
C	250	15	MNU09659	Mus musculus chaperonI	1.63e+03		C	323	15	1.1	1275	14	RNBMP2	B.napus mRNA for glyox	1.63e+03
C	251	15	PRKMTCTB	Promops centralis mito	1.63e+03		C	324	16	1.1	1288	18	BNGMDH	X.laevis mRNA for calr	1.63e+03
C	252	15	AF019776	Staphylococcus hyicus	1.63e+03		C	325	15	1.1	1291	16	XLGALR	CDNA encoding IL-8 rec	1.63e+03
C	253	15	MUSANTH21	Mouse thymus leukemia	1.63e+03		C	326	15	1.1	1299	25	E07262	Oryza sativa peroxidas	1.63e+03
C	254	15	I20600	Sequence 13 from paten	1.63e+03		C	327	15	1.1	1306	18	AF014467	Mus musculus endoprote	1.63e+03
C	255	15	590 25	A.caudatus L. (ACI) mr	4.15e+02		C	328	15	1.1	1306	14	MXPACE4M1	X.laevis mRNA for calr	1.63e+03
C	256	16	ACLIAMP2	Millettia richardiana	4.15e+02		C	329	15	1.1	1307	16	XCALRET	Sequence 2 from Patent	1.63e+03
C	257	16	AF004786	Millettia dura phytoc	4.15e+02		C	330	15	1.1	1324	25	I03610	CDNA encoding human tu	1.63e+03
C	258	16	AF004785	Carmichaelia sp. 'Lavi	4.15e+02		C	331	15	1.1	1324	25	E00702	Chicken mRNA for catal	4.15e+02
C	259	16	CSU78839	Mundulea sericea phyto	4.15e+02		C	332	16	1.1	1338	16	CHK130KDC	A.thaliana protein pho	4.15e+02
C	260	16	MSU78066	Piscidia piscipula phy	4.15e+02		C	333	15	1.1	1349	18	ATRPPOHB	Sequence 1 from patent	1.63e+03
C	261	16	AF004791	Millettia grandis phyt	4.15e+02		C	334	16	1.1	1352	25	I32827	Chironomus thummi clon	1.63e+03
C	262	15	ABU78843	Austrosteensia blackii	1.63e+03		C	335	15	1.1	1356	17	CFU14628	xenopus mRNA for alpha	1.63e+03
C	263	16	SAU78837	Sophora affinis phytoc	4.15e+02		C	336	15	1.1	1364	16	XLFODA2	Pig cofilin mRNA, comp	1.63e+03
C	264	16	AF004797	Lonchocarpus eriocarin	4.15e+02		C	337	15	1.1	1390	15	PIGCOFIL	Mus musculus GDP disso	1.63e+03
C	265	15	AF004782	Ostryocarpus stuhlman	4.15e+02		C	338	15	1.1	1391	14	MUSGDPBETA	Rattus norvegicus mRNA	1.63e+03
C	266	15	XLBGILR	Xenopus laevis mRNA fo	1.63e+03		C	339	15	1.1	1399	14	RSBBE	Mus musculus beta-gala	4.15e+02
C	267	16	600 21	Human immunodeficiency	4.15e+02		C	340	15	1.1	1418	14	MU55060	M.musculus Pax-8 gene,	4.15e+02
C	268	16	607 14	Rat insulin 1 gene, ex	4.15e+02		C	341	16	1.1	1419	14	MMPAX81	Human immunodeficiency	1.63e+03
C	269	15	639 21	Foot and mouth disease	1.63e+03		C	342	15	1.1	1419	21	HYGP120ZZ	a.nidulans mt small ri	4.15e+02
C	270	15	673 15	Sus scrofa retinoic ac	4.15e+02		C	343	15	1.1	1437	18	EMEMTRGS	Mus musculus protein p	1.63e+03
C	271	16	678 18	Saccharomyces cerevisi	4.15e+02		C	344	15	1.1	1438	14	MUSDIST2M1A	Oryctolagus cuniculus	1.63e+03
C	272	16	688 15	S.scrofa gpi gene for	4.15e+02		C	345	15	1.1	1444	15	RABTRIL	Rat PP-192 gene for ca	4.15e+02
C	273	15	689 14	M.musculus Vli gene (1	1.63e+03		C	346	16	1.1	1456	14	RATPP1G2	Oryctolagus cuniculus	1.63e+03
C	274	15	693 17	Dictyostelium discoide	1.63e+03		C	347	15	1.1	1456	15	OCU24216	Rat PP-192 gene for ca	4.15e+02
C	275	15	693 25	Sequence 6 from Patent	1.63e+03		C	348	15	1.1	1459	15	BIFET	Oryctolagus cuniculus	1.63e+03
C	276	15	702 25	Sequence 30 from Paten	1.63e+03		C	349	15	1.1	1476	25	AA3747	B.taurus mRNA for fetu	1.63e+03
C	277	16	708 18	Orpinomyces sp. cyclop	4.15e+02		C	350	15	1.1	1486	15	RABPRCAMU	Sequence 3 from Patent	1.63e+03
C	278	16	721 14	Rat gene for insulin (4.15e+02		C	351	16	1.1	1487	19	PRCADADA	Rabbit calcium-depende	4.15e+02
C	279	16	752 15	Rabbit rearranged Ig h	4.15e+02		C	352	16	1.1	1488	23	XXU14012	Plasmid R (from C.dive	4.15e+02
C	280	16	770 16	G.gallus HMG-14a gene	4.15e+02		C	353	16	1.1	1495	17	MMU52826	Synthetic construct gl	4.15e+02
C	281	16	801 14	Microxus mimus mitoch	4.15e+02		C	354	15	1.1	1498	17	CTU14627	Mus musculus syndecan-	4.15e+02
C	282	16	804 21	Potato Virus Y (Potato	4.15e+02		C	355	15	1.1	1498	18	ALFRPE15A	Chironomus thummi hemo	1.63e+03
C	283	16	826 17	Onchocerca volvulus cy	4.15e+02		C	356	16	1.1	1502	14	MMG1P1R	Medicago sativa middle	1.63e+03
C	284	16	828 16	Gallus gallus homeodom	4.15e+02		C	357	15	1.1	1507	17	AFU06469	Mus musculus mRNA for	4.15e+02
C	285	16	860 15	Bovine mRNA for beta-c	4.15e+02		C	358	16	1.1	1508	14	S78217	Sarcocystis hirsuta 18	1.63e+03
C	286	16	872 16	Gallus gallus HMG-14 p	4.15e+02		C	359	16	1.1	1510	14	ABO08534	protein phosphatase 1	4.15e+02
C	287	15	883 16	Chicken MRLC mRNA for	1.63e+03		C	360	16	1.1	1513	15	DVLINELIRT	Rattus norvegicus mRNA	4.15e+02
C	288	15	892 25	DNA sequence of human	1.63e+03		C	361	15	1.1	1544	19	HAARNA	D.virginiana partial L	1.63e+03
C	289	16	899 21	Avian erythroblastosis	4.15e+02		C	362	15	1.1	1546	19	D50648	Haloanaerobium lacuros	4.15e+02
C	290	15	921 18	A.thaliana mRNA for pr	1.63e+03		C	363	15	1.1	1546	15	SSRYR1B	Erythrobacter longus p	4.15e+02
C	291	16	944 14	Mus musculus platelet-	4.15e+02		C	364	15	1.1	1547	15	RNU94710	S.scrofa RYR1 gene for	1.63e+03
C	292	15	949 18	A.thaliana mRNA for va	1.63e+03		C	365	15	1.1	1547	15	PIGVITRON	Rattus norvegicus type	4.15e+02
C	293	15	954 15	Capra hircus MCI-R gen	1.63e+03		C	366	15	1.1	1555	15	D61396	Pig mRNA for vitronect	1.63e+03
C	294	15	954 15	CCMC1R	1.63e+03		C	367	15	1.1	1555	15	D61396	Porcine mRNA for vitro	1.63e+03
C	295	15	962 19	B.doshiaie glta gene (s	1.63e+03		C	368	16	1.1	1564	18	ATCSMRNA	A.thaliana mRNA for cy	1.63e+03
C	296	15	977 14	Mus musculus (C40c) he	1.63e+03		C	369	16	1.1	1597	18	NTL19R1B	N.tabacum (cv.Samsun N	4.15e+02
C	297	15	981 14	R.norvegicus mRNA for	1.63e+03		C	370	15	1.1	1617	18	NGAZURIN	Neisseria gonorrhoeae	4.15e+02
C	298	15	997 16	Chicken mRNA insertion	1.63e+03		C	371	16	1.1	1618	18	LJGPAL	i.japonicus gpal mRNA.	1.63e+03
C	299	15	1014 18	P.sativum mRNA for typ	1.63e+03		C	372	16	1.1	1620	16	SCYPL162C	S.cerevisiae chromosom	4.15e+02
C	300	16	1035 21	Human immunodeficiency	1.63e+02		C	373	15	1.1	1641	18	YSCARPA0	G.gallus mRNA for vitr	4.15e+02
C	301	16	1062 21	Human herpesvirus 7 UI	4.15e+02		C	374	15	1.1	1653	18	YSCSIT4A	S.cerevisiae acidic r	1.63e+03
C	302	15	1068 15	Oryctolagus cuniculus	1.63e+03		C	375	15	1.1	1669	19	BCU94743	Bacillus cereus hemoly	1.63e+03
C	303	15	1077 14	Mus musculus beta-gala	1.63e+03		C	376	16	1.1	1680	21	REAEV34E	Avian Erythroblastosis	4.15e+02
C	304	15	1086 18	S.cerevisiae ccpl gene	1.63e+03		C	377	16	1.1	1688	23	AF044078	Synthetic construct tr	4.15e+02
C	305	15	1103 18	Porphyrin tenara gene f	1.63e+03		C	378	15	1.1	1699	16	DRU57656	Danio rerio lipoprotei	1.63e+03
C	306	15	1108 18	S.cerevisiae chromosom	1.63e+03		C	379	15	1.1	1720	18	YSCIL10F	S.cerevisiae L10e prot	1.63e+03

C	380	16	1.1	1722	15	FDTNEA	Feline gene for feline	4.15e+02
C	381	16	1.1	1731	14	AF006617	Rattus norvegicus micr	4.15e+02
C	382	16	1.1	1731	25	I55059	Sequence 13 from paten	4.15e+02
C	383	15	1.1	1736	14	RATSRI3	Rat SRI3 myelin protei	1.63e+03
C	384	15	1.1	1736	14	S55427	myelin protein SRI3=gr	1.63e+03
C	385	16	1.1	1740	18	LIGPROA	L.luteus mRNA for alph	4.15e+02
C	386	15	1.1	1755	16	D82053	Cynops pyrrhogaster mr	1.63e+03
C	387	16	1.1	1761	15	HRSDHE	Horse alcohol dehydrog	4.15e+02
C	388	15	1.1	1762	21	FLAENM76HA	Influenza A/equine/New	1.63e+03
C	389	15	1.1	1766	18	YSCSIP2	Saccharomyces cerevisi	1.63e+03
C	390	16	1.1	1770	16	ORZALAR	Oryzias latipes alphas	4.15e+02
C	391	16	1.1	1775	18	CPCCMC1	Cryptococcus flavus mr	4.15e+02
C	392	16	1.1	1775	18	S45137	CMC1=carboxymethylcell	4.15e+02
C	393	16	1.1	1775	18	PSU97043	Pisum sativum G protei	4.15e+02
C	394	16	1.1	1788	21	ACBYERBBA	Avian erythroblastosis	4.15e+02
C	395	15	1.1	1799	17	OCTOMEGCRY	Octopus dofleini omega	1.63e+03
C	396	15	1.1	1800	14	MUSGAS3A	Mouse growth arrest sp	1.63e+03
C	397	16	1.1	1806	14	RATGLPR	Rattus norvegicus gluc	4.15e+02
C	398	16	1.1	1806	14	RNHRGLP1	R.norvegicus mRNA for	4.15e+02
C	399	15	1.1	1812	15	BOVOSTP	Bovine oestrogen sulfo	1.63e+03
C	400	15	1.1	1812	15	BTOSTR	B.taurus mRNA for oest	1.63e+03
C	401	15	1.1	1816	14	RNCD25MR	R.norvegicus mRNA for	1.63e+03
C	402	16	1.1	1818	19	CCU59414	Clostridium celluloipa	4.15e+02
C	403	16	1.1	1825	17	AB006455	Patinopecten yessoensi	4.15e+02
C	404	15	1.1	1838	18	NTIPTVP17	N.tabacum mRNA for ino	1.63e+03
C	405	15	1.1	1864	18	ATGGS	A.thaliana mRNA for pu	1.63e+03
C	406	16	1.1	1875	14	RATGLUCREC	Rat glucagon receptor	4.15e+02
C	407	15	1.1	1878	17	SFU03071	Sarcocystis fusiformis	1.63e+03
C	408	16	1.1	1889	17	DROGPAD	D.melanogaster G prote	4.15e+02
C	409	15	1.1	1901	19	MTU37405	Methanobacterium therm	1.63e+03
C	410	16	1.1	1904	19	MC010	M.capricolum DNA for C	4.15e+02
C	411	16	1.1	1909	25	I66446	Sequence 3 from patent	4.15e+02
C	412	15	1.1	1912	18	PRULHP	Prunus persica (clone	1.63e+03
C	413	16	1.1	1914	17	SE18SRRN	S.elegans gene encodin	4.15e+02
C	414	15	1.1	1917	15	BTU21660	Bos taurus phosphatidy	1.63e+03
C	415	15	1.1	1917	18	MIANRN	A.nidulans mitochondr	1.63e+03
C	416	15	1.1	1929	18	CHATGSH1	A.thaliana Chloroplast	1.63e+03
C	417	15	1.1	1936	18	SCYOR123C	S.cerevisiae chromosom	1.63e+03
C	418	15	1.1	1944	14	MUSGLURECB	R.norvegicus (Sprague	1.63e+03
C	419	16	1.1	1950	19	SEU43247	Mus musculus glucagon	4.15e+02
C	420	15	1.1	1950	19	SEU43248	Salmonella enterica in	1.63e+03
C	421	15	1.1	1950	19	EHU78319	Salmonella enterica in	1.63e+03
C	422	15	1.1	1958	17	ATUCHVA	Entamoeba histolytica	1.63e+03
C	423	16	1.1	1969	19	RNU15660	A.tumefaciens attachme	4.15e+02
C	424	15	1.1	1996	14	RYU15660	Rattus norvegicus orph	1.63e+03
C	425	15	1.1	2008	18	SCYGL208W	S.cerevisiae chromosom	1.63e+03
C	426	16	1.1	2020	18	SCYJR011C	S.cerevisiae chromosom	4.15e+02
C	427	16	1.1	2031	18	YSPB	Yeast gene for RNA pol	4.15e+02
C	428	16	1.1	2032	16	CRARED	Carassius auratus red	1.63e+03
C	429	15	1.1	2043	15	S82652	biglycan core protein	1.63e+03
C	430	16	1.1	2046	17	DMDIFF6	D.melanogaster mRNA fo	4.15e+02
C	431	16	1.1	2086	18	YSCDPH2A	Saccharomyces cerevisi	4.15e+02
C	432	15	1.1	2091	21	ACBERBBH	Avian erythroblastosis	4.15e+02
C	433	15	1.1	2094	21	S78506	Forl1 region, R-fragme	1.63e+03
C	434	16	1.1	2096	17	AF031414	Caenorhabditis elegans	4.15e+02
C	435	16	1.1	2116	14	S75952	glucagon-like peptide	4.15e+02
C	436	15	1.1	2118	17	HCY14233	Haemonchus contortus m	1.63e+03
C	437	16	1.1	2127	25	I05724	Sequence 12 from Paten	4.15e+02
C	438	15	1.1	2134	16	XLCTGT	X.laevis Cctg mRNA.	1.63e+03
C	439	16	1.1	2147	25	I08174	Sequence 1 from Patent	4.15e+02
C	440	16	1.1	2178	17	DROSEP1HP	Drosophila melanogaste	4.15e+02
C	441	16	1.1	2189	25	A19048	H.sapiens mRNA for thr	4.15e+02
C	442	16	1.1	2194	15	BOVPAF	Bovine mRNA for PAF ac	4.15e+02
C	443	16	1.1	2200	14	MUSPIMLK	Mouse mRNA for PPIgam	4.15e+02
C	444	16	1.1	2208	21	S69372	.env [Rous Associa	4.15e+02
C	445	16	1.1	2209	17	LB094966	Leishmania braziliensi	4.15e+02
C	446	16	1.1	2220	18	ZMBIAA	Z.mays B-I gene for B	4.15e+02
C	447	16	1.1	2224	14	RATPIIG1	Rat PP-1g1 gene for ca	4.15e+02
C	448	16	1.1	2269	14	MMU90267	Mus musculus CDK5 acti	1.63e+03
C	449	15	1.1	2278	14	MUSPKI	Mus musculus inhibitor	1.63e+03
C	450	16	1.1	2294	18	MMU53456	Mus musculus protein p	4.15e+02
C	451	15	1.1	2327	18	AF030290	Arabidopsis thaliana p	1.63e+03
C	452	15	1.1	2334	25	I57970	Sequence 1 from patent	1.63e+03

526	15	1.1	3537	26	AC003306	*** SEQUENCING IN PROG	1.63e+03	599	16	1.1	5291	19	MLUSTROA	M.luteus str operon en	4.15e+02
527	16	1.1	3558	16	GGUSTIDNA	G.gallus USIL-1 DNA se	4.15e+02	600	16	1.1	5326	14	MUSGURECA	Mus musculus glucagon	4.15e+02
528	15	1.1	3615	16	D83273	Cyprinus carpio mRNA f	1.63e+03	601	16	1.1	5350	14	MMAM3EAA2	Mus musculus laminin b	4.15e+02
529	15	1.1	3658	14	AF035045	Mus musculus Maxik pot	1.63e+03	602	15	1.1	5362	14	MUSMHSUPC	Mouse MHC sex-limited	1.63e+03
530	15	1.1	3682	21	PVUMVIN83	Puumala virus M-segmen	1.63e+03	603	15	1.1	5371	14	MM091967	Mus musculus platelet	1.63e+03
531	15	1.1	3730	25	I34014	Sequence 8 from patent	1.63e+03	604	16	1.1	5425	14	RATINSI	Rat insulin-I (Ins-1)	4.15e+02
532	15	1.1	3743	14	RATPTK3D	Rattus norvegicus tyro	1.63e+03	605	15	1.1	5479	14	MMH2KK	Mouse H-2K(k) gene of	1.63e+03
533	15	1.1	3750	19	U93704	Riftia pachyptila endo	1.63e+03	606	15	1.1	5491	18	ATATK1	A.thaliana Atk-1 gene.	1.63e+03
534	15	1.1	3783	17	CEGPA2G	Caenorhabditis elegans	1.63e+03	607	16	1.1	5552	17	DROPLC21A	D.melanogaster phospho	4.15e+02
535	16	1.1	3840	19	PDBCI	P. denitrificans bcl g	1.63e+03	608	16	1.1	5559	14	RNGREXS2	Rattus norvegicus gluc	4.15e+02
536	15	1.1	3865	19	ECOPLSB	E.coli plsb and dgk ge	4.15e+02	609	15	1.1	5562	17	CEVITELA	C.elegans gene for vit	1.63e+03
537	15	1.1	3874	19	RCFBC	Rhodopseudomonas sphae	1.63e+03	610	15	1.1	5565	14	MM15A3A	M.musculus mRNA for la	4.15e+02
538	15	1.1	3876	17	BMOSP2	Silkworm (B.mori) stor	1.63e+03	611	16	1.1	5581	14	RNSTAM	Rat s-laminin mRNA.	4.15e+02
539	15	1.1	3911	18	SCYJL162C	S.cerevisiae chromosom	1.63e+03	612	15	1.1	5651	15	RABAMA	Rabbit serum amyloid A	1.63e+03
540	15	1.1	3920	17	DRO25DC97Z	Drosophila melanogaste	1.63e+03	613	16	1.1	5702	14	RNMAP2	Rat map2 gene for micr	4.15e+02
541	15	1.1	3923	14	MUSB14GT1	Mouse N-acetylglucosam	1.63e+03	614	16	1.1	5731	14	RNMAPP2	Rat mRNA for microtubu	4.15e+02
542	15	1.1	3947	19	MBU77466	Mycobacterium bovis BC	1.63e+03	615	16	1.1	5736	14	RNMAPP2R	Rat mRNA for microtubu	4.15e+02
543	15	1.1	3955	18	YSCRAD25A	Saccharomyces cerevisi	1.63e+03	616	15	1.1	5746	15	SSTEN	S.scrofa mRNA for tena	1.63e+03
544	16	1.1	3959	18	SCYJR010W	S.cerevisiae chromosom	4.15e+02	617	15	1.1	5794	19	WZJ14952	Weeksella zoohelcum Ac	1.63e+03
545	15	1.1	3969	14	MUSMHD2D	Mouse MHC class I D-re	1.63e+03	618	15	1.1	5799	18	TVDNALPGT	T.versicolor Dfg I and	4.15e+02
546	15	1.1	3980	19	ALTDAGA	A.haloplanktis D-alani	1.63e+03	619	15	1.1	5831	18	SOYNOD26A	Glycine max cv. Dare n	1.63e+03
547	15	1.1	3983	17	CEIFDR3	C.elegans IF44 gene fo	1.63e+03	620	15	1.1	5850	16	GGU62026	Gallus gallus cardiac	1.63e+03
548	15	1.1	4007	19	RCPETG	Rhodopseudomonas capsu	1.63e+03	621	15	1.1	5900	19	AF034614	Zymomonas mobilis carb	1.63e+03
549	15	1.1	4023	14	MMU41282	Mus musculus galactose	1.63e+03	622	15	1.1	6008	25	IL8304	Sequence 5 from patent	1.63e+03
550	16	1.1	4028	15	OCATGL1	Rabbit alpha-1-globin	4.15e+02	623	15	1.1	6014	14	YSCUBPIT	Saccharomyces cerevisi	1.63e+03
551	15	1.1	4029	17	IOU10338	Ilyanassa obsoleta RNA	1.63e+03	624	16	1.1	6018	14	AF025425	Mus musculus RNA polym	4.15e+02
552	16	1.1	4031	15	RABHBAPT	Rabbit alpha-globin ge	1.63e+03	625	16	1.1	6027	19	MKY14428	Methanopyrus kandleri	4.15e+02
553	15	1.1	4079	15	AF023128	Cryptolagus cuniculus	1.63e+03	626	16	1.1	6027	19	AF025425	Rattus norvegicus RNA	4.15e+02
554	15	1.1	4146	25	I57017	S.cerevisiae chromosom	1.63e+03	627	15	1.1	6161	14	MMV17393	Mus musculus class Ib	1.63e+03
555	15	1.1	4147	18	ATU50400	Arabidopsis thaliana p	1.63e+03	628	15	1.1	6175	21	HSVT1IEP	Feline herpesvirus typ	1.63e+03
556	15	1.1	4182	18	SCYOR162C	Sequence 1 from patent	1.63e+03	629	15	1.1	6225	18	HVCPMIT	H.vulgaris gene encodin	1.63e+03
557	15	1.1	4200	25	I34008	Sequence 1 from patent	1.63e+03	630	16	1.1	6331	14	MMR200KP	M.musculus mRNA for 20	4.15e+02
558	15	1.1	4299	25	I26663	Rattus norvegicus Pg10	4.15e+02	631	16	1.1	6465	14	AEVPPNA	Avian erythroblastosis	1.63e+02
559	15	1.1	4368	14	RNU76717	Arabidopsis thaliana g	1.63e+03	632	16	1.1	6556	21	NPOCAPA	Mouse mRNA for plexin	4.15e+02
560	16	1.1	4374	18	ATU53856	Drosophila melanogaste	1.63e+03	633	16	1.1	6563	16	CHKERBBF	O.pseudotsugata multic	4.15e+02
561	15	1.1	4415	17	DROKCHAN	Rattus norvegicus gamm	1.63e+03	634	16	1.1	6642	25	I64799	Sequence 5 from patent	1.63e+03
562	15	1.1	4489	14	RNU17096	Caenorhabditis elegans	4.15e+02	635	15	1.1	6730	14	MD8949	Mouse mRNA for plexin	1.63e+03
563	15	1.1	4497	17	AF016854	B.bronchiseptica bvg 1	4.15e+02	636	15	1.1	6831	14	MMTENASC	Mouse mRNA for tenasci	1.63e+03
564	16	1.1	4534	19	BBBVGAS	D.discoideum racGAP ge	4.15e+02	637	15	1.1	6843	25	I64800	Sequence 6 from patent	1.63e+03
565	16	1.1	4535	17	DDY10159	P.vulgata alpha-tubuli	1.63e+03	638	15	1.1	6900	19	BPBGVAS	B.parapertussis bvg lo	4.15e+02
566	15	1.1	4545	17	PVAT4G	Rattus norvegicus Spra	4.15e+02	639	16	1.1	7129	18	SCCATCB	S.cerevisiae DPr2, YCN	1.63e+02
567	16	1.1	4595	14	RNU10096	Mus musculus kidney-sp	4.15e+02	640	15	1.1	7129	18	ZMU77346	Zea mays lethal leaf-s	1.63e+02
568	16	1.1	4605	14	MMU94518	Mus musculus kidney-sp	4.15e+02	641	15	1.1	7350	25	II4735	Sequence 14 from paten	4.15e+02
569	16	1.1	4655	14	MMU20974	Mus musculus kidney-sp	4.15e+02	642	16	1.1	7573	21	GPCDNPO	Guinea Pig Cyomegalov	4.15e+02
570	16	1.1	4655	14	MMU20975	Mus musculus seed coat	1.63e+03	643	15	1.1	7687	21	MRU01834	Multimammate rat papil	1.63e+03
571	16	1.1	4655	14	MMU20973	Glycine max seed coat	4.15e+02	644	15	1.1	7762	19	BTU55042	Bos taurus myosin X, c	1.63e+03
572	16	1.1	4700	18	AF014502	Mouse MHC class I H-2D	1.63e+03	645	15	1.1	7872	14	BAAMYLA	B.acidocaldarius amy g	4.15e+02
573	15	1.1	4718	14	MUSMHE2DK	Mouse C4/SLP hybrid 1	1.63e+03	646	16	1.1	7909	17	MMABCI	Plasmodium falciparum	1.63e+03
574	15	1.1	4730	14	MUSC4SLP1	Mouse C4/SLP hybrid 2	1.63e+03	647	15	1.1	7913	15	BOVCMPPR	Bovine cation-independ	1.63e+03
575	15	1.1	4750	15	OCNKCC2B	Oryctolagus cuniculus	4.15e+02	648	15	1.1	7942	21	HPV52	R.norvegicus (Sprague	1.63e+03
576	16	1.1	4750	15	OCNKCC2A	Oryctolagus cuniculus	4.15e+02	649	15	1.1	8014	14	RNTEST6	Human immunodeficienc	4.15e+02
577	16	1.1	4750	15	OCNKCC2F	Oryctolagus cuniculus	4.15e+02	650	15	1.1	8017	18	ATU76670	Arabidopsis thaliana r	1.63e+03
578	16	1.1	4758	17	DDU23478	Dictyostelium discoide	4.15e+02	651	15	1.1	8089	19	STMDAUABCE	Streptomyces sp. aklay	4.15e+02
579	16	1.1	4763	14	MUSMHQ89DB	Mouse MHC qa-2,3 class	1.63e+03	652	16	1.1	9000	21	HIV1U26942	Human immunodeficienc	4.15e+02
580	15	1.1	4768	16	CHKTR0SS04	Chicken tropomyosin be	1.63e+03	653	15	1.1	9022	21	HIVNY5CG	Human immunodeficienc	4.15e+02
581	15	1.1	4785	18	MIPCTRATP	Emericella nidulans hy	4.15e+02	654	16	1.1	9201	23	SYNSVPHEP	Cloning vector cosmid	4.15e+02
582	15	1.1	4819	18	AF001273	Cloning vector PEUK-C1	4.15e+02	655	16	1.1	9623	21	SIVAGM677A	Simian (African green	4.15e+02
583	15	1.1	4892	23	XXU02429	PSVL cloning vector, c	4.15e+02	656	16	1.1	9698	21	PVU09509	Potato virus Y common	4.15e+02
584	16	1.1	4896	19	STRGTFIC	House mouse; Musculus	1.63e+03	657	16	1.1	9709	21	HIVNL43	Human immunodeficiency	4.15e+02
585	16	1.1	4957	14	D87117	Microcystis aeruginosa	1.63e+03	658	15	1.1	9811	21	CIVCG	Chimpanzee immunodef	1.63e+03
586	15	1.1	5071	19	MA2PMA2	Aeromonas caviae phac	4.15e+02	659	15	1.1	9901	19	U67530	Methanococcus jannasch	1.63e+03
587	15	1.1	5071	15	D88825	S.scrofa mRNA for Na/D	1.63e+03	660	15	1.1	10028	19	U67503	Methanococcus jannasch	1.63e+03
588	16	1.1	5110	14	MMPDGBSR	Mouse pre-PDGF recepto	4.15e+02	661	15	1.1	10029	19	STRGTFBC	S.mutans glucosyltrans	4.15e+02
589	15	1.1	5125	14	RNANTANT	Rat anti gene for aden	1.63e+03	662	15	1.1	10035	21	AF024514	Acyrthosiphon pisum vi	1.63e+03
590	16	1.1	5147	21	AF038616	Simian virus 40 strain	4.15e+02	663	15	1.1	10105	19	AE000946	Archaeoglobus fulgidus	1.63e+03
591	15	1.1	5187	14	MUSMHLA	Mouse MHC class I T3-d	1.63e+03	664	15	1.1	10194	15	GOTGLOBE	Goat beta globin locus	4.15e+02
592	16	1.1	5243	21	SV40XX	SV40 genome.	4.15e+02	665	15	1.1	10199	18	AF009516	Petunia x hybrida tran	1.63e+03
593	16	1.1	5243	21	SV4CG	Simian virus 40 comple	4.15e+02	666	16	1.1	10338	19	U67464	Methanococcus jannasch	4.15e+02
594	15	1.1	5264	14	RNU61261	Rattus norvegicus lam1	1.63e+03	667	16	1.1	10512	19	HPAE000639	Helicobacter pylori se	4.15e+02

C	672	16	1.1	10622	15	RABGLBIN	Rabbit zeta-1 globin (4.15e+02																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																							
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C	818	16	1.1	46105	17	CELCS5C3	Caenorhabditis elegans	4.15e+02	C	891	16	1.1	120201	26	HS506	Human DNA sequence ***	4.15e+02
C	819	15	1.1	46462	17	CELCS3F10	Caenorhabditis elegans	1.63e+03	C	892	16	1.1	120787	18	AC002292	Genomic sequence of Ar	4.15e+02
C	820	15	1.1	47388	26	AC000090	*** SEQUENCING IN PROG	1.63e+03	C	893	15	1.1	122176	14	AC003997	Mouse BAC mbac20 from	1.63e+03
C	821	15	1.1	47512	26	CER03E1	Caenorhabditis elegans	1.63e+03	C	894	15	1.1	123080	26	HS510H16	Human DNA sequence ***	1.63e+03
C	822	15	1.1	47554	17	CELD1007	Caenorhabditis elegans	1.63e+03	C	895	16	1.1	124000	26	AC004060	*** SEQUENCING IN PROG	4.15e+02
C	823	16	1.1	47785	17	CELF45E4	Caenorhabditis elegans	4.15e+02	C	896	16	1.1	127098	26	HS971N18	Human DNA sequence ***	4.15e+02
C	824	15	1.1	48985	26	CEW03G8	Caenorhabditis elegans	1.63e+03	C	897	16	1.1	128000	26	AC004046	*** SEQUENCING IN PROG	4.15e+02
C	825	15	1.1	50984	18	SCXVORFS	S.cerevisiae DNA of 51	1.63e+03	C	898	16	1.1	128208	26	AC003040	*** SEQUENCING IN PROG	4.15e+02
C	826	16	1.1	51776	26	HSN91G8	*** SEQUENCING IN PROG	4.15e+02	C	899	16	1.1	128393	26	HS14GH21	Human DNA sequence ***	4.15e+02
C	827	16	1.1	53419	14	MMU35323	Mus musculus H2-M alph	4.15e+02	C	900	15	1.1	128607	26	HS31314	Human DNA sequence ***	1.63e+03
C	828	16	1.1	53517	26	AC002405	Homo sapiens; HTGS pha	4.15e+02	C	901	16	1.1	131047	26	AC002421	*** SEQUENCING IN PROG	4.15e+02
C	829	16	1.1	53533	19	BSY09476	B.subtilis 54kb genom	4.15e+02	C	902	15	1.1	131193	26	HS510D11	Human DNA sequence ***	1.63e+03
C	830	16	1.1	54606	26	AC000053	*** SEQUENCING IN PROG	4.15e+02	C	903	16	1.1	131936	26	AC003063	*** SEQUENCING IN PROG	4.15e+02
C	831	16	1.1	55786	18	SCLACHXVI	S.cerevisiae chromosom	4.15e+02	C	904	16	1.1	131990	21	OPU75930	Orgyia pseudotsugata n	4.15e+02
C	832	15	1.1	57677	26	HSU151E3	Human DNA sequence ***	1.63e+03	C	905	15	1.1	132367	26	AC002355	*** SEQUENCING IN PROG	1.63e+03
C	833	15	1.1	57892	18	AB005241	Arabidopsis thaliana g	1.63e+03	C	906	15	1.1	133661	21	U93872	Kaposi's sarcoma-assoc	4.15e+02
C	834	16	1.1	61001	18	AB010699	Arabidopsis thaliana g	4.15e+02	C	907	16	1.1	133687	26	AC002093	*** SEQUENCING IN PROG	4.15e+02
C	835	16	1.1	63093	18	ATU63815	Arabidopsis thaliana A	4.15e+02	C	908	16	1.1	134706	26	HS230G1	Human DNA sequence ***	1.63e+03
C	836	15	1.1	65958	18	AB009056	Arabidopsis thaliana g	1.63e+03	C	909	15	1.1	135194	26	AC004099	*** SEQUENCING IN PROG	4.15e+02
C	837	16	1.1	68302	18	SCE9781	Saccharomyces cerevisi	4.15e+02	C	910	15	1.1	136254	19	ECOUW82	E. coli; the region fr	1.63e+03
C	838	15	1.1	68537	26	HS824T19	Human DNA sequence ***	1.63e+03	C	911	15	1.1	136685	26	HS16915	Human DNA sequence ***	1.63e+03
C	839	15	1.1	69316	26	HSAC001233	*** SEQUENCING IN PROG	1.63e+03	C	912	15	1.1	137404	26	AC002375	Homo sapiens; HTGS pha	1.63e+03
C	840	15	1.1	70640	26	CEH32K21	Caenorhabditis elegans	1.63e+03	C	913	15	1.1	137500	26	HS340N1	Human DNA sequence ***	1.63e+03
C	841	15	1.1	75317	18	SC4357	S.cerevisiae chromosom	4.15e+02	C	914	15	1.1	138120	26	HS418A9	Human DNA sequence ***	1.63e+03
C	842	16	1.1	78054	26	HSAC000376	*** SEQUENCING IN PROG	4.15e+02	C	915	15	1.1	138187	14	MMMH461	Mus musculus Major His	1.63e+03
C	843	16	1.1	78616	14	AC000398	Genomic sequence from	4.15e+02	C	916	15	1.1	139467	19	D90905	Synechocystis sp. PCC6	1.63e+03
C	844	15	1.1	78844	18	AB006708	Arabidopsis thaliana g	1.63e+03	C	917	15	1.1	140596	26	HS745E8	Human DNA sequence ***	1.63e+03
C	845	15	1.1	79150	17	AC002513	Arabidopsis thaliana g	1.63e+03	C	918	15	1.1	141744	19	ECU28377	Escherichia coli K-12	1.63e+03
C	846	16	1.1	80101	17	AC004115	Drosophila melanogaste	4.15e+02	C	919	15	1.1	142282	26	AC004123	*** SEQUENCING IN PROG	1.63e+03
C	847	15	1.1	81189	26	AC003034	*** SEQUENCING IN PROG	1.63e+03	C	920	16	1.1	142828	26	HS782G3	Human DNA sequence ***	1.63e+03
C	848	15	1.1	81189	26	AC003034	*** SEQUENCING IN PROG	1.63e+03	C	921	15	1.1	144184	26	HS167P19	Human DNA sequence ***	1.63e+03
C	849	15	1.1	81729	17	L49405	Drosophila melanogaste	1.63e+03	C	922	16	1.1	144763	26	CEY40D7	Caenorhabditis elegans	4.15e+02
C	850	15	1.1	82415	18	AB005244	Arabidopsis thaliana g	1.63e+03	C	923	16	1.1	144861	21	HHU43400	Human herpesvirus-7 (H	4.15e+02
C	851	15	1.1	82484	18	ATAC002341	Arabidopsis thaliana c	1.63e+03	C	924	15	1.1	145788	26	HS192P9	Human DNA sequence ***	1.63e+03
C	852	16	1.1	83594	18	AB008268	Arabidopsis thaliana g	4.15e+02	C	925	16	1.1	146360	26	HS104C13	Human DNA sequence ***	4.15e+02
C	853	15	1.1	87500	19	AF027868	Bacillus subtilis chro	1.63e+03	C	926	15	1.1	146360	26	HS104C13	Human DNA sequence ***	1.63e+03
C	854	15	1.1	89350	18	ATT12H17	Arabidopsis thaliana D	1.63e+03	C	927	16	1.1	146505	18	F21M12	Sequence of BAC F21M12	4.15e+02
C	855	16	1.1	90143	26	HSAC001232	*** SEQUENCING IN PROG	4.15e+02	C	928	15	1.1	148583	26	CEY17D7	Caenorhabditis elegans	1.63e+03
C	856	16	1.1	90557	26	CEY7A5	Caenorhabditis elegans	4.15e+02	C	929	16	1.1	148583	26	CEY17D7	Caenorhabditis elegans	1.63e+03
C	857	16	1.1	91564	26	AC003062	*** SEQUENCING IN PROG	4.15e+02	C	930	15	1.1	149940	26	HS453C12	Human DNA sequence ***	1.63e+03
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C	860	16	1.1	93695	18	ATF2109	Arabidopsis thaliana D	4.15e+02	C	933	16	1.1	152708	26	HS964D12	Human DNA sequence ***	4.15e+02
C	861	15	1.1	94292	26	HS286B10	Human DNA sequence ***	1.63e+03	C	934	16	1.1	153080	21	AF037218	Human herpesvirus 7 st	4.15e+02
C	862	15	1.1	94292	26	HS286B10	Human DNA sequence ***	1.63e+03	C	935	15	1.1	154746	21	HSV2HG52	Herpes simplex virus t	1.63e+03
C	863	16	1.1	95134	26	HS265J14	Human DNA sequence ***	4.15e+02	C	936	16	1.1	157255	26	AC003036	Homo sapiens; HTGS pha	4.15e+02
C	864	16	1.1	95456	26	AC002092	*** SEQUENCING IN PROG	4.15e+02	C	937	15	1.1	157684	14	AC004093	Mus musculus (129SV) D	1.63e+03
C	865	16	1.1	95568	26	CEH05L14	Caenorhabditis elegans	4.15e+02	C	938	16	1.1	158635	26	HS407F17	Human DNA sequence ***	4.15e+02
C	866	15	1.1	97000	26	AC004059	Caenorhabditis elegans	1.63e+03	C	939	15	1.1	159500	26	HS18601	Human DNA sequence ***	1.63e+03
C	867	16	1.1	98940	26	AC003118	*** SEQUENCING IN PROG	4.15e+02	C	940	15	1.1	160839	26	HS329A5	Human DNA sequence ***	1.63e+03
C	868	16	1.1	100145	26	AC003104	*** SEQUENCING IN PROG	4.15e+02	C	941	15	1.1	160839	26	HS329A5	Human DNA sequence ***	1.63e+03
C	869	15	1.1	100639	26	AC002417	*** SEQUENCING IN PROG	1.63e+03	C	942	16	1.1	164775	26	AC003669	Homo sapiens; HTGS pha	4.15e+02
C	870	16	1.1	101778	26	CEY49A10	Caenorhabditis elegans	4.15e+02	C	943	15	1.1	165279	26	HS262D12	Human DNA sequence ***	1.63e+03
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C	872	15	1.1	106929	26	HS821D11	Human DNA sequence ***	1.63e+03	C	945	15	1.1	166924	18	MIATGENB	A.thaliana mitochondri	1.63e+03
C	873	16	1.1	108847	18	ATAF002109	Arabidopsis thaliana c	4.15e+02	C	946	15	1.1	167034	26	HS7706	Human DNA sequence ***	1.63e+03
C	874	15	1.1	110000	26	CEY39A1	Caenorhabditis elegans	1.63e+03	C	947	16	1.1	170000	26	AC004055	*** SEQUENCING IN PROG	4.15e+02
C	875	15	1.1	110000	26	CEY106G6	Caenorhabditis elegans	1.63e+03	C	948	15	1.1	170000	26	AC004067	*** SEQUENCING IN PROG	1.63e+03
C	876	15	1.1	110000	26	AC003035	Homo sapiens; HTGS pha	1.63e+03	C	949	15	1.1	170000	26	AC004055	*** SEQUENCING IN PROG	1.63e+03
C	877	15	1.1	110102	18	ATP28J12	Arabidopsis thaliana D	1.63e+03	C	950	15	1.1	170215	26	AC004127	*** SEQUENCING IN PROG	1.63e+03
C	878	15	1.1	110409	26	AC002290	*** SEQUENCING IN PROG	1.63e+03	C	951	16	1.1	170789	26	CEY76A2	Caenorhabditis elegans	4.15e+02
C	879	15	1.1	110838	26	AC003661	*** SEQUENCING IN PROG	1.63e+03	C	952	16	1.1	171797	26	HS6802	Human DNA sequence ***	4.15e+02
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C	881	16	1.1	111390	18	AC000348	Genomic sequence for A	4.15e+02	C	954	15	1.1	174877	26	AC002060	*** SEQUENCING IN PROG	1.63e+03
C	882	15	1.1	114144	18	ATU78721	Arabidopsis thaliana c	4.15e+02	C	955	16	1.1	176195	19	ECOUW89	E. coli chromosomal re	4.15e+02
C	883	16	1.1	114471	26	HS239K6	Human DNA sequence ***	1.63e+03	C	956	16	1.1	179000	26	HSAC002059	*** SEQUENCING IN PROG	4.15e+02
C	884	15	1.1	114505	18	F20P5	Sequence of BAC F20P5	1.63e+03	C	957	15	1.1	179000	26	HSAC002059	*** SEQUENCING IN PROG	1.63e+03
C	885	15	1.1	114747	26	HS422H11	Human DNA sequence ***	1.63e+03	C	958	16	1.1	179017	26	HS102D24	Human DNA sequence ***	4.15e+02
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C	887	15	1.1	117261	26	HS426N21	Human DNA sequence ***	1.63e+03	C	960	15	1.1	186306	26	CEY6E2	Caenorhabditis elegans	1.63e+03
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C	889	16	1.1	119704	18	OSCHLPLXX	O.sineusis complete ch	4.15e+02	C	962	15	1.1	188959	26	HS37E16	Human DNA sequence ***	1.63e+03
C	890	15	1.1	120000	26	HSAC000001	*** SEQUENCING IN PROG	1.63e+03	C	963	15	1.1	190350	26	HS230I19	Human DNA sequence ***	1.63e+03

C	964	16	1.1	190350	26	HS230119	Human DNA sequence ***	4.15e+02
C	965	15	1.1	190667	26	AC004025	Homo sapiens; HTGS pha	1.63e+03
C	966	15	1.1	194000	26	AC000016	*** SEQUENCING IN PROG	1.63e+03
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C	978	15	1.1	213420	19	BSUB0014	Bacillus subtilis comp	1.63e+03
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C	985	15	1.1	233780	19	BSUB0010	Bacillus subtilis comp	1.63e+03
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C	988	16	1.1	251364	14	MMAE000664	Mus musculus; TCR beta	4.15e+02
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C	996	16	1.1	320751	26	AC003978	Homo sapiens; HTGS pha	4.15e+02
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C	998	15	1.1	332000	26	CEY102A5	Caenorhabditis elegans	1.63e+03
C	999	15	1.1	338534	19	ECOUW93	Escherichia coli K-12	1.63e+03
C	1000	16	1.1	340723	26	CEY46G5	Caenorhabditis elegans	4.15e+02

ALIGNMENTS

RESULT	1	MUSKAPOPRE	1410 bp	mRNA	ROD	13-DEC-1993
LOCUS		Mouse kappa opioid receptor mRNA, complete cds.				
DEFINITION		L11065				
ACCESSION		9348248				
KEYWORDS		kappa opioid receptor.				
SOURCE		Mus musculus				
ORGANISM		Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.				
REFERENCE		1 (bases 1 to 1410)				
AUTHORS		Yasuda,K., Raynor,K., Kong,H., Breder,C.D., Takeda,J., Reisine,T. and Bell,G.I.				
TITLE		Cloning and functional comparison of kappa and delta opioid receptors from mouse brain				
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740 (1993)				
MEDLINE		93342064				
FEATURES		Location/Qualifiers				
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BASE COUNT		322	a	360	c	337	g	391	t	
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Db	61	GCATCAGGAACGTGACCCATCAGGGCTGAACAGCTACTCAGGATCTAAAGTGTGACTT	120							
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Db	121	GGAAGCTGACGGTGACTTGGGAAGGAGGTCCCAATCAGCGATCTGGAGCTGACGGC	180							
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QY	1381		1410

RESULT 2

LOCUS S81111 1288 bp mRNA 02-AUG-1996

DEFINITION kappa-opioid receptor [alternatively spliced] [mice, C58/J, R1.1 thymoma cells, mRNA Partial, 1288 nt].

ACCESSION S81111

NID 91478285

KEYWORDS

SOURCE Mus sp. C58/J R1.1 thymoma cells.

ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 1288)

AUTHORS Belkowski,S.M., Zhu,J., Liu-Chen,L.Y., Eisenstein,T.K., Adler,M.W. and Rogers,T.J.

TITLE Sequence of kappa-opioid receptor cDNA in the R1.1 thymoma cell line

JOURNAL J. Neuroimmunol. 62 (1), 113-117 (1995)

MEDLINE 96084989

REMARK Genbank staff at the National Library of Medicine created this entry [NCBI glibsq 175931] from the original journal article.

COMMENT This sequence comes from Fig. 3.

FEATURES

location/Qualifiers

1..1288

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97..1239 /db_xref="taxon:10095"

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97..1239 /gene="kappa-opioid receptor"

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BASE COUNT	283	a	336	c	305	g	364	t
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Query Match	85.7%; Score 1208; DB 14; Length 1288;							
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Db	861	TGTCCGGCTCCTGTCTGGCTCCCGAGAGAGAGACCGAAATCTCCGCCGATCACCAAGCT	920					
QY	950	TGTCCGGCTCCTGTCTGGCTCCCGAGAGAGAGACCGAAATCTCCGCCGATCACCAAGCT	1009					
Db	921	GGTGTGTAGTAGTGTGAGTCTTCATCATCTGTGTGGACCCCATTCACATCTTATCTCT	980					
QY	1010	GGTGTGTAGTAGTGTGAGTCTTCATCATCTGTGTGGACCCCATTCACATCTTATCTCT	1069					
Db	981	GGTGAGAGCTCTGGGAAGACCTCCACAGACAGACAGCTGCCCTCTCCAGCTATTATTCTG	1040					
QY	1070	GGTGAGAGCTCTGGGAAGACCTCCACAGACAGACAGCTGCCCTCTCCAGCTATTATTCTG	1129					
Db	1041	TATTGCTTTGGTTATACCAACAGAGCTGAATCCTGTCTCTATGCTTCTGTGATGA	1100					

QY 1130 TATTGCTTGGGTTATACCAACAGCAGCCGTGAATCCTGTCTCTATGCGCTTCTGATGA 1189

Db 1101 AAACITCAAGCGGTTTITAGGACTTCTGCTTCCCTATTAAGATGCGAATGAGCGCCA 1160

QY 1190 AAACITCAAGCGGTTTITAGGACTTCTGCTTCCCTATTAAGATGCGAATGAGCGCCA 1249

Db 1161 GAGCACCATTAGAGTTAGAAACACAGTTCAGATCCTGCTTCCATGAGAGATGTGGAGG 1220

QY 1250 GAGCACCATTAGAGTTAGAAACACAGTTCAGATCCTGCTTCCATGAGAGATGTGGAGG 1309

Db 1221 GATGAATTAAGCCATGACTAGTCTGTTGAATGTCTTCTATTTGTTCTCCAGGTAGAGA 1280

QY 1310 GATGAATTAAGCCATGACTAGTCTGTTGAATGTCTTCTATTTGTTCTCCAGGTAGAGA 1369

Db 1281 AGAGTTCA 1288

QY 1370 AGAGTTCA 1377

RESULT 3

LOCUS S77868S3 1186 bp DNA ROD 26-SEP-1995

DEFINITION kappa opiod receptor [mice, Genomic, 1186 nt, segment 3 of 3].

ACCESSION S77872

NID 9998531

KEYWORDS

SEGMENT 3 of 3

SOURCE Mus sp.

ORGANISM Mus sp.

REFERENCE 1 (bases 1 to 1186)

AUTHORS Liu,H.C., Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Loh,H.H. and Wei,L.N.

TITLE Cloning and promoter mapping of mouse kappa opiod receptor gene

JOURNAL Biochem. Res. Commun. 209 (2), 639-647 (1995)

MEDLINE 95251663

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 166539] from the original journal article.

FEATURES

source location/Qualifiers

1..1186

/organism="Mus sp."

/db_xref="taxon:10095"

join(S77868:537..1894,S77869:371..723,289..>821)

join(S77868:913..1894,S77869:371..723,289..>821)

join(S77868:919..1894,S77869:371..723,289..>821)

order(S77868:1638..2074,S77869:1..1109,1..821)

/gene="kappa opiod receptor, KOR"

join(S77868:1638..1894,S77869:371..723,289..821)

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/note="This sequence comes from Fig. 2. Author-given protein sequence is in conflict with the conceptual translation; mismatch(365[E->Q]); KOR"

/codon_start=1

/product="kappa opiod receptor"

/db_xref="PID:9998532"

/translation="MESPIQIFRGGDPPTGPTCSPSACLIPNSSSWFPNWAESDSNGSVGS

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LADALVTTMPFQSAVYLMNSWPFQDVLCIKIVISIDYNNMFTSIFLTMTMSVDRYIAV

CHPVKALDERTPKAKLINICIMWLASSVGSISATVIGTKVRDVEDVIECSLOFPDE

YSWVDLFMKICVEFAFVLPVLIIVCYTLMILRLSVRLISGSREKDRNLRLTKLY

LYVVAVFIIICWTPIHIFILVEALIGSTSHSTAALSSYFCIALGYTNSLNPLYAFLD

ENFRRCFRDFCFPIKMRERQSTNRVNTVEDPASMRDVGGMKNKPV"

BASE COUNT 310 a 272 c 254 g 350 t

ORIGIN

Query Match 43.8%; Score 617; DB 14; Length 1186;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 617; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 287 AGATGTGATGATCAATGAATGCTCCTTGAGATTTCCTGATGATGAATATTCCTGTGGGA 346

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QY 794 AGATGTGATGATCAATGAATGCTCCTTGCACTTTCCTGATGATGAATATTCCTGTGGGA 853

Db 347 TCTCTTCATGAAGATCTGTGCTCTGCTTGGCTTTGTGATCCAGCTCATCATCAT 406

QY 854 TCTCTTCATGAAGATCTGTGCTCTGCTTGGCTTTGTGATCCAGCTCATCATCAT 913

Db 407 TGTCTGTACACCTGATGATCCCTGCGCTGAAGAAGTGCCGCTCTGTGCTCCCG 466

QY 914 TGTCTGTACACCTGATGATCCCTGCGCTGAAGAAGTGCCGCTCTGTGCTCCCG 973

Db 467 AGAGAAGACCGAAATCTCCGCCGATACCAAGCTGTGCTGTAGTAGTTCAGTCTT 526

QY 974 AGAGAAGACCGAAATCTCCGCCGATACCAAGCTGTGCTGTAGTAGTTCAGTCTT 1033

Db 527 CATCATCTGTGGACCCCATTCACATCTTTATCCCTGTGTGAGGCTCTGGGAAGCACCTC 586

QY 1034 CATCATCTGTGGACCCCATTCACATCTTTATCCCTGTGTGAGGCTCTGGGAAGCACCTC 1093

Db 587 CCACAGCACAGCTGCCCTCTCCAGCTATTTCTGTATTGCCCTGGTTATACCAACAG 646

QY 1094 CCACAGCACAGCTGCCCTCTCCAGCTATTTCTGTATTGCCCTGGTTATACCAACAG 1153

Db 647 CAGCCTGAATCCTGTCTCTATAGCCCTTCTGTGATGAAAACCTTCAAGCGGTTTAGGGA 706

QY 1154 CAGCCTGAATCCTGTCTCTATAGCCCTTCTGTGATGAAAACCTTCAAGCGGTTTAGGGA 1213

Db 707 CTTCGTCTTCCCTATTAGATGCGAATGAGCGCCAGACACCAATAGAGTTAGAAACAC 766

QY 1214 CTTCGTCTTCCCTATTAGATGCGAATGAGCGCCAGACACCAATAGAGTTAGAAACAC 1273

Db 767 AGTTCAGATCCTGCTTCCATGAGAGATGTGGAGGATGAATTAAGCCATAGACTAGT 826

QY 1274 AGTTCAGATCCTGCTTCCATGAGAGATGTGGAGGATGAATTAAGCCATAGACTAGT 1333

Db 827 CGTGAATCTCTCTTATTGTCTCTCCAGTAGAGAAGAGTTCATCATCTTGGTTAAC 886

QY 1334 CGTGAATCTCTCTTATTGTCTCTCCAGTAGAGAAGAGTTCATCATCTTGGTTAAC 1393

Db 887 CCAGATTACAACCTGCAG 903

QY 1394 CCAGATTACAACCTGCAG 1410

RESULT 4

LOCUS MUSMORGP3 638 bp DNA ROD 12-APR-1996

DEFINITION Mouse MORGD gene for kappa-opiod receptor, exon 3.

ACCESSION D31665

NID 9643595

KEYWORDS

SEGMENT 3 of 3

SOURCE Mus musculus

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 638)

AUTHORS Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,T.

TITLE Structure and chromosomal mapping of genes for the mouse

JOURNAL +kappa-opiod receptor and an opiod receptor homolog (MOR-C)

Biochemical and Biophysical Research Communication 205, 1353-1357 (1994)

2 (bases 1 to 638)

Takeshima,H.

Direct Submission

Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi Takeshima, Tokyo Institute of Psychiatry, Department of Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan (Tel:03-3304-5701(ex.312); Fax:03-3329-8035)

Submitted (28-May-1994) to DDBJ by:

Hiroshi Takeshima

Department of Neurochemistry

Tokyo Institute of Psychiatry

2-1-8 Kamikitazawa, Setagaya-ku
Tokyo 156

Japan
Phone: 03-3304-5701 x312
Fax: 03-3329-8035.

FEATURES
source location/Qualifiers
1..638

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="phage lambda fixit"
join(D31663:111..367,D31664:89..441,28..560)
/codon_start=1
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/db_xref="PID:d1007079"
/db_xref="PID:g808876"
/translation="MESPQIFRGDPPTCSPSACLLPNSSSWFPMWAEPSNSGVGS
EDQLESALISPAIPYITITAVSVFVGVGLVNSLVMFVIRYTKMTATNTYENLA
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CHPVKALDFRTPPLKAKIINICIMWLASSVGISAVIGGTVKREDVDVIECLIQPDDE
YSWDLFMKICVVFPAFVIVLIIIVCYTILMLRLKSVRLSGSREKDRNIRITKLV
LVVAVFIIICWTFPIHIFILVEALIGSTSHSTALSSYFCIALGYTNSLNPVLYAFLD
ENFKRCFRDFCFPIKMERQSTNVRNTVQDPASMRDVGGMKPV"
28..560

exon
/note="third protein coding sequence (P3)"
/number=3

BASE COUNT 141 a 154 c 151 g 192 t
ORIGIN Chromosome 1 A2-3.

Query Match 37.3%; Score 526; DB 14; Length 638;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 586; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 51 TTGCAGTTTCTGATGATGAATATTCCTGGTGGATCTCTTCATGAAGATCTGTGCTC 110
QY 819 TTGCAGTTTCTGATGATGAATATTCCTGGTGGATCTCTTCATGAAGATCTGTGCTC 878
Db 111 GTCTTGCTTGTGTAICCCAGTCTCATCATCATGTGCTGCTACACCCGTGATGATCCTG 170
QY 879 GTCTTGCTTGTGTAICCCAGTCTCATCATCATGTGCTGCTACACCCGTGATGATCCTG 938
Db 171 CGCTGAAGAGTGTCCGGCTGCTGCTGGCTCCCGAGAGAAGACCGAAATCTCCGCCGC 230
QY 939 CGCTGAAGAGTGTCCGGCTGCTGCTGGCTCCCGAGAGAAGACCGAAATCTCCGCCGC 998
Db 231 ATCACCAGCTGTGCTGTAGTAGTTGCAGTCTTCATCATCATGTGGAACCCCATTCAC 290
QY 999 ATCACCAGCTGTGCTGTAGTAGTTGCAGTCTTCATCATCATGTGGAACCCCATTCAC 1058
Db 291 ATCTTATCTCTGTGGAGGCTCTGGGAAGCACCTCCACAGCAGAGCTGCCCTCTCCAGC 350
QY 1059 ATCTTATCTCTGTGGAGGCTCTGGGAAGCACCTCCACAGCAGAGCTGCCCTCTCCAGC 1118
Db 351 TATTATTTCTGTATTGCTTGGGTTATACCAACAGCAGCCGTGAATCCTGTTCTCTATGCC 410
QY 1119 TATTATTTCTGTATTGCTTGGGTTATACCAACAGCAGCCGTGAATCCTGTTCTCTATGCC 1178
Db 411 TTCTGTGATGAAAACITCAAGCGGTGTTTAGGAGCTTCTGCTCCCTATTAGATGCGA 470
QY 1179 TTCTGTGATGAAAACITCAAGCGGTGTTTAGGAGCTTCTGCTCCCTATTAGATGCGA 1238
Db 471 ATGAGCGCCAGAGCACCAATAGAGTTAGAACAACAGATTCAGATCCTGCTTCCATGAGA 530
QY 1239 ATGAGCGCCAGAGCACCAATAGAGTTAGAACAACAGATTCAGATCCTGCTTCCATGAGA 1298
Db 531 GATGTGGAGGAGGATGAATAAGCCAGTATGACTAGTGTGGAATGTCTTCTTATGTCT 590
QY 1299 GATGTGGAGGAGGATGAATAAGCCAGTATGACTAGTGTGGAATGTCTTCTTATGTCT 1358
Db 591 CCAGGTAGAGAAGAGTCAATGATCTGTTTAAACCAGATTAACAAT 638
QY 1359 CCAGGTAGAGAAGAGTCAATGATCTGTTTAAACCAGATTAACAAT 1406

RESULT 5
LOCUS MUSMORGP2 488 bp DNA ROD 12-APR-1996
DEFINITION Mouse MORGD gene for kappa-opioid receptor, exon 2.
ACCESSION D31664
NID g643594
KEYWORDS G-protein associated; kappa opioid receptor; opioid drugs and peptides-binding; transmembrane protein.

SEGMENT
SOURCE Mus musculus DNA, clone_lib:phage lambda fixit.
ORGANISM Mus musculus

REFERENCE
AUTHORS Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,T.
TITLE Structure and chromosomal mapping of genes for the mouse -kappa-opioid receptor and an opioid receptor homolog (MOR-C)
JOURNAL Biochemical and Biophysical Research Communication 205, 1353-1357 (1994)

REFERENCE
AUTHORS Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,T.
TITLE Structure and chromosomal mapping of genes for the mouse -kappa-opioid receptor and an opioid receptor homolog (MOR-C)
JOURNAL Biochemical and Biophysical Research Communication 205, 1353-1357 (1994)
2 (bases 1 to 488)
Takeshima,H.
Direct Submission
Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi Takeshima, Tokyo Institute of Psychiatry, Department of Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan (Tel:03-3304-5701(ex.312), Fax:03-3329-8035)
Submitted (28-May-1994) to DDBJ by:
Hiroshi Takeshima
Department of Neurochemistry
Tokyo Institute of Psychiatry
2-1-8 Kamikitazawa, Setagaya-ku
Tokyo 156
Japan
Phone: 03-3304-5701 x312
Fax: 03-3329-8035.

COMMENT

FEATURES
source location/Qualifiers
1..488

/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="phage lambda fixit"
89..441
/note="second protein coding sequence (P2)"
/number=2

BASE COUNT 129 a 103 c 97 g 159 t
ORIGIN Chromosome 1 A2-3.

Query Match 25.1%; Score 354; DB 14; Length 488;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 88 GATACACGAAGATGAAGACCGCAACCAACATCTACATATTAAACCTGGCTTGGCAGATG 147
QY 442 GATACACGAAGATGAAGACCGCAACCAACATCTACATATTAAACCTGGCTTGGCAGATG 501
Db 148 CTTGGTTACTACCACTATGCCCTTTCAGAGTGTGCTACTTGATGAATTCTTGCCCTT 207
QY 502 CTTGGTTACTACCACTATGCCCTTTCAGAGTGTGCTACTTGATGAATTCTTGCCCTT 561
Db 208 TTGGAGATGTGCTATGCAAGATTGTCATTTCCATTGACTACTACACAIGTTTACAGCA 267
QY 562 TTGGAGATGTGCTATGCAAGATTGTCATTTCCATTGACTACTACACAIGTTTACAGCA 621
Db 268 TATTCACTTGACCATGATGAGTGTGACCGCTACATTTGCTGTGTCACACCTGTGAAG 327
QY 622 TATTCACTTGACCATGATGAGTGTGACCGCTACATTTGCTGTGTCACACCTGTGAAG 681
Db 328 CTTTGGACTTCCGAACACCTTTGAAGAAGCAAGATCATCAACATCTGCATTTGGCTCTGG 387
QY 682 CTTTGGACTTCCGAACACCTTTGAAGAAGCAAGATCATCAACATCTGCATTTGGCTCTGG 741
Db 388 CATCATCTGTTGTTATATCAGCATAGTCTCTGGAGGCAACCAAGTCAAGGGAAG 441
QY 742 CATCATCTGTTGTTATATCAGCATAGTCTCTGGAGGCAACCAAGTCAAGGGAAG 795

RESULT 5 S77868S2 1109 bp DNA ROD 26-SEP-1995
LOCUS kappa opiod receptor [mice, Genomic, 1109 nt, segment 2 of 3].
DEFINITION S77869
ACCESSION 9998530
NID
KEYWORDS
SEGMENT 2 of 3
SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE 1 (bases 1 to 1109)
AUTHORS Liu,H.C., Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Loh,H.H.
and Wei,L.N.
TITLE Cloning and promoter mapping of mouse kappa opiod receptor gene
JOURNAL Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
MEDLINE 95251663
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsg 166534] from the original journal article.
This sequence comes from Fig. 2.
FEATURES
source 1..1109
/organism="Mus sp."
/db_xref="taxon:10095"
BASE COUNT 331 a 213 c 204 g 361 t
ORIGIN
Query Match 25.1%; Score 354; DB 14; Length 1109;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 354; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

JOURNAL
REFERENCE 2 (bases 1 to 432)
AUTHORS Grandy,D.K.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-1994) David K. Grandy, Vollum Institute, Oregon
Health Sciences, University, 3181 S.W. Sam Jackson Park Road,
Portland, OR 97201, USA
FEATURES
source 1..432
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/db_xref="taxon:10090"
/clone="R21mg1"
/clone_lib="Stratagene lambda FIX"
/sex="male"
/dev_stage="adult"
14..366
/gene="oprk1"
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/note="encodes putative transmembrane domains II, III and
IV"
/codon_start=2
/evidence=experimental
/product="kappa opiod receptor"
/db_xref="PID:g9595937"
/translation="YTKMKTATNIYIFNLTLADALVTTMFEQSAVYLMSWPFQDVL
CKTVISIGYYNMFSTISIFLITMMSVDRIYAVCHPVKALDPRIPLKAKIINICIMWLASS
VGISAIVLGGTKVRE"
BASE COUNT 114 a 92 c 85 g 141 t
ORIGIN
Query Match 19.5%; Score 275; DB 14; Length 432;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 61 CTTTGGCAGATGCTTTGGTTACTTACCACCTATGCCCTTTCAGAGTGCCTGCTACTTGATGA 120
QY 490 CTTTGGCAGATGCTTTGGTTACTTACCACCTATGCCCTTTCAGAGTGCCTGCTACTTGATGA 549
Db 121 ATTCTTGGCCCTTTTGGAGATGTGCTATGCAAGATTGTCATTTCCATTGGCTACTACACAA 180
QY 550 ATTCTTGGCCCTTTTGGAGATGTGCTATGCAAGATTGTCATTTCCATTGGCTACTACACAA 609
Db 181 TGTTTACCAGCATATTCACCTTGACCATGATGATGTGGACCGCTACATTCGCTGTGCC 240
QY 610 TGTTTACCAGCATATTCACCTTGACCATGATGATGTGGACCGCTACATTCGCTGTGCC 669
Db 241 ACCCTGTGAAGCTTTTGGACTTCCGAACACCTTTGAAGCAAGATCATCAACATCTGCA 300
QY 670 ACCCTGTGAAGCTTTTGGACTTCCGAACACCTTTGAAGCAAGATCATCAACATCTGCA 729
Db 301 TTTGGCTCCTGGCATCATCTGTTGTATATACAGGATAGTCCCTTGAGGCAACCAAGTCA 360
QY 730 TTTGGCTCCTGGCATCATCTGTTGTATATACAGGATAGTCCCTTGAGGCAACCAAGTCA 789
Db 361 GGGAG 366
QY 790 GGGAG 795

RESULT 8
LOCUS MUSMORGDPI 423 bp DNA ROD 12-APR-1995
DEFINITION Mouse MORGD gene for kappa-opiod receptor, exon 1.
ACCESSION D31663
NID 9643593
KEYWORDS g-protein associated; kappa opiod receptor; opiod drugs and
peptides-binding; transmembrane protein.
SEGMENT 1 of 3
SOURCE Mus musculus DNA, clone_lib:phage lambda fixII.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 423)
AUTHORS Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,T.
TITLE Structure and chromosomal mapping of genes for the mouse
JOURNAL +kappa-opioid receptor and an opioid receptor homolog (MOR-C)
Biochemical and Biophysical Research Communication 205, 1353-1357
(1994)
REFERENCE 2 (bases 1 to 423)
AUTHORS Takeshima,H.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi
Takeshima, Tokyo Institute of Psychiatry, Department of
Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan
(Tel:03-3304-5701(ex.312), Fax:03-3329-8035)
Submitted (28-May-1994) to DDBJ by:
Hiroshi Takeshima
Department of Neurochemistry
Tokyo Institute of Psychiatry
2-1-8 Kamikitazawa, Setagaya-ku
Tokyo 156
Japan
Phone: 03-3304-5701 x312
Fax: 03-3329-8035.

FEATURES
source location/Qualifiers
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="phage lambda fixII"
111..367
/note="first protein coding sequence (P1)"
/number=1

BASE COUNT 64 a 126 c 116 g 117 t
ORIGIN Chromosome 1 A2-3.

Query Match 19.4%; Score 273; DB 14; Length 423;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 95 AGCTGCAGCGCTCACCATGGAGTCCCCCATTCAGATCTTCCGAGAGATCCAGGCCCTAC 154
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QY 170 AGCTGCAGCGCTCACCATGGAGTCCCCCATTCAGATCTTCCGAGAGATCCAGGCCCTAC 229
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Db 155 CTGCTCTCCAGTGCCTTGCCTTCTCCCCCAACAGCAGCTCTGTGTTCCCAACTGGGCAGA 214
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QY 230 CTGCTCTCCAGTGCCTTGCCTTCTCCCCCAACAGCAGCTCTGTGTTCCCAACTGGGCAGA 289
|||
Db 215 ATCCGACAGTAATGGCAGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGCGCATCTC 274
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QY 290 ATCCGACAGTAATGGCAGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGCGCATCTC 349
|||
Db 275 TCCGGCCATCCCTGTATATCATCACCGCTGTCTACTCTGTGTAATTGGTGGGCTTAGT 334
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QY 350 TCCGGCCATCCCTGTATATCATCACCGCTGTCTACTCTGTGTAATTGGTGGGCTTAGT 409
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Db 335 GGGCAATTCTCTGTGCATGTTGTGCATCATCCG 367
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QY 410 GGGCAATTCTCTGTGCATGTTGTGCATCATCCG 442
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RESULT 9
LOCUS S77868s1 2074 bp DNA ROD 26-SEP-1995
DEFINITION kappa opioid receptor [mice, Genomic, 2074 nt, segment 1 of 3].
ACCESSION S77868
MID g998529
KEYWORDS
SEGMENT 1 of 3
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.

REFERENCE 1 (bases 1 to 2074)
AUTHORS Liu,H.C., Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Loh,H.H.
and Wei,L.N.
TITLE Cloning and promoter mapping of mouse kappa opioid receptor gene
JOURNAL Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
MEDLINE 95251663
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsg 166530] from the original journal article.
This sequence comes from Fig. 2.

FEATURES
source location/Qualifiers
1..2074
/organism="Mus sp."
/db_xref="taxon:10095"

BASE COUNT 492 a 485 c 564 g 533 t
ORIGIN

Query Match 19.4%; Score 273; DB 14; Length 2074;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1622 AGTCGACGGCTCACCATGGAGTCCCCCATTCAGATCTTCCGAGAGATCCAGGCCCTAC 1681
|||
QY 170 AGTCGACGGCTCACCATGGAGTCCCCCATTCAGATCTTCCGAGAGATCCAGGCCCTAC 229
|||
Db 1682 CTGCTCTCCAGTGCCTTGCCTTCTCCCCCAACAGCAGCTCTGTGTTCCCAACTGGGCAGA 1741
|||
QY 230 CTGCTCTCCAGTGCCTTGCCTTCTCCCCCAACAGCAGCTCTGTGTTCCCAACTGGGCAGA 289
|||
Db 1742 ATCCGACAGTAATGGCAGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGCGCATCTC 1801
|||
QY 290 ATCCGACAGTAATGGCAGTGTGGGCTCAGAGGATCAGCAGCTGGAGTCCGCGCATCTC 349
|||
Db 1802 TCCGGCCATCCCTGTATATCATCACCGCTGTCTACTCTGTGTAATTGGTGGGCTTAGT 1861
|||
QY 350 TCCGGCCATCCCTGTATATCATCACCGCTGTCTACTCTGTGTAATTGGTGGGCTTAGT 409
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Db 1862 GGGCAATTCTCTGTGCATGTTGTGCATCATCCG 1894
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QY 410 GGGCAATTCTCTGTGCATGTTGTGCATCATCCG 442
|||

RESULT 10
LOCUS RATRORD 1273 bp mRNA ROD 21-DEC-1993
DEFINITION Rat mRNA for opioid receptor, complete cds.
ACCESSION D16534
MID g409390
KEYWORDS
SOURCE G-protein coupled receptor; opioid receptor; transmembrane protein.
Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone
pROR2.
ORGANISM Rattus norvegicus
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 1273)
AUTHORS Nishi,M., Takeshima,H., Fukuda,K., Kato,S. and Mori,K.
TITLE cDNA cloning and pharmacological characterization of an opioid
JOURNAL receptor with high affinities for kappa-subtype-selective ligands
MEDLINE FEBS Lett. 330 (1), 77-80 (1993)
93380575
REFERENCE 2 (bases 1 to 1273)
AUTHORS Takeshima,H.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1993) to the DDBJ/EMBL/GenBank databases. Hiroshi
Takeshima, International Institute for Advanced Studies; c/o
Shimadzu Corporation N-80, 1 Nishinokyo-Kuawahara-cho, Kyoto 604,
Japan (Tel:075-823-1208, Fax:075-811-8186)
Submitted (19-JUN-1993) to DDBJ by:
Hiroshi Takeshima
International Institute
for Advanced Studies
c/o Shimadzu Corporation
N-80
1 Nishinokyo-Kuawahara-cho

Kyoto 604
Japan
Phone: 075-823-1208
Fax: 075-811-8186.

FEATURES
source
Location/Qualifiers
1. .1273

/organism="Rattus norvegicus"
/strain="Wistar"
/db_xref="taxon:10116"
/dev_stage="adult"
/tissue_type="brain"
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49. .1191
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/db_xref="PID:g415310"
/translation="MESPIQIRGEPEGPTCAPSACLPNSSSWFPNWAESDSNGSVGS
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Matches 529; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

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LOCUS R4TKORIA 1358 bp mRNA ROD 21-OCT-1993
DEFINITION Rat kappa opioid receptor mRNA, complete cds.

ACCESSION L22001
NID 9409236
KEYWORDS kappa opioid receptor; opioid receptor.
SOURCE Rattus norvegicus whole brain cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.

REFERENCE 1 (bases 1 to 1358)
AUTHORS Chen, Y., Mestek, A., Liu, J. and Yu, L.
TITLE Molecular cloning of a rat kappa opioid receptor reveals sequence similarities to the mu and delta opioid receptors
JOURNAL Biochem. J. 295, 625-628 (1993)
MEDLINE 94059008

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QY 414 AATCTCTGTGTCATGTTGTGCATCATCCGATACACAAAGATGAAGACCGCAACACATC 473
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QY 834 GATGAATATTCCTGTGTGGACCTCTTCATGAAGATCTGTCTCTGCTTTGCCCTTGT 892


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LOCUS      R12KOR1B      2094 bp      mRNA
DEFINITION Rattus norvegicus kappa opioid receptor (KOR-1) mRNA, complete cds.
ACCESSION  L22536
NID        9425188
KEYWORDS   G-protein coupled receptor; kappa opioid receptor; transmembrane
SOURCE     Rattus norvegicus (strain Sprague-Dawley) (library: lambda gt10)
            adult brain (striatum) cDNA to mRNA.
ORGANISM   Rattus norvegicus
            Eukaryota; Eukaryota; Eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae;
            Murinae; Rattus.
REFERENCE  1 (bases 1 to 2094)
AUTHORS   Li,S., Zhu,J., Chen,C., Chen,Y.-W., de Riel,J.K., Ashby,B. and
            Liu-Chen,L.-Y.
TITLE     Molecular cloning and expression of a rat k opioid receptor
JOURNAL   Biochem. J. 295, 629-633 (1993)
MEDLINE   94059009
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RESULT 13
LOCUS      E08874      2481 bp      RNA
DEFINITION cDNA coding rat kappa-opioid receptor.
ACCESSION  E08874
NID        92176978
KEYWORDS   JP 1995070191-A/1.
SOURCE     Rattus sp.
ORGANISM   Rattus sp.
            Eukaryota; Eukaryota; Eukaryotes; Metazoa; Chordata;
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            Murinae; Rattus.
REFERENCE  1 (bases 1 to 2481)
AUTHORS   Kimimichi,S.
TITLE     RECEPTOR PROTEIN, ITS PRODUCTION AND USE THEREOF
JOURNAL   Patent: JP 1995070191-A 1 14-MAR-1995;
            TAKEDA CHEM IND LTD
COMMENT    OS Rattus sp. (rat)
            PN JP 1995070191-A/1
            PD 14-MAR-1995
            PF 30-JUL-1993 JP 1993190261
            PR 09-JUL-1993 JP 93P 170591
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            PC C07K14/47, C12N1/21, C12N15/09, C12P21/02//A61K38/00, A61K38/00,
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RESULT 14
LOCUS RATKOR 2481 bp mRNA ROD 02-DEC-1993
DEFINITION Rattus norvegicus mRNA for kappa opioid receptor, complete cds.
ACCESSION D16829
NID 9404115
KEYWORDS kappa opioid receptor.
SOURCE Rattus norvegicus CDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 2481)
AUTHORS Minami,M., Toya,T., Katao,Y., Maekawa,K., Nakamura,S., Onogi,T.,
Kaneko,S. and Satoh,M.
TITLE Cloning and expression of a cDNA for the rat kappa-opioid receptor
JOURNAL FEBS Lett. 329 (3), 291-295 (1993)
MEDLINE 93374033
REFERENCE 2 (bases 1 to 2481)
AUTHORS Minami,M.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases.
MEDLINE Masabumi Minami, Faculty of Pharmaceutical Sciences, Kyoto
REFERENCE University, Department of Pharmacology; Kyoto, Kyoto 606-01, Japan
AUTHORS (E-mail:f51250@sakura.kudpc.kyoto-u.ac.jp, Tel:075-753-4546,
JOURNAL Fax:075-753-4586)
COMMENT Submitted (21-JUL-1993) to DDBJ by:
Masabumi Minami
Department of Pharmacology
Faculty of Pharmaceutical Sciences
Kyoto University
Kyoto, Kyoto 606-01
Japan
Phone: 075-753-4546
Fax: 075-753-4586.
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Best Local Similarity 98.1%; Pred. No. 1.90e-252;
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QY 354 GCCATCCCTGTTATCATCACCGCTGCTACTCTGTGTGTGTGTGTGGCTTAGTGGGC 413
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RESULT 15
LOCUS RNU00442 4742 bp mRNA ROD 25-MAY-1994
DEFINITION Rattus norvegicus kappal opioid receptor mRNA, complete cds.
ACCESSION U00442
NID 9403486
KEYWORDS .
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 4742)
AUTHORS Meng,F., Xie,G.-X., Thompson,R.C., Mansour,A., Goldstein,A.,
Watson,S.J. and Akil,H.
TITLE Cloning and pharmacological characterization of a rat kappa opioid
JOURNAL receptor
PROC. NATL. ACAD. SCI. U.S.A. 90, 9954-9958 (1993)
MEDLINE 94052210
REFERENCE 2 (bases 1 to 4742)
AUTHORS Meng,F.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-1993) Fan Meng, Mental Health Research Institute,
University of Michigan, 205 Zina Pitcher Place, Ann Arbor, Michigan
48109, USA
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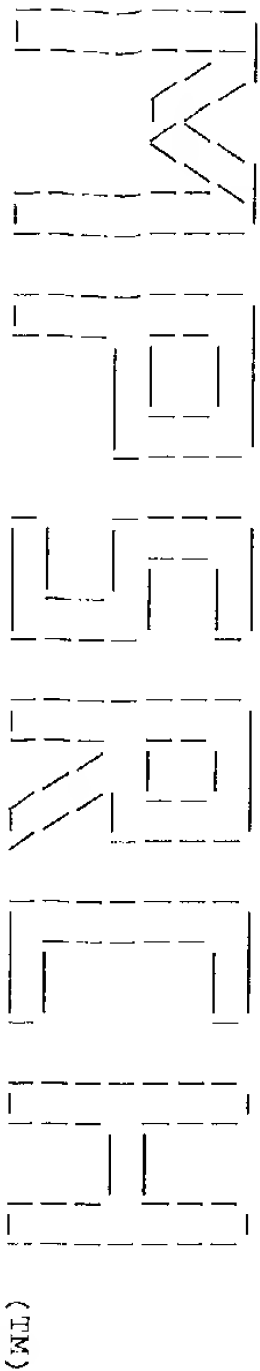
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1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 7.967; Variance 2.921; scale 2.727
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1410	100.0	1410	13	Q75926	Mouse kappa opioid re	0.00e+00
2	229	16.2	2481	15	Q86725	Mammalian kappa opioi	8.00e-228
3	32	2.3	1000	13	Q75931	Human kappa opioid re	4.01e-12
4	32	2.3	1142	20	T12550	Human kappa opioid re	4.01e-12
5	31	2.2	2447	10	Q56702	Partial sequence of t	3.20e-11
6	29	2.1	822	5	Q29156	Brain somatostatin re	1.92e-09
7	25	1.8	1330	13	Q75928	Mouse opioid receptor	5.12e-06
8	25	1.8	1567	14	Q89233	Rat opioid receptor c	5.12e-06
9	25	1.8	2600	14	Q90096	Mouse kappa-3 opioid	5.12e-06
10	25	1.8	2705	15	Q92972	Rat opiorph receptor	5.12e-06
11	23	1.6	1821	10	Q56700	Sequence of murine de	2.20e-04
12	23	1.6	2216	11	Q66656	Murine delta opioid r	2.20e-04
13	23	1.6	2272	13	Q75927	Mouse delta opioid re	2.20e-04
14	20	1.4	36	20	T12551	Human kappa opioid re	4.66e-02
15	20	1.4	39	20	T12554	Human kappa opioid re	4.66e-02

16	20	1.4	1610	14	Q89226	Human mu opioid recep	4.66e-02
17	20	1.4	1618	14	Q89223	Transcription regulat	4.66e-02
18	20	1.4	1618	14	Q89222	Rat mu opioid recepto	4.66e-02
19	20	1.4	2070	12	Q79199	Rat mu-subtype opioi	4.66e-02
20	20	1.4	2160	15	Q93102	Human mu opiate recep	4.66e-02
21	18	1.3	20	14	Q89231	Rat opioid receptor p	1.31e+00
22	18	1.3	829	10	Q56703	Partial sequence of t	1.31e+00
23	17	1.2	21	20	T12553	Human kappa opioid re	6.37e+00
24	17	1.2	376	19	T22429	Human gene signature	6.37e+00
25	17	1.2	1324	20	T18876	Human TcL-1 cDNA.	6.37e+00
26	17	1.2	1796	7	Q45658	Murine somatostatin r	6.37e+00
27	17	1.2	1981	10	Q56705	Partial sequence of t	6.37e+00
28	17	1.2	2028	4	Q26421	Gene for beta-IG-MI.	6.37e+00
29	17	1.2	2061	12	Q77669	Variant cyclomaltohex	6.37e+00
30	17	1.2	7960	1	N90568	Ovine Y-chromosomal D	6.37e+00
31	17	1.2	10564	21	T03854	Human fibrinogen gamm	6.37e+00
32	17	1.2	11715	1	N81564	Genomic sequence enco	6.37e+00
33	17	1.2	11724	2	N70102	Complete genomic sequ	6.37e+00
34	17	1.2	11725	33	T79723	Human protein C gene.	6.37e+00
35	17	1.2	11725	22	T32796	Human protein C gene.	6.37e+00
36	15	1.1	15	13	Q75942	Primer 3-i-loop-F for	1.23e+02
37	15	1.1	15	24	T49640	Human CETP HH ribozym	1.23e+02
38	15	1.1	15	13	Q75937	Primer N-R to amplify	1.23e+02
39	15	1.1	20	8	Q51059	Human glucokinase exo	1.23e+02
40	15	1.1	20	14	Q89232	Rat opioid receptor p	1.23e+02
41	15	1.1	30	6	Q38864	Arg134>Pro hgh DNA.	1.23e+02
42	15	1.1	33	24	T49331	5 bp insert enhancer	1.23e+02
43	15	1.1	36	20	T13181	Human insulin coding	1.23e+02
44	15	1.1	37	32	T62889	Human or monkey kappa	1.23e+02
45	15	1.1	37	6	Q35917	Human/monkey kappa li	1.23e+02
46	15	1.1	46	11	Q80661	CC49 V-light primer 3	1.23e+02
47	15	1.1	50	2	Q12959	Template linker probe	1.23e+02
48	15	1.1	50	30	T74409	HIV template linker p	1.23e+02
49	16	1.1	88	4	N10118	Gene encoding human 1	2.90e+01
50	16	1.1	90	4	N10117	Insulin B-chain duple	2.90e+01
51	15	1.1	130	5	Q32209	BDNF, salmon.	1.23e+02
52	16	1.1	134	2	N61204	Sequence of avian ery	2.90e+01
53	16	1.1	186	29	T65663	Polymorphic repeat se	2.90e+01
54	16	1.1	202	1	N81094	Sequence of a synthet	1.23e+02
55	15	1.1	211	8	Q61036	Human brain Expressed	1.23e+02
56	15	1.1	261	20	T17831	Optimised insulin cod	1.23e+02
57	15	1.1	270	5	Q29167	HLA-Bw 52 exon 2 alph	1.23e+02
58	15	1.1	277	20	T22193	Human gene signature	1.23e+02
59	15	1.1	290	18	T19174	Human gene signature	1.23e+02
60	15	1.1	290	20	T22470	Human gene signature	1.23e+02
61	16	1.1	326	8	Q60130	Human brain Expressed	2.90e+01
62	15	1.1	331	15	Q99371	Rat allogaft inflamm	1.23e+02
63	16	1.1	336	13	Q81503	OPDE 30 kDa subunit g	2.90e+01
64	15	1.1	339	11	Q68657	CC49 V-light.	1.23e+02
65	15	1.1	343	21	T25365	Human gene signature	1.23e+02
66	16	1.1	354	3	N40255	Sequence encoding pro	2.90e+01
67	15	1.1	359	8	Q59710	Human brain Expressed	1.23e+02
68	15	1.1	370	8	Q59401	Human brain Expressed	1.23e+02
69	15	1.1	375	22	T35131	Diminished expression	1.23e+02
70	15	1.1	400	8	Q59771	Human brain Expressed	1.23e+02
71	15	1.1	420	33	T80693	Type II topoisomerase	1.23e+02
72	15	1.1	476	4	Q24122	Human gene encoding G	1.23e+02
73	15	1.1	484	1	N91631	Sequence of new sigma	1.23e+02
74	15	1.1	507	11	Q62692	CDNA sequence of both	1.23e+02
75	15	1.1	507	1	N91440	CDNA sequence of both	1.23e+02
76	15	1.1	538	33	T73917	E6-binding protein E6	1.23e+02
77	15	1.1	538	17	T08639	HPV E6-binding protei	1.23e+02
78	15	1.1	590	5	Q32995	Ac-AMP2.	1.23e+02
79	15	1.1	590	11	Q70119	Antimicrobial Ac-AMP2	1.23e+02
80	15	1.1	609	2	N70099	Sequence of DNA fragm	1.23e+02
81	15	1.1	623	33	T70417	Mouse rhodopsin cDNA	1.23e+02
82	15	1.1	629	33	T70430	Human peripherin cDNA	1.23e+02
83	15	1.1	641	4	N30130	Sequence of VP3 gene	1.23e+02
84	15	1.1	652	5	Q30731	Neutrophil-derived DN	1.23e+02
85	15	1.1	693	27	T37435	Non-structural protei	1.23e+02
86	15	1.1	702	4	N30148	Sequence encoding ant	1.23e+02
87	15	1.1	734	18	T20481	Human gene signature	1.23e+02
88	15	1.1					

C	89	15	1.1	738	12	Q70612	IL-6 binding inhibito	1.23e+02		162	15	1.1	2165	11	Q68660	CC49 VL-L-VH-L-V	1.23e+02
C	90	15	1.1	741	8	Q45080	Human glucokinase gen	1.23e+02	C	163	16	1.1	2167	21	T31553	Human ice-ced-3 homol	2.90e+01
C	91	15	1.1	754	2	N60072	Sequence encoding hum	1.23e+02	C	164	16	1.1	2174	14	Q79972	Human interleukin-1 b	2.90e+01
C	92	15	1.1	795	1	Q04263	Encodes Colon Cancer	1.23e+02	C	165	16	1.1	2189	3	Q20349	Thromboplastin clone	2.90e+01
C	93	16	1.1	801	1	Q06637	Coat protein gene of	2.90e+01	C	166	15	1.1	2242	28	T58403	Human heat shock prot	1.23e+02
C	94	16	1.1	801	6	Q36838	Potato virus Y coat p	2.90e+01	C	167	16	1.1	2254	11	Q66167	Seven transmembrane r	2.90e+01
C	95	15	1.1	847	15	Q86972	Clone contg. yeast p	1.23e+02	C	168	15	1.1	2319	29	T60489	Chicken liver alpha-N	1.23e+02
C	96	15	1.1	847	2	Q10546	Yeast peptidyl-prolyl	1.23e+02	C	169	15	1.1	2319	12	Q73728	Chicken liver alpha-N	1.23e+02
C	97	15	1.1	847	15	Q86965	Clone contg. yeast p	1.23e+02	C	170	15	1.1	2334	29	T66121	Chicken alpha-N-acety	1.23e+02
C	98	15	1.1	854	1	Q03296	Sequence of clone c71	1.23e+02	C	171	15	1.1	2344	3	Q51427	Human FACC CDNA clone	1.23e+02
C	99	15	1.1	858	13	Q80340	DNA fragment function	1.23e+02	C	172	15	1.1	2380	3	Q14982	Human FACC CDNA clone	1.23e+02
C	100	15	1.1	877	10	Q56738	Sequence of CC49 sing	1.23e+02	C	173	15	1.1	2400	28	T59642	Human prostaglandin H	1.23e+02
C	101	15	1.1	885	10	Q62008	SSO2 gene.	2.90e+01	C	174	15	1.1	2421	9	Q54621	Mammalian vesicle mem	1.23e+02
C	102	15	1.1	892	2	N60706	Sequence encoding hum	1.23e+02	C	175	15	1.1	2475	27	T49003	Tumour necrosis facto	1.23e+02
C	103	15	1.1	897	27	T49878	Porcine trypsinogen c	1.23e+02	C	176	16	1.1	2485	14	Q79971	Human interleukin-1 b	2.90e+01
C	104	15	1.1	914	2	N60076	Sequence encoding hum	1.23e+02	C	177	16	1.1	2491	14	Q79968	Human interleukin-1 b	2.90e+01
C	105	15	1.1	1029	4	Q26960	Human platelet activa	1.23e+02	C	178	15	1.1	2521	3	Q20542	Mouse retinoic acid r	1.23e+02
C	106	16	1.1	1125	11	Q65603	Pre-hutFrh CDNA.	2.90e+01	C	179	16	1.1	2580	8	Q49165	84 kD ISGF-3alpha gen	2.90e+01
C	107	15	1.1	1164	2	Q12871	Polynhedin-soluble IA	1.23e+02	C	180	16	1.1	2607	14	Q89337	Human Stat84 CDNA.	2.90e+01
C	108	15	1.1	1200	17	Q99949	Recombinant high affi	1.23e+02	C	181	16	1.1	2607	22	T31277	Human STAT1-beta CDNA	2.90e+01
C	109	15	1.1	1200	5	Q30011	Sequence encoding a h	1.23e+02	C	182	15	1.1	2617	5	Q29753	DNA sequence encoding	1.23e+02
C	110	15	1.1	1299	11	Q63919	Interleukin 8 (IL-8)	1.23e+02	C	183	15	1.1	2629	24	T35593	Sequence encoding tob	1.23e+02
C	111	15	1.1	1313	27	T51049	Human adipocyte compl	1.23e+02	C	184	15	1.1	2740	3	Q20541	Mouse retinoic acid r	1.23e+02
C	112	15	1.1	1323	2	N60363	Endoglucanase (60 kDa	1.23e+02	C	185	15	1.1	2749	11	Q63492	S-Locus receptor (ser	1.23e+02
C	113	15	1.1	1331	10	Q58207	Sequence encoding hum	1.23e+02	C	186	15	1.1	2862	30	T61592	Murine c-IAP.	1.23e+02
C	114	15	1.1	1346	10	Q58208	Sequence of CC49 sing	1.23e+02	C	187	15	1.1	2923	31	T76529	DNA encoding macropha	1.23e+02
C	115	15	1.1	1347	33	T86173	Human hd53 U1 nucleot	1.23e+02	C	188	15	1.1	2943	2	N70160	Sequence encoding elo	1.23e+02
C	116	15	1.1	1352	12	Q70299	Mutant human tissue f	2.90e+01	C	189	15	1.1	2944	1	N80159	Insert of lambda 3 en	1.23e+02
C	117	16	1.1	1352	12	Q84924	Mutant human tissue f	2.90e+01	C	190	15	1.1	2967	14	Q87171	Natural resistance-as	1.23e+02
C	118	16	1.1	1352	12	T61373	Mutant human tissue f	2.90e+01	C	191	16	1.1	3066	8	Q05872	Rat glucagon-like pep	2.90e+01
C	119	16	1.1	1352	28	Q56737	Sequence of CC49 sing	1.23e+02	C	192	15	1.1	3089	17	T05575	MEK3 CDNA.	1.23e+02
C	120	15	1.1	1373	5	Q30013	Sequence encoding a 1	1.23e+02	C	193	15	1.1	3150	9	Q51428	Human FACC CDNA clone	1.23e+02
C	121	15	1.1	1373	17	Q99951	Recombinant high affi	1.23e+02	C	194	15	1.1	3247	28	T63080	Active clone XI of Ig	1.23e+02
C	122	15	1.1	1430	17	T15579	ICE-like apoptosis pr	2.90e+01	C	195	15	1.1	3261	33	T80100	Mouse KF-1 gene.	1.23e+02
C	123	16	1.1	1456	21	T31552	Human ice-ced-3 homol	2.90e+01	C	196	15	1.1	3373	4	Q24433	Tak E3 region.	1.23e+02
C	124	16	1.1	1473	30	Q86542	HIV integrase-LexA (I	1.23e+02	C	197	15	1.1	3373	2	T12229	Ad41 E3 region.	1.23e+02
C	125	16	1.1	1476	16	Q86542	Wilson disease exon 1	1.23e+02	C	198	15	1.1	3451	26	T28492	P. aeruginosa detecti	1.23e+02
C	126	15	1.1	1480	3	N30040	Sequence encoding bov	1.23e+02	C	199	15	1.1	3486	29	T47757	Pathogenic staphyloco	1.23e+02
C	127	15	1.1	1500	13	Q76311	Plasmid pTF271 encode	2.90e+01	C	200	15	1.1	3560	15	Q30849	Human tyk2 kinase cod	1.23e+02
C	128	16	1.1	1515	12	Q77721	p58 CDNA clone.	1.23e+02	C	201	15	1.1	3690	14	Q30849	Type III procollagen	1.23e+02
C	129	15	1.1	1557	14	Q81505	Human glucagon-like 1	2.90e+01	C	202	15	1.1	3730	18	T03195	Group B streptococcal	1.23e+02
C	130	16	1.1	1588	21	T31005	Rat cardiac alpha myo	1.23e+02	C	203	15	1.1	3848	24	T45417	Group B streptococcal	1.23e+02
C	131	15	1.1	1623	6	Q38253	HCV CKS-NS5F recombin	1.23e+02	C	204	15	1.1	3923	1	Q03463	P. suis leukotoxin ge	1.23e+02
C	132	15	1.1	1623	6	Q38268	HCV CKS-NS5F fusion g	1.23e+02	C	205	16	1.1	3943	14	Q89336	Human Stat91 CDNA.	2.90e+01
C	133	15	1.1	1623	6	Q38238	HCV CKS-NS5F recombin	1.23e+02	C	206	16	1.1	3943	22	T31276	Human STAT1-alpha cdn	2.90e+01
C	134	15	1.1	1626	3	Q21680	PHCV-48 - recombinant	1.23e+02	C	207	16	1.1	3977	8	Q49165	91 kD ISGF-3alpha gen	2.90e+01
C	135	15	1.1	1660	5	Q32869	Human PMP-22 CDNA.	1.23e+02	C	208	15	1.1	4146	20	T09026	Arabidopsis thaliana	1.23e+02
C	136	16	1.1	1731	33	T84446	Rat STCH chaperone pr	2.90e+01	C	209	15	1.1	4173	31	T73214	Grapevine leafroll vi	1.23e+02
C	137	15	1.1	1736	5	Q32870	Rat PMP CDNA.	1.23e+02	C	210	15	1.1	4200	18	T03190	Group B Streptococcal	1.23e+02
C	138	15	1.1	1748	26	T49319	Wnt-10b-delta gene.	1.23e+02	C	211	15	1.1	4203	2	Q14000	Leukotoxin genes.	1.23e+02
C	139	15	1.1	1829	21	T34367	Plasmid pJC265 (ATCC	1.23e+02	C	212	15	1.1	4346	24	T45897	Serine kinase SRPK1 c	1.23e+02
C	140	15	1.1	1829	3	Q14627	Human Glioblastoma ce	1.23e+02	C	213	15	1.1	4392	20	T10166	Feline infectious per	1.23e+02
C	141	15	1.1	1848	14	Q86998	Aminopeptidase O12 cl	1.23e+02	C	214	15	1.1	4455	6	Q39177	PVX ORF1 encoding a r	1.23e+02
C	142	15	1.1	1871	2	Q12869	Lymphocyte Activation	1.23e+02	C	215	15	1.1	4488	8	Q51426	Human FACC CDNA clone	1.23e+02
C	143	15	1.1	1872	11	Q66176	Seven transmembrane r	1.23e+02	C	216	15	1.1	4529	8	Q46121	Porcine sodium ion/gl	1.23e+02
C	144	15	1.1	1875	10	Q58758	Rat glucagon receptor	2.90e+01	C	217	15	1.1	4708	3	N50415	Human acetyl choline	1.23e+02
C	145	16	1.1	1878	28	T63079	Active clone Y1 of Ig	1.23e+02	C	218	15	1.1	4756	16	Q86541	Human acetyl choline	1.23e+02
C	146	15	1.1	1881	33	T59892	Coding sequence for t	1.23e+02	C	219	15	1.1	4975	12	Q73445	Wilson disease gene.	1.23e+02
C	147	15	1.1	1905	8	Q47835	Murine interleukin 9	1.23e+02	C	220	15	1.1	4989	20	T29608	IGF-I receptor.	1.23e+02
C	148	15	1.1	1909	8	Q48986	Human glucagon-like p	2.90e+01	C	221	15	1.1	4989	19	T13329	Human type I insulin-	1.23e+02
C	149	15	1.1	1912	2	Q10388	Encodes skin-specific	1.23e+02	C	222	15	1.1	4989	24	Q99245	Insulin like growth f	1.23e+02
C	150	15	1.1	1913	18	T05202	Murine retinoic acid	1.23e+02	C	223	15	1.1	4989	12	Q73702	Human Irf-1 receptor.	1.23e+02
C	151	15	1.1	1914	12	Q77984	Heavy subunit of rat	1.23e+02	C	224	15	1.1	5187	19	T14218	Mouse patched gene.	1.23e+02
C	152	15	1.1	2052	33	T80101	Mouse KR-1 gene open	1.23e+02	C	225	15	1.1	5288	19	T14220	Human patched gene.	1.23e+02
C	153	15	1.1	2097	27	T49006	Tumour necrosis facto	1.23e+02	C	226	15	1.1	5421	14	Q85678	Wilson's disease gene	1.23e+02
C	154	15	1.1	2111	21	T12940	RPDL. transcriptional	1.23e+02	C	227	15	1.1	5437	10	Q64218	Mutant tissue factor	2.90e+01
C	155	15	1.1	2127	26	T49318	Wnt-10b gene.	1.23e+02	C	228	16	1.1	5460	20	T16508	Human tissue factor.	1.23e+02
C	156	16	1.1	2127	1	N81104	Sequence of human tis	2.90e+01	C	229	15	1.1	6008	7	Q41289	Ubiquitin-specific pr	1.23e+02
C	157	16	1.1	2141	33	T68488	Human tissue factor c	2.90e+01	C	230	15	1.1	6008	7	T84509	Human LDL receptor an	1.23e+02
C	158	16	1.1	2147	1	N92782	CDNA of entire human	2.90e+01	C	231	15	1.1	7183	33	Q06074	Sequence encoding the	1.23e+02
C	159	16	1.1	2147	1	N81953	Encodes human tissue	1.23e+02	C	232	15	1.1	7184	11	Q70050	ptx gene of Pasteurel	1.23e+02
C	160	16	1.1	2165	11	Q68659	CC49 VL-L-VH-L-VL-L-V	1.23e+02	C	233	15	1.1	7184	11	Q70050	CC49 VL-L-VH-L-V	1.23e+02
C	161	15	1.1						C	234	15	1.1					

C	235	16	1.1	7350	17	Q98955	Complete B-G gene enc	2.90e+01	308	14	1.0	283	13	Q78988	Human immunoglobulin	4.79e+02
C	236	15	1.1	7360	24	T43072	Wheat acetyl-CoA carb	1.23e+02	309	14	1.0	291	22	T25886	Human gene signature	4.79e+02
C	237	16	1.1	7399	5	Q33479	HDPACK1.	2.90e+01	310	14	1.0	295	22	T26677	Human gene signature	4.79e+02
C	238	15	1.1	7824	28	T63073	7.8 kb fragment of pN	1.23e+02	311	14	1.0	297	1	N92584	CEM kappa promoter of	4.79e+02
C	239	15	1.1	8201	20	T12170	pUG4-5-CDK-BP cDNA cl	1.23e+02	312	14	1.0	302	19	T09832	Tomato genomic DNA, D	4.79e+02
C	240	15	1.1	8738	31	T72327	Lactobacillus bacteri	1.23e+02	313	14	1.0	303	20	T23565	Human gene signature	4.79e+02
C	241	15	1.1	8791	23	T37090	Human T cell inositol	1.23e+02	314	14	1.0	308	8	Q61356	Human brain Expressed	4.79e+02
C	242	15	1.1	9071	3	Q22370	U266-Lambda gene and	1.23e+02	315	14	1.0	317	2	Q10903	Synthetic HIV-2 gp 36	4.79e+02
C	243	15	1.1	9071	3	Q22491	Human U266 Lambda gen	1.23e+02	316	14	1.0	318	8	Q59588	Human brain Expressed	4.79e+02
C	244	15	1.1	9192	2	Q11943	Nucleotide sequence o	2.90e+01	317	14	1.0	319	19	T21953	Human gene signature	4.79e+02
C	245	16	1.1	9709	16	Q26140	HIV-1 proviral clone	1.23e+02	318	14	1.0	322	8	Q61160	Human brain Expressed	4.79e+02
C	246	16	1.1	9709	3	Q22488	Mouse bone morphogene	1.23e+02	319	14	1.0	322	8	T09832	Human gene signature	4.79e+02
C	247	15	1.1	15144	29	T47715	IgG-Fc binding protei	1.23e+02	320	14	1.0	330	27	T35302	Human immunodeficienc	4.79e+02
C	248	15	1.1	16382	28	T63074	Human deoxycydidylate	1.23e+02	321	14	1.0	333	22	T26687	Human gene signature	4.79e+02
C	249	15	1.1	20303	30	T71699	Human deoxycydidylate	1.23e+02	322	14	1.0	333	8	Q59791	Human brain Expressed	4.79e+02
C	250	15	1.1	26764	30	T71696	AcNPV genomic DNA clo	1.23e+02	323	14	1.0	341	20	T23290	Human gene signature	4.79e+02
C	251	15	1.1	133894	17	T13635	Mycoplasma genitalium	1.23e+02	324	14	1.0	342	7	Q43695	Sequence of intron 46	4.79e+02
C	252	15	1.1	580073	27	T58840	Human CERP HH ribozym	4.79e+02	325	14	1.0	349	8	Q60437	Human brain Expressed	4.79e+02
C	253	14	1.0	15	24	T49727	Human CERP HH ribozym	4.79e+02	326	14	1.0	357	29	T39996	Human gamma-signalin	4.79e+02
C	254	14	1.0	18	13	Q78329	crYA(c) terminator P	4.79e+02	327	14	1.0	363	33	T67327	Human brain Expressed	4.79e+02
C	255	14	1.0	20	10	Q57790	Primer pair 5B MYC de	4.79e+02	328	14	1.0	365	8	Q59687	Human brain Expressed	4.79e+02
C	256	14	1.0	21	14	Q83684	Epsilon opioiid recept	4.79e+02	329	14	1.0	368	15	Q87447	Variola major virus s	4.79e+02
C	257	14	1.0	24	4	Q24949	PCR primer vpuE for a	4.79e+02	330	14	1.0	369	18	T19957	Human gene signature	4.79e+02
C	258	14	1.0	24	12	Q72200	Human PACAP receptor	4.79e+02	331	14	1.0	374	18	T19100	Human gene signature	4.79e+02
C	259	14	1.0	25	28	T59305	Primer for 5'-end of	4.79e+02	332	14	1.0	377	1	Q03265	DNA probe for the det	4.79e+02
C	260	14	1.0	26	23	T38625	Chimaeric human/murin	4.79e+02	333	14	1.0	377	8	Q61026	Human brain Expressed	4.79e+02
C	261	14	1.0	26	15	Q94511	Human/murine chimeric	4.79e+02	334	14	1.0	379	15	Q94521	Human/murine chimeric	4.79e+02
C	262	14	1.0	26	15	Q94512	Human/murine chimeric	4.79e+02	335	14	1.0	379	15	Q94514	Human/murine chimeric	4.79e+02
C	263	14	1.0	26	23	T38626	Chimaeric human/murin	4.79e+02	336	14	1.0	379	15	Q94520	Human/murine chimeric	4.79e+02
C	264	14	1.0	28	16	Q99509	Mouse Fas ligand gene	4.79e+02	337	14	1.0	379	23	T38635	Chimaeric human/murin	4.79e+02
C	265	14	1.0	28	7	Q43669	Sequence of 146F an a	4.79e+02	338	14	1.0	379	23	T38627	Chimaeric human/murin	4.79e+02
C	266	14	1.0	30	2	Q13759	D2 receptor probe.	4.79e+02	339	14	1.0	379	23	T38631	Chimaeric human/murin	4.79e+02
C	267	14	1.0	30	20	T18355	G-protein coupled rec	4.79e+02	340	14	1.0	379	15	T38634	Chimaeric human/murin	4.79e+02
C	268	14	1.0	31	12	Q78156	BayM capsid protein	4.79e+02	341	14	1.0	379	15	Q94513	Human/murine chimeric	4.79e+02
C	269	14	1.0	33	33	T91668	Mistletoe lectin RML	4.79e+02	342	14	1.0	379	15	Q94517	Human/murine chimeric	4.79e+02
C	270	14	1.0	33	22	T17818	Primer #5 for secreto	4.79e+02	343	14	1.0	379	23	T38628	Chimaeric human/murin	4.79e+02
C	271	14	1.0	37	5	Q28820	Anti-tumour ribozyme	4.79e+02	344	14	1.0	403	11	Q45439	KM641 J chain variabl	4.79e+02
C	272	14	1.0	37	5	Q28822	Ribozyme.	4.79e+02	345	14	1.0	403	14	Q83707	Human beta-globulin reg	4.79e+02
C	273	14	1.0	37	11	Q68654	CC49 V-light primer 3	4.79e+02	346	14	1.0	403	6	Q37057	Rat immunoglobulin H	4.79e+02
C	274	14	1.0	38	9	Q55262	Stable hairpin ribozy	4.79e+02	347	14	1.0	412	8	Q60101	Human brain Expressed	4.79e+02
C	275	14	1.0	38	14	Q88038	U6-type RNA polymeras	4.79e+02	348	14	1.0	415	14	Q86062	MuLV modified LTR.	4.79e+02
C	276	14	1.0	40	9	Q50717	ERM HIV target sequen	4.79e+02	349	14	1.0	415	1	Q86062	Synthetic gene for hu	4.79e+02
C	277	14	1.0	40	14	Q83090	HIVPCV12 No. 13 enzym	4.79e+02	350	14	1.0	415	1	N90274	DNA encoding human granu	4.79e+02
C	278	14	1.0	42	5	Q28821	Anti-tumour ribozyme	4.79e+02	351	14	1.0	417	3	N40018	DNA encoding fusion p	4.79e+02
C	279	14	1.0	42	26	T45962	24-Hydroxylase gene p	4.79e+02	352	14	1.0	423	33	T80665	Type II topoisomerase	4.79e+02
C	280	14	1.0	45	17	T00676	Primer 259 for human	4.79e+02	353	14	1.0	429	23	T37122	GM-CSF (N- and O-link	4.79e+02
C	281	14	1.0	45	18	T07608	RT-PCR primer/probe 2	4.79e+02	354	14	1.0	432	4	Q24294	Ovine GM-CSF gene.	4.79e+02
C	282	14	1.0	48	2	Q11624	Probe S3 complementar	4.79e+02	355	14	1.0	434	24	T38480	Rat petrin cDNA clone	4.79e+02
C	283	14	1.0	55	4	Q25727	N-terminal extracellu	4.79e+02	356	14	1.0	435	23	T37123	GM-CSF (N-linked site	4.79e+02
C	284	14	1.0	56	5	Q28823	Anti-tumour ribozyme	4.79e+02	357	14	1.0	435	23	T37121	GM-CSF (N-linked site	4.79e+02
C	285	14	1.0	83	10	Q45281	Sequence of a D10 RNA	4.79e+02	358	14	1.0	459	1	Q04737	Sequence encoding pol	4.79e+02
C	286	14	1.0	87	10	Q77150	Human genome fragment	4.79e+02	359	14	1.0	459	1	Q04738	Sequence encoding pol	4.79e+02
C	287	14	1.0	90	7	Q47048	GM-CSF oligomer, sens	4.79e+02	360	14	1.0	459	18	T19065	Human gene signature	4.79e+02
C	288	14	1.0	99	24	T30893	Primer 23 for 95 kd p	4.79e+02	361	14	1.0	477	32	T60777	Mablinin MBL1IT cDNA	4.79e+02
C	289	14	1.0	103	5	Q33960	Downstream sequence c	4.79e+02	362	14	1.0	477	32	T60775	Mablinin MBLI cDNA fr	4.79e+02
C	290	14	1.0	105	23	T15319	PVLBS2p67120 fragmen	4.79e+02	363	14	1.0	479	24	T38482	Rat petrin cDNA clone	4.79e+02
C	291	14	1.0	107	31	T60683	Beta chain of Class I	4.79e+02	364	14	1.0	479	10	Q56261	Brevibacterium derive	4.79e+02
C	292	14	1.0	111	31	T47135	Beta chain of Class I	4.79e+02	365	14	1.0	484	27	T61384	Human fibrosin cDNA.	4.79e+02
C	293	14	1.0	119	16	T01088	VLfns-gp160IIIB const	4.79e+02	366	14	1.0	484	27	T33599	Human fibrosin cDNA.	4.79e+02
C	294	14	1.0	121	10	Q45279	Sequence of a D10 DNA	4.79e+02	367	14	1.0	495	15	Q86357	Human granulocyte mac	4.79e+02
C	295	14	1.0	147	19	T20281	Human gene signature	4.79e+02	368	14	1.0	495	1	N91709	DNA sequence of wild	4.79e+02
C	296	14	1.0	157	6	Q39881	Expressed Sequence Ta	4.79e+02	369	14	1.0	496	12	Q67878	Vaccinia E3L promoter	4.79e+02
C	297	14	1.0	157	8	Q59293	Human brain Expressed	4.79e+02	370	14	1.0	498	2	N70929	Sequence encoding pro	4.79e+02
C	298	14	1.0	169	20	T23044	Human gene signature	4.79e+02	371	14	1.0	514	15	Q86358	Human granulocyte mac	4.79e+02
C	299	14	1.0	174	13	Q75364	Gibberellin-20-oxida	4.79e+02	372	14	1.0	514	2	Q12781	hGM-CSF1leu23Asp27Glu	4.79e+02
C	300	14	1.0	210	1	N92594	Nucleotide sequence f	4.79e+02	373	14	1.0	522	2	Q11771	Sequence encoding rec	4.79e+02
C	301	14	1.0	223	19	T22710	Human gene signature	4.79e+02	374	14	1.0	534	30	T71702	Human deoxycydidylate	4.79e+02
C	302	14	1.0	225	10	Q76679	Human genome fragment	4.79e+02	375	14	1.0	548	19	T12186	pUG4-5-CDK-BP cDNA cl	4.79e+02
C	303	14	1.0	234	8	Q60481	Human brain Expressed	4.79e+02	376	14	1.0	552	17	Q94247	Cysteine proteinase c	4.79e+02
C	304	14	1.0	249	8	Q59469	Human brain Expressed	4.79e+02	377	14	1.0	564	16	Q89755	Plasmid PAR6 partial	4.79e+02
C	305	14	1.0	256	20	T22205	Human gene signature	4.79e+02	378	14	1.0	564	15	Q87557	Human T cell lymphotr	4.79e+02
C	306	14	1.0	258	3	N40019	DNA encoding fusion p	4.79e+02	379	14	1.0	565	2	N70930	Sequence encoding pro	4.79e+02
C	307	14	1.0	258	4	Q24952	HIV-1 vpu gene amplif	4.79e+02	380	14	1.0	573	29	T67537	H. pylori inner membr	4.79e+02

381	14	1.0	574	14	Q86063	MuTV modified LTR.	4.79e+02	454	14	1.0	921	12	Q74442	sacs positive regulat	4.79e+02
382	14	1.0	582	5	Q32239	Human NT-4, clone 4-2	4.79e+02	455	14	1.0	922	1	Q04259	Encodes Colon Cancer	4.79e+02
383	14	1.0	582	9	Q54717	Human NT-4 DNA isolat	4.79e+02	456	14	1.0	925	23	T27151	Human Machado-Joseph	4.79e+02
384	14	1.0	590	7	Q42320	EAFC coagulation sequ	4.79e+02	457	14	1.0	925	23	T39062	Chimeric endoglucanas	4.79e+02
385	14	1.0	591	13	Q78955	Human immunoglobulin	4.79e+02	458	14	1.0	927	28	T39062	Chimeric endoglucanas	4.79e+02
386	14	1.0	596	16	Q99026	Chelating peptide-HPV	4.79e+02	459	14	1.0	935	2	N70784	HSRV glycoprotein G (4.79e+02
387	14	1.0	596	4	Q27124	DNA encoding a Met-hg	4.79e+02	460	14	1.0	942	21	T18013	Beta-ionone 4-methyle	4.79e+02
388	14	1.0	606	13	Q78960	Human immunoglobulin	4.79e+02	461	14	1.0	951	30	T68792	Melanocortin-1 recept	4.79e+02
389	14	1.0	608	1	N90364	Fish growth hormone g	4.79e+02	462	14	1.0	953	3	Q28858	Odorant receptor clon	4.79e+02
390	14	1.0	627	6	Q37629	Native PLRV coat prot	4.79e+02	463	14	1.0	954	35	T73913	E6-binding protein E6	4.79e+02
391	14	1.0	627	6	Q37630	Modified PLRV coat pr	4.79e+02	464	14	1.0	957	21	T29932	Human striata A3 aden	4.79e+02
392	14	1.0	637	9	Q53460	PLRV integument prote	4.79e+02	465	14	1.0	957	17	T00647	Human A3 adenosine re	4.79e+02
393	14	1.0	633	31	T60688	CDNA encoding soluble	4.79e+02	466	14	1.0	957	13	Q78087	Hepatitis C virus cor	4.79e+02
394	14	1.0	636	5	Q29867	Pheromone receptor cl	4.79e+02	467	14	1.0	957	18	Q48428	Human A3 adenosine re	4.79e+02
395	14	1.0	648	6	Q35444	Cysteine protease gen	4.79e+02	468	14	1.0	957	18	T07651	Human A3 adenosine recep	4.79e+02
396	14	1.0	651	8	Q35446	Cysteine protease cod	4.79e+02	469	14	1.0	971	4	Q23666	Neurotrophic factor 4	4.79e+02
397	14	1.0	651	8	Q48029	Potato Leaf Roll Viru	4.79e+02	470	14	1.0	975	24	T39912	Maize acetyl CoA carb	4.79e+02
398	14	1.0	654	31	T60686	CDNA encoding soluble	4.79e+02	471	14	1.0	981	12	Q74278	Human transaldolase p	4.79e+02
399	14	1.0	661	2	N70561	Sequence encoding gra	4.79e+02	472	14	1.0	982	1	Q04258	Sequence of VH-alpha-	4.79e+02
400	14	1.0	661	2	N60246	Human granulocyte mac	4.79e+02	473	14	1.0	1000	1	Q04473	Potato leaf roll viru	4.79e+02
401	14	1.0	665	2	N70571	Sequence encoding hum	4.79e+02	474	14	1.0	1000	1	Q04473	Potato leaf roll viru	4.79e+02
402	14	1.0	667	2	N70570	Sequence encoding hum	4.79e+02	475	14	1.0	1014	6	Q38091	NS1-19857 fusion codi	4.79e+02
403	14	1.0	668	1	N80049	Sequence of the E.col	4.79e+02	476	14	1.0	1031	28	T39074	Chimeric endoglucanas	4.79e+02
404	14	1.0	672	11	Q67943	HIV2(gp32)-CD44 exon	4.79e+02	477	14	1.0	1047	15	Q91109	Human ileal/renal bil	4.79e+02
405	14	1.0	685	1	Q04264	Encodes Colon Cancer	4.79e+02	478	14	1.0	1048	28	T39073	Chimeric endoglucanas	4.79e+02
406	14	1.0	702	31	T60704	CDNA encoding soluble	4.79e+02	479	14	1.0	1058	4	Q26405	Humicola insolens DSM	4.79e+02
407	14	1.0	711	29	T62512	Primitised anti-human	4.79e+02	480	14	1.0	1060	5	Q31181	Alkaline endoglucanas	4.79e+02
408	14	1.0	712	15	Q92528	N. alata arabinogalac	4.79e+02	481	14	1.0	1060	5	Q31181	Alkaline endoglucanas	4.79e+02
409	14	1.0	726	31	T77788	G-protein coupled rec	4.79e+02	482	14	1.0	1060	8	Q49941	H. insolens cellulase	4.79e+02
410	14	1.0	731	18	Q99804	PR-1 like gene PR-1mz	4.79e+02	483	14	1.0	1060	5	Q30067	Endoglucanase enzyme.	4.79e+02
411	14	1.0	738	29	N71049	Sequence encoding hum	4.79e+02	484	14	1.0	1060	4	Q26380	Endoglucanase #1.	4.79e+02
412	14	1.0	759	29	T68254	H. pylori cytoplasmic	4.79e+02	485	14	1.0	1060	7	Q41732	Dye transfer inhibiti	4.79e+02
413	14	1.0	763	1	Q04018	Granulocyte macrophag	4.79e+02	486	14	1.0	1060	3	Q14856	Humicola insolens DSM	4.79e+02
414	14	1.0	767	13	Q78990	Human immunoglobulin	4.79e+02	487	14	1.0	1060	5	Q29934	Endoglucanase gene.	4.79e+02
415	14	1.0	773	2	N80223	Sequence encoding hum	4.79e+02	488	14	1.0	1060	5	Q30072	43kD endoglucanase ge	4.79e+02
416	14	1.0	773	2	N82363	Sequence encoding hum	4.79e+02	489	14	1.0	1060	4	Q25932	Cellulase contained i	4.79e+02
417	14	1.0	773	2	N60457	Colony stimulating fa	4.79e+02	490	14	1.0	1065	15	Q25932	Plasmid pSI4001 alpha	4.79e+02
418	14	1.0	774	33	T91660	Prepro mistletoe lect	4.79e+02	491	14	1.0	1108	8	Q46149	reca gene.	4.79e+02
419	14	1.0	781	2	N93172	CDNA encoding human	4.79e+02	492	14	1.0	1111	12	Q74280	Human transaldolase p	4.79e+02
420	14	1.0	783	2	N93066	Clone encoding bovine	4.79e+02	493	14	1.0	1143	10	Q58820	NANBH virus gene frag	4.79e+02
421	14	1.0	787	2	N60364	Human granulocyte mac	4.79e+02	494	14	1.0	1168	23	T41942	Src SH3 binding prote	4.79e+02
422	14	1.0	787	14	Q84865	Clone pcd-human-GM-CS	4.79e+02	495	14	1.0	1173	7	Q43896	NANB hepatitis virus	4.79e+02
423	14	1.0	795	20	T12164	Partial pJG4-5-CDK-BP	4.79e+02	496	14	1.0	1190	4	Q23665	Neurotrophic factor 4	4.79e+02
424	14	1.0	798	15	Q88193	PRRS virus (Spanish s	4.79e+02	497	14	1.0	1191	27	T33600	Human fibrosin cDNA i	4.79e+02
425	14	1.0	798	20	T14427	PRRSV Ielystad ORF-3.	4.79e+02	498	14	1.0	1191	27	T61385	Human Fibrosin cDNA i	4.79e+02
426	14	1.0	810	2	N71121	Sequence encoding pig	4.79e+02	499	14	1.0	1203	14	Q87971	Factor-XA cDNA.	4.79e+02
427	14	1.0	813	3	Q20270	Human GM-CSF/IL-3 fus	4.79e+02	500	14	1.0	1213	28	T61895	Human 14-3-3 beta or	4.79e+02
428	14	1.0	813	2	Q10949	GM-CSF/IL-3 fusion pr	4.79e+02	501	14	1.0	1225	22	T33325	American elm chitinas	4.79e+02
429	14	1.0	813	4	Q24524	GM-CSF/IL-3 fusion pr	4.79e+02	502	14	1.0	1239	17	T00645	Human A2a adenosine r	4.79e+02
430	14	1.0	813	4	Q27810	PIXY 321.	4.79e+02	503	14	1.0	1239	18	T07649	Human adenosine recep	4.79e+02
431	14	1.0	815	1	Q04269	Sequence encoding CC8	4.79e+02	504	14	1.0	1239	21	T29930	Human ventricicle A2a a	4.79e+02
432	14	1.0	818	1	Q04268	Sequence encoding CC4	4.79e+02	505	14	1.0	1239	21	Q48415	Human A2a adenosine r	4.79e+02
433	14	1.0	819	6	Q38089	19857 Osp A DNA.	4.79e+02	506	14	1.0	1244	7	Q45656	Murine somatostatin r	4.79e+02
434	14	1.0	825	3	Q20271	Human IL-3/GM-CSF fus	4.79e+02	507	14	1.0	1259	13	Q75360	Gibberellin-20-oxida	4.79e+02
435	14	1.0	825	4	Q24525	IL-3/GM-CSF fusion pr	4.79e+02	508	14	1.0	1265	7	Q45654	Murine somatostatin r	4.79e+02
436	14	1.0	825	4	Q27811	PIXY 344.	4.79e+02	509	14	1.0	1265	31	T69550	Rat pheromone recepto	4.79e+02
437	14	1.0	825	2	Q10950	IL-3/GM-CSF fusion pr	4.79e+02	510	14	1.0	1270	10	Q44340	Sequence encoding a p	4.79e+02
438	14	1.0	858	1	Q04260	Encodes Colon Cancer	4.79e+02	511	14	1.0	1316	29	T61679	Human alpha(1,3)-fuc	4.79e+02
439	14	1.0	862	7	Q45595	Sequence encoding mur	4.79e+02	512	14	1.0	1316	9	Q56911	DNA encoding a glycos	4.79e+02
440	14	1.0	865	7	Q45594	Sequence encoding mur	4.79e+02	513	14	1.0	1320	13	Q80916	Plasmodium falciparum	4.79e+02
441	14	1.0	867	21	T18014	Beta-ionone 4-methyle	4.79e+02	514	14	1.0	1320	5	Q30998	Serrate gene.	4.79e+02
442	14	1.0	873	23	T27149	Human Machado-Joseph	4.79e+02	515	14	1.0	1323	31	T60700	CDNA encoding soluble	4.79e+02
443	14	1.0	879	4	Q24437	Mutated mature VWF 44	4.79e+02	516	14	1.0	1326	1	N90772	Coding strand of cDNA	4.79e+02
444	14	1.0	882	9	Q51189	Homeotic gene "green	4.79e+02	517	14	1.0	1332	14	Q87443	Vaccinia virus semaph	4.79e+02
445	14	1.0	885	28	T39075	Chimeric endoglucanas	4.79e+02	518	14	1.0	1333	3	Q20499	Encodes fibrinogenoly	4.79e+02
446	14	1.0	889	5	Q29700	PTOM75.	4.79e+02	519	14	1.0	1344	31	T60705	CDNA encoding soluble	4.79e+02
447	14	1.0	891	2	N60919	Sequence encoding por	4.79e+02	520	14	1.0	1371	23	T29383	Hamster flank organ d	4.79e+02
448	14	1.0	891	12	Q78155	Barley yellow mosaic	4.79e+02	521	14	1.0	1380	28	T51051	Human amine receptor	4.79e+02
449	14	1.0	894	28	T39061	Chimeric endoglucanas	4.79e+02	522	14	1.0	1389	12	Q70737	TATA-binding protein-	4.79e+02
450	14	1.0	906	4	Q25910	HIV endonuclease DNA.	4.79e+02	523	14	1.0	1390	2	Q13751	Peptidylglycine alpha	4.79e+02
451	14	1.0	907	2	N70905	Human kallikrein-like	4.79e+02	524	14	1.0	1395	8	Q50415	Human antithrombin II	4.79e+02
452	14	1.0	911	2	N71002	Sequence encoding a h	4.79e+02	525	14	1.0	1398	20	T03700	Cotton UDP glucose sy	4.79e+02
453	14	1.0	916	3	Q20375	Sequence encoding the	4.79e+02	526	14	1.0	1399	8	Q51424	Human vitamin D recep	4.79e+02

C	527	14	1.0	1408	16	Q91761	Mouse Rad51 gene, enc	4.79e+02	C	600	14	1.0	1922	3	Q21172	Human CD19 antigen co	4.79e+02
	528	14	1.0	1409	3	N50474	Sequence of brain spe	4.79e+02	C	601	14	1.0	1922	22	T14712	Human CD19 antigen CD	4.79e+02
	529	14	1.0	1413	9	Q54885	Etherase gene.	4.79e+02	C	602	14	1.0	1928	22	T36140	Guinea pig L-asparagi	4.79e+02
	530	14	1.0	1447	10	Q58686	Human hippocampal cho	4.79e+02	C	603	14	1.0	1969	29	T64531	Glutamate dehydrogena	4.79e+02
C	531	14	1.0	1473	5	Q30002	HCNP precursor gene #	4.79e+02	C	604	14	1.0	1969	15	Q98751	DNA encoding murine s	4.79e+02
C	532	14	1.0	1473	29	T64548	NADP-specific glutama	4.79e+02	C	605	14	1.0	1970	17	T00613	DNA encoding lucifera	4.79e+02
C	533	14	1.0	1489	2	Q10323	Antithrombin III cDNA	4.79e+02		606	14	1.0	1982	5	Q30687	Arylglycerol-beta-ary	4.79e+02
C	534	14	1.0	1496	4	Q28119	P.falciparum LSA gene	4.79e+02		607	14	1.0	1985	7	Q21172	Dopamine transporter	4.79e+02
C	535	14	1.0	1506	29	T64547	NADP-specific glutama	4.79e+02		608	14	1.0	1989	16	Q92945	Schizosaccharomyces p	4.79e+02
C	536	14	1.0	1515	19	T07072	Adhesive protein gene	4.79e+02	C	609	14	1.0	1989	12	Q70810	Protein kinase (Hhp2+	4.79e+02
	537	14	1.0	1518	14	Q83682	Epsilon opioid recept	4.79e+02	C	610	14	1.0	2009	20	T11379	Cytochrome P450 2C9 c	4.79e+02
	538	14	1.0	1518	24	T37313	Aromatic acyl transfe	4.79e+02	C	611	14	1.0	2010	1	N91379	Intron 1 from human f	4.79e+02
	540	14	1.0	1523	1	Q04757	Sequence encoding bat	4.79e+02	C	612	14	1.0	2012	12	Q71448	Attr 20 murine prohom	4.79e+02
	541	14	1.0	1527	29	N81741	Batroxobin gene	4.79e+02	C	613	14	1.0	2012	7	Q43249	Sequence of AtTr20 mur	4.79e+02
C	542	14	1.0	1527	5	T67337	H. pylori cytoplasmic	4.79e+02		614	14	1.0	2018	17	T00755	Recombinant C.albican	4.79e+02
C	543	14	1.0	1533	13	Q30974	HIV gp160-SF2C precu	4.79e+02	C	615	14	1.0	2020	18	T04707	ALVAC recombinant VCP	4.79e+02
C	544	14	1.0	1537	5	Q81497	HIV-1 SF2 gp120 gene.	4.79e+02	C	616	14	1.0	2028	18	T04708	ALVAC recombinant VCP	4.79e+02
C	545	14	1.0	1575	12	Q30973	HIV gp160-RF precursor	4.79e+02		617	14	1.0	2032	5	Q29937	PEP4 gene encoding Pi	4.79e+02
C	546	14	1.0	1578	32	T79597	Human PACAP receptor	4.79e+02		618	14	1.0	2043	8	Q51425	Rat vitamin D recepto	4.79e+02
C	547	14	1.0	1578	24	T42223	TARA-binding protein	4.79e+02		619	14	1.0	2048	14	Q85985	Zea mays pPFX-ZM1 gen	4.79e+02
C	548	14	1.0	1588	31	T72721	Human TATA-binding pr	4.79e+02	C	620	14	1.0	2058	2	N60739	Sequence encoding cyc	4.79e+02
C	549	14	1.0	1599	3	N30203	PAP-GM-CSF immunostim	4.79e+02	C	621	14	1.0	2058	11	Q62599	Human cytoplasmic NAD	4.79e+02
C	550	14	1.0	1610	31	T72724	Sequence encoding hum	4.79e+02	C	622	14	1.0	2060	18	T04709	COPAK recombinant vcp	4.79e+02
C	551	14	1.0	1629	21	T18011	p53-GM-CSF immunostim	4.79e+02	C	623	14	1.0	2071	10	Q56945	A. niger pH 2.5 acid	4.79e+02
C	552	14	1.0	1630	2	N60813	Beta-ionone 4-methyl	4.79e+02	C	624	14	1.0	2071	10	Q58121	pH 2.5 acid phosphata	4.79e+02
C	553	14	1.0	1632	12	Q71341	Sequence encoding tis	4.79e+02	C	625	14	1.0	2078	30	T47698	Banana polyphenol oxi	4.79e+02
C	554	14	1.0	1633	9	Q51227	Human basigin I immun	4.79e+02	C	626	14	1.0	2090	7	Q42383	TGF-beta receptor ty	4.79e+02
C	555	14	1.0	1634	7	Q45653	Human MSH-R gene.	4.79e+02	C	627	14	1.0	2095	10	Q64830	TGF-beta receptor typ	4.79e+02
C	556	14	1.0	1648	6	Q40502	Human somatostatin re	4.79e+02	C	628	14	1.0	2096	29	T64543	NADP-specific glutama	4.79e+02
C	557	14	1.0	1656	12	Q72194	Human ALT gene.	4.79e+02	C	629	14	1.0	2099	29	T64530	NADP-specific glutama	4.79e+02
C	558	14	1.0	1657	7	Q45503	Human PACAP receptor	4.79e+02	C	630	14	1.0	2116	6	T64542	Tomato hsp80 cDNA seq	4.79e+02
C	559	14	1.0	1659	12	Q72193	Sequence encoding an	4.79e+02	C	631	14	1.0	2137	29	T64549	NADP-specific glutama	4.79e+02
C	560	14	1.0	1659	12	Q72195	Human PACAP receptor	4.79e+02	C	632	14	1.0	2140	29	T64529	NADP-specific glutama	4.79e+02
C	561	14	1.0	1664	12	Q72207	Human PACAP receptor	4.79e+02	C	633	14	1.0	2148	12	Q73222	BOPCar I, bovine para	4.79e+02
C	562	14	1.0	1680	15	Q74150	Plasmid pSI4001 alpha	4.79e+02	C	634	14	1.0	2151	29	T68080	H. pylori cell envelo	4.79e+02
C	563	14	1.0	1685	21	T30395	Borage delta-6-desatu	4.79e+02	C	635	14	1.0	2156	2	Q11562	Partial endothelial p	4.79e+02
C	564	14	1.0	1695	18	T05877	CDNA encoding transfo	4.79e+02	C	636	14	1.0	2175	5	Q29268	Fungal signal recogni	4.79e+02
C	565	14	1.0	1695	22	T36138	Guinea pig L-asparagi	4.79e+02	C	637	14	1.0	2175	5	Q29268	Human calcium channel	4.79e+02
C	566	14	1.0	1702	15	Q97236	Rhizobium delta gene.	4.79e+02	C	638	14	1.0	2175	31	T49307	Nucleotide sequence o	4.79e+02
C	567	14	1.0	1738	6	Q40503	Rat ALT gene.	4.79e+02	C	639	14	1.0	2196	12	Q71197	Human protein-kinase-	4.79e+02
C	568	14	1.0	1745	12	Q72209	Human PACAP receptor	4.79e+02	C	640	14	1.0	2200	17	T04115	Simian-human hybrid T	4.79e+02
C	569	14	1.0	1747	5	Q30959	AdhB encoding alcohol	4.79e+02	C	641	14	1.0	2206	1	Q03510	Human Transforming gr	4.79e+02
C	570	14	1.0	1747	29	T47179	zymomonas mobilis alc	4.79e+02	C	642	14	1.0	2207	1	Q03511	Hybrid transforming g	4.79e+02
C	571	14	1.0	1748	12	Q72208	Human PACAP receptor	4.79e+02	C	643	14	1.0	2207	3	Q05127	Human TGF-Betal/TGF-B	4.79e+02
C	572	14	1.0	1748	12	Q72210	Human PACAP receptor	4.79e+02	C	644	14	1.0	2208	1	Q20291	Sequence encoding hyb	4.79e+02
C	573	14	1.0	1755	11	Q64088	Mouse gene participat	4.79e+02	C	645	14	1.0	2217	1	N90768	Sequence of human tra	4.79e+02
C	574	14	1.0	1761	8	Q46054	Sequence of tomato po	4.79e+02	C	646	14	1.0	2222	11	Q68556	Murine pro-hormone co	4.79e+02
C	575	14	1.0	1765	14	Q81703	Cell adhesion protein	4.79e+02	C	647	14	1.0	2236	5	Q32247	Bovine Viral Diarrhoe	4.79e+02
C	576	14	1.0	1765	6	Q37734	AAMP-1 cDNA.	4.79e+02	C	648	14	1.0	2258	15	T11380	Cytochrome P450 2C9 c	4.79e+02
C	577	14	1.0	1767	21	T26980	Aspergillus oryzae ta	4.79e+02	C	649	14	1.0	2263	20	Q91108	Hamster ileal/renal b	4.79e+02
C	578	14	1.0	1770	1	Q06266	Promoter region and s	4.79e+02	C	650	14	1.0	2271	1	Q06844	Amlyase gene from Str	4.79e+02
C	579	14	1.0	1779	29	T68171	H. pylori transporter	4.79e+02	C	651	14	1.0	2291	1	N80309	Entire amylase gene.	4.79e+02
C	580	14	1.0	1779	2	Q13322	PLRV Sac1-EcoRI fragm	4.79e+02	C	652	14	1.0	2294	28	T60957	Maize tapetum-specifi	4.79e+02
C	581	14	1.0	1796	17	T03734	TNF-R p55IC/Fas-IC-bi	4.79e+02	C	653	14	1.0	2376	12	T45037	Chick chondroitin 6-s	4.79e+02
C	582	14	1.0	1800	21	T31542	Mouse immunoglobulin	4.79e+02	C	654	14	1.0	2376	25	Q69030	Murine TrkC gene.	4.79e+02
C	583	14	1.0	1800	16	Q91769	Coding sequence of PE	4.79e+02	C	655	14	1.0	2376	5	Q34582	Partial sequence of a	4.79e+02
C	584	14	1.0	1804	33	T48550	Mouse tub gene.	4.79e+02	C	656	14	1.0	2376	5	Q28669	Encodes mouse trkC.	4.79e+02
C	585	14	1.0	1809	13	Q73757	Hydrogen peroxide-gen	4.79e+02	C	657	14	1.0	2376	20	T26998	N. meningitidis serot	4.79e+02
C	586	14	1.0	1830	23	T18383	Human Fas-associated	4.79e+02	C	658	14	1.0	2379	20	T26999	Her2-GM-CSF immunosti	4.79e+02
C	587	14	1.0	1830	17	T03731	TNF-R p75IC-binding p	4.79e+02	C	659	14	1.0	2385	31	T72725	Mouse Khcs cDNA.	4.79e+02
C	588	14	1.0	1833	16	Q98988	DNA encoding protein	4.79e+02	C	660	14	1.0	2389	28	T62793	Sequence encoding the	4.79e+02
C	589	14	1.0	1835	28	T62654	Rat p65 oncofoetal pr	4.79e+02	C	661	14	1.0	2397	2	N70599	V.harveyi luxAB genes	4.79e+02
C	590	14	1.0	1836	24	T33630	B.lautus endol core c	4.79e+02	C	662	14	1.0	2409	12	Q69033	Murine TrkC K3 isofor	4.79e+02
C	591	14	1.0	1854	3	Q14842	Human adrenal gland c	4.79e+02	C	663	14	1.0	2418	17	T15598	Laccase-LCC1 gene.	4.79e+02
C	592	14	1.0	1855	30	T66381	Mouse inositol polyph	4.79e+02	C	664	14	1.0	2434	21	T17044	Bacillus thuringiens	4.79e+02
C	593	14	1.0	1876	28	Q37488	gig-1 coding sequence	4.79e+02	C	665	14	1.0	2439	31	T63354	Bacillus subtilis epr	4.79e+02
C	594	14	1.0	1888	6	N91471	1.9 kb Ro (Ro/SSA) an	4.79e+02	C	666	14	1.0	2439	1	Q04542	Extracellular proteas	4.79e+02
C	595	14	1.0	1890	1	Q54624	Mammalian vesicle mem	4.79e+02	C	667	14	1.0	2439	29	T59381	Epr gene encoding ext	4.79e+02
C	596	14	1.0	1898	9	Q51094	JM haemagglutinin.	4.79e+02	C	668	14	1.0	2452	9	Q04788	Rat thyroid hormone r	4.79e+02
C	597	14	1.0	1919	8	N90612	CD19 cDNA.	4.79e+02	C	669	14	1.0	2455	1	Q04788	Rat D2 dopamine recep	4.79e+02
C	598	14	1.0	1921	1	T38556	Human CD19 cDNA.	4.79e+02	C	670	14	1.0	2460	32	T62919	Mael gene encoding ma	4.79e+02
C	599	14	1.0	1922	24	T38556	Human CD19 cDNA.	4.79e+02	C	671	14	1.0	2460	32	T62919	Malate permease mael	4.79e+02
										672	14	1.0	2460	25	T42611		

673	14	1.0	2468	6	Q39090	XR5 coding sequence.	4.79e+02	746	14	1.0	3526	33	T80106	Human KF-1 gene clone	4.79e+02
674	14	1.0	2468	6	Q39090	XR5 coding sequence.	4.79e+02	747	14	1.0	3528	15	Q91740	Rat alpha-d composite	4.79e+02
675	14	1.0	2469	16	Q29944	Schizosaccharomyces p	4.79e+02	748	14	1.0	3588	21	T30396	Synechocystis delta-6	4.79e+02
676	14	1.0	2469	12	Q70809	Protein kinase (Hhpl+	4.79e+02	749	14	1.0	3588	7	Q40057	Bacterial delta-6-des	4.79e+02
677	14	1.0	2474	31	T70840	Mouse apoptosis inhib	4.79e+02	750	14	1.0	3592	15	Q91715	Human cfr cDNA clone.	4.79e+02
678	14	1.0	2484	26	T47139	Ionotropic glutamate	4.79e+02	751	14	1.0	3597	15	Q91715	Rat alpha-d subunit c	4.79e+02
679	14	1.0	2493	20	T29511	GST-II-27 promoter.	4.79e+02	752	14	1.0	3661	28	T63081	Active clone V11 of I	4.79e+02
680	14	1.0	2514	20	T30308	Mouse Sox-9 cDNA.	4.79e+02	753	14	1.0	3697	30	T61556	Human signal mediator	4.79e+02
681	14	1.0	2515	13	Q75304	Unique region of huma	4.79e+02	754	14	1.0	3697	30	Q10324	Human Natriuretic pep	4.79e+02
682	14	1.0	2521	28	T47252	Bacillus subtilis ext	4.79e+02	755	14	1.0	3754	13	Q84782	Protein-tyrosine-kin	4.79e+02
683	14	1.0	2553	13	Q76018	DNA encoding gp120 fr	4.79e+02	756	14	1.0	3803	15	Q91714	Mouse alpha-d subunit	4.79e+02
684	14	1.0	2553	1	N80949	HIV protein HT6.	4.79e+02	757	14	1.0	3808	18	T04701	PHIV32 fragment contg	4.79e+02
685	14	1.0	2561	2	Q10400	D2 dopamine receptor	4.79e+02	758	14	1.0	3812	2	Q10991	Partial sequence of m	4.79e+02
686	14	1.0	2568	1	N90767	Sequence of human tra	4.79e+02	759	14	1.0	3812	1	N92734	Partial nucleotide se	4.79e+02
687	14	1.0	2569	3	Q20290	Sequence encoding hum	4.79e+02	760	14	1.0	3827	29	T63125	Glutathione S-transfe	4.79e+02
688	14	1.0	2569	1	Q05126	Human TGF-Beta2-442 p	4.79e+02	761	14	1.0	3827	11	Q66591	GST II-27 gene promot	4.79e+02
689	14	1.0	2571	14	Q76020	DNA encoding gp120 fr	4.79e+02	762	14	1.0	3861	1	Q05979	Recombinant AcNPV-HIV	4.79e+02
690	14	1.0	2575	9	Q54641	Human A2a adenosine r	4.79e+02	763	14	1.0	3865	6	Q37101	Bovine transglutamina	4.79e+02
691	14	1.0	2592	17	T04116	Human transforming gr	4.79e+02	764	14	1.0	3901	12	Q71190	PLRV genomic fragment	4.79e+02
692	14	1.0	2595	2	N70259	Sequence of env gene	4.79e+02	765	14	1.0	3931	7	Q42594	Rat betaglycan (bg7).	4.79e+02
693	14	1.0	2597	14	Q79135	Bovine male enhanced	4.79e+02	766	14	1.0	3934	20	T30309	Human SOX-9 cDNA.	4.79e+02
694	14	1.0	2598	1	N80948	HIV protein HT7.	4.79e+02	767	14	1.0	3962	14	Q92522	Human mammary carcin	4.79e+02
695	14	1.0	2607	5	Q31985	Pisium sativum L. PAL	4.79e+02	768	14	1.0	3962	14	Q92520	Human mammary carci	4.79e+02
696	14	1.0	2610	1	N93060	cDNA of plasmid pXA45	4.79e+02	769	14	1.0	3969	28	T62655	DNA encoding protein	4.79e+02
697	14	1.0	2633	2	Q10351	PLUXSPAFC-2 encoding	4.79e+02	770	14	1.0	4004	1	Q05680	bPGS1245 gene.	4.79e+02
698	14	1.0	2642	2	Q10350	PLUXSPAFC-1 encoding	4.79e+02	771	14	1.0	4067	10	Q63192	Human adeno-associate	4.79e+02
699	14	1.0	2662	6	Q37757	PVMO51.	4.79e+02	772	14	1.0	4113	1	Q06644	Human adeno-associate	4.79e+02</

C	819	14	1.0	6971	24	T38740	Moraxella outer membr	4.79e+02	892	14	1.0	31122	7	Q40705	Bacillus subtilis str	4.79e+02
	820	14	1.0	7032	15	Q84662	Human neuronal calciu	4.79e+02	893	14	1.0	53577	28	T18551	Human polycystic kidn	4.79e+02
	821	14	1.0	7089	15	Q84663	Human neuronal calciu	4.79e+02	894	14	1.0	133894	17	T13635	AcNPV genomic DNA clo	4.79e+02
	822	14	1.0	7158	23	T27394	Hepatitis E virus str	4.79e+02	895	14	1.0	580073	27	T58840	Mycoplasma genitalium	4.79e+02
	823	14	1.0	7168	10	Q45197	HEV strain SAR-55 cDN	4.79e+02	C	896	13		33	T87255	Interleukin-4 2'F RNA	1.70e+03
	824	14	1.0	7171	2	Q14413	Composite sequence fr	4.79e+02	C	897	13		33	T87185	Interleukin-4 2'F RNA	1.70e+03
	825	14	1.0	7195	2	Q14412	Forward strand of Bur	4.79e+02	C	898	13		33	T87180	Interleukin-4 2'F RNA	1.70e+03
	826	14	1.0	7470	24	T39905	DNA encoding mouse ce	4.79e+02	C	899	13		33	T87206	Interleukin-4 2'F RNA	1.70e+03
	827	14	1.0	7608	16	T74118	Maize acetyl CoA carb	4.79e+02	C	900	13		33	T58888	Bispecific tetraalen	1.70e+03
	828	14	1.0	7625	31	T71323	Hybrid activation vec	4.79e+02	C	901	13		33	T50658	Rabbit CERP hairpin r	1.70e+03
	829	14	1.0	7726	2	N70834	L-Tryptophan producti	4.79e+02	C	902	13		33	T72136	Vector pUC19MCH frag	1.70e+03
	830	14	1.0	7742	32	T84745	Bordetella pertussis	4.79e+02	C	903	13		33	T60425	Potato starch branchi	1.70e+03
	831	14	1.0	8043	14	Q85924	Human protein tyrosin	4.79e+02	C	904	13		33	T79781	Human mature interfer	1.70e+03
	832	14	1.0	8075	24	T31984	Invertebrate calicium	4.79e+02	C	905	13		33	T47917	Human mature interfer	1.70e+03
	833	14	1.0	8075	24	T31981	Neuronal invertebrate	4.79e+02	C	906	13		33	T47918	Human mature interfer	1.70e+03
	834	14	1.0	8316	12	Q74450	myoD retroviral expre	4.79e+02	C	907	13		33	T31590	Probe (BLUR2) for Alu	1.70e+03
	835	14	1.0	8355	24	T35524	Human interferon-beta	4.79e+02	C	908	13		33	N80150	Plasmid pC21a insert	1.70e+03
	836	14	1.0	8654	14	O55138	Staphylococcus epide	4.79e+02	C	909	13		33	N95402	Sequence of new sigma	1.70e+03
	837	14	1.0	9046	15	T02792	Zucchini ACC synthase	4.79e+02	C	910	13		33	T64563	Mouse thymus and acti	1.70e+03
	838	14	1.0	9060	3	Q15132	Transcription factor	4.79e+02	C	911	13		33	T75083	Human mature growth h	1.70e+03
	839	14	1.0	9088	2	N60476	Sequence of lymphaden	4.79e+02	C	912	13		33	T75094	Sinapis alba flowerin	1.70e+03
	840	14	1.0	9115	12	Q74449	myoD retroviral expre	4.79e+02	C	913	13		33	Q73017	5' end of CH14-2a16-1	1.70e+03
	841	14	1.0	9193	2	N60365	Sequence of LAV virus	4.79e+02	C	914	13		33	T58248	Hepatitis Type-C viru	1.70e+03
	842	14	1.0	9213	2	N60288	Sequence of the HTLV-	4.79e+02	C	915	13		33	T58531	Nucleotide sequence o	1.70e+03
	843	14	1.0	9213	2	N60288	Sequence of the HTLV-	4.79e+02	C	916	13		33	T43312	Ospa variant #1 codin	1.70e+03
	844	14	1.0	9299	29	T47716	Mouse bone morphogene	4.79e+02	C	917	13		33	T38531	Chlamydia trachomatis	1.70e+03
	845	14	1.0	9326	4	Q25051	DNA complementary to	4.79e+02	C	918	13		33	Q94034	HV18 gene promoter re	1.70e+03
	846	14	1.0	9360	1	Q02830	CDNA to HIV-2 RNA.	4.79e+02	C	919	13		33	T58122	Human CD40L mutein co	1.70e+03
	847	14	1.0	9425	7	Q45921	HTLV-III DNA (Clone B	4.79e+02	C	920	13		33	T58123	CDNA encoding yeast G	1.70e+03
	848	14	1.0	9425	7	Q45919	HTLV-III DNA (Clone B	4.79e+02	C	921	13		33	T42665	Histidine tagged vero	1.70e+03
	849	14	1.0	9425	7	Q45921	HTLV-III DNA (Clone B	4.79e+02	C	922	13		33	T73693	DNA encoding phenylal	1.70e+03
	850	14	1.0	9425	7	Q45919	HTLV-III DNA (Clone B	4.79e+02	C	923	13		33	T41788	Fusion peptide #3 hav	1.70e+03
	851	14	1.0	9427	7	Q45920	HTLV-III DNA (Clone B	4.79e+02	C	924	13		33	T74024	Ethylene synthase enc	1.70e+03
	852	14	1.0	9427	7	Q45920	HTLV-III DNA (Clone B	4.79e+02	C	925	13		33	Q25060	PSbeta-318 clone.	1.70e+03
	853	14	1.0	9473	1	N92768	HIV-2 variant HIV-D19	4.79e+02	C	926	13		33	T74888	Xenopus neurogenic di	1.70e+03
	854	14	1.0	9515	14	Q55145	Pseudomonas aeruginos	4.79e+02	C	927	13		33	Q91637	Mouse sonic hedgehog	1.70e+03
	855	14	1.0	9534	17	T17419	Merosin CDNA.	4.79e+02	C	928	13		33	O50561	Asparaginylendopeptid	1.70e+03
	856	14	1.0	9589	6	Q38218	NANBH virus strain HC	4.79e+02	C	929	13		33	T86003	Maize 5-enolpyruvylsh	1.70e+03
	857	14	1.0	9629	18	T14600	PXJCL-hGM-CSF express	4.79e+02	C	930	13		33	T85995	Maize 5-enolpyruvylsh	1.70e+03
	858	14	1.0	9633	1	N80890	Sequence of CDNA clon	4.79e+02	C	931	13		33	T86002	Maize 5-enolpyruvylsh	1.70e+03
	859	14	1.0	9636	12	Q67190	P. talciparum transmi	4.79e+02	C	932	13		33	T85994	Maize 5-enolpyruvylsh	1.70e+03
	860	14	1.0	9693	1	N92119	Sequence of clone HIV	4.79e+02	C	933	13		33	T72215	Maize 5-enolpyruvylsh	1.70e+03
	861	14	1.0	9718	19	T14180	Attenuated HIV-1 stra	4.79e+02	C	934	13		33	Q11190	Grapevine leafroll vl	1.70e+03
	862	14	1.0	9737	2	N60140	Sequence of ARV-2 (9B	4.79e+02	C	935	13		33	T85993	Immunoglobulin gamma	1.70e+03
	863	14	1.0	9737	2	T33898	HIV-1 SF2 genome.	4.79e+02	C	936	13		33	Q62841	Maize 5-enolpyruvylsh	1.70e+03
	864	14	1.0	9737	5	Q31936	ARV-2 proviral DNA fr	4.79e+02	C	937	13		33	T75076	CDNA encoding aspartyl	1.70e+03
	865	14	1.0	9745	2	N60240	HTLV-III virus (HIV v	4.79e+02	C	938	13		33	T59528	Alpha4 subunit of mut	1.70e+03
	866	14	1.0	9745	2	N60240	HTLV-III virus (HIV v	4.79e+02	C	939	13		33	T59527	Alpha4 subunit of hor	1.70e+03
	867	14	1.0	9746	3	Q14752	HIV-1(MN-ST1) env pro	4.79e+02	C	940	13		33	T59528	Human growth hormone	1.70e+03
	868	14	1.0	9746	26	T58550	Human Immunodeficienc	4.79e+02	C	941	13		33	T59528	Plant potassium chann	1.70e+03
	869	14	1.0	9749	7	Q45922	HTLV-III DNA (Clone H	4.79e+02	C	942	13		33	T62826	Human growth hormone	1.70e+03
	870	14	1.0	9749	7	Q45922	HTLV-III DNA (Clone H	4.79e+02	C	943	13		33	Q51345	Human Aurora-2 cDNA.	1.70e+03
	871	14	1.0	10163	32	T61085	Full-length HIV-2KR p	4.79e+02	C	944	13		33	Q73117	Nucleotide sequence o	1.70e+03
	872	14	1.0	10614	15	Q89555	Hamster cholesterol 7	4.79e+02	C	945	13		33	T67234	S. cerevisiae origin	1.70e+03
	873	14	1.0	10660	14	Q89555	Spinocerebellar ataxi	4.79e+02	C	946	13		33	T85402	CDNA encoding glycosy	1.70e+03
	874	14	1.0	10723	31	T49304	CDNA encoding polypro	4.79e+02	C	947	13		33	T67290	Scytalidium thermophi	1.70e+03
	875	14	1.0	10723	31	T49303	CDNA sequence encodin	4.79e+02	C	948	13		33	T49305	Human cadherin-8 codi	1.70e+03
	876	14	1.0	11478	32	T79784	Full length potato st	4.79e+02	C	949	13		33	T73282	Porcine TrkC K2 isofe	1.70e+03
	877	14	1.0	11478	32	T79805	Full length potato st	4.79e+02	C	950	13		33	T73282	DNA encoding Bacillus	1.70e+03
	878	14	1.0	11492	1	N70543	Complete sequence of	4.79e+02	C	951	13		33	T77045	Alanyl-tRNA synthetas	1.70e+03
	879	14	1.0	12923	3	N90338	Sequence of human mus	4.79e+02	C	952	13		33	T67234	DNA encoding Bacillus	1.70e+03
	880	14	1.0	13633	7	Q40862	VAC-beta (genomic - p	4.79e+02	C	953	13		33	T85402	Bacillus caldotenax D	1.70e+03
	881	14	1.0	14176	33	T84564	Swinepox virus HindII	4.79e+02	C	954	13		33	T67770	Rat FabpI gut-specific	1.70e+03
	882	14	1.0	15101	17	T16239	Lelystad virus genom	4.79e+02	C	955	13		33	T73696	S. cerevisiae origin	1.70e+03
	883	14	1.0	15101	17	T16239	Lelystad virus genom	4.79e+02	C	956	13		33	T75432	Xenopus beta-signalin	1.70e+03
	884	14	1.0	15108	5	Q32002	Lelystad Agent genome	4.79e+02	C	957	13		33	T75434	Chicken derived neurit	1.70e+03
	885	14	1.0	15108	5	Q32002	Lelystad Agent genome	4.79e+02	C	958	13		33	T75434	Human kidney inward r	1.70e+03
	886	14	1.0	15223	29	T63430	Respiratory syncytial	4.79e+02	C	959	13		33	T73280	DNA encoding macropha	1.70e+03
	887	14	1.0	16079	2	N70753	Sequence of segment o	4.79e+02	C	960	13		33	T67318	MEF2.	1.70e+03
	888	14	1.0	17327	7	Q44278	Serglycin - proteogly	4.79e+02	C	961	13		33	T31792		
	889	14	1.0	21126	2	N60970	TL-DNA region of A.rh	4.79e+02	C	962	13		33	T84537		
	890	14	1.0	21126	2	N60970	TL-DNA region of A.rh	4.79e+02	C	963	13		33	T76529		
	891	14	1.0	22481	24	T11658	PEDF full length segu	4.79e+02	C	964	13		10	Q58740		

C	965	13	0.9	2992	31	T67285	Soluble starch synthase	1.70e+03
C	966	13	0.9	3136	32	T85406	Rat full length cadherin	1.70e+03
C	967	13	0.9	3164	32	T85401	Human cadherin-5 ccdi	1.70e+03
C	968	13	0.9	3182	4	Q25799	hLIF-R.	1.70e+03
C	969	13	0.9	3192	17	T08222	X region antisense he	1.70e+03
C	970	13	0.9	3225	32	T78402	Feline immunodeficien	1.70e+03
C	971	13	0.9	3225	32	T49091	Feline immunodeficien	1.70e+03
C	972	13	0.9	3349	32	T51256	Human AD4 gene genom	1.70e+03
C	973	13	0.9	3373	31	T76768	Human alpha 1,2 fuco	1.70e+03
C	974	13	0.9	3394	33	T84484	Human alpha-1 collagen	1.70e+03
C	975	13	0.9	3561	31	T77277	Bacillus thuringiens	1.70e+03
C	976	13	0.9	3780	29	T61864	c-abl gene.	1.70e+03
C	977	13	0.9	4004	32	T51260	Human AD4 gene genom	1.70e+03
C	978	13	0.9	4049	2	N70682	Sequence of cry-1-1 g	1.70e+03
C	979	13	0.9	4173	31	T72214	Grapevine leafroll vi	1.70e+03
C	980	13	0.9	4320	32	T73388	DNA encoding HSP72 an	1.70e+03
C	981	13	0.9	4360	32	T36284	DNA encoding crystal	1.70e+03
C	982	13	0.9	4373	31	T72719	Pyruvate:flavodoxin o	1.70e+03
C	983	13	0.9	4438	2	Q13073	Modified CrYA(b) gen	1.70e+03
C	984	13	0.9	4577	33	T72813	Mouse SPT6 CDNA.	1.70e+03
C	985	13	0.9	4739	32	T78203	Physiologically activ	1.70e+03
C	986	13	0.9	4932	33	T72811	Human homologue of ye	1.70e+03
C	987	13	0.9	5274	2	N70679	Sequence encoding pse	1.70e+03
C	988	13	0.9	5836	33	T84444	Human prostate-speci	1.70e+03
C	989	13	0.9	5836	15	Q96296	Human prostate-speci	1.70e+03
C	990	13	0.9	5864	33	T72812	Human SPT6 CDNA.	1.70e+03
C	991	13	0.9	5962	32	T79596	TATA-binding protein	1.70e+03
C	992	13	0.9	6524	32	T77803	CDNA encoding wild ty	1.70e+03
C	993	13	0.9	6527	32	T77806	CDNA encoding variant	1.70e+03
C	994	13	0.9	6558	33	T79882	Tomato. immunity 2 gen	1.70e+03
C	995	13	0.9	6843	33	T84509	Human LDL receptor an	1.70e+03
C	996	13	0.9	7052	32	T77805	CDNA encoding variant	1.70e+03
C	997	13	0.9	9880	31	T68647	Halobacterium halobiu	1.70e+03
C	998	13	0.9	10380	31	T67164	Human alpha-N-acetyl	1.70e+03
C	999	13	0.9	12687	31	T70125	Equine arteritis viru	1.70e+03
C	1000	13	0.9	40875	32	T80043	Insert from cosmid 10	1.70e+03

ALIGNMENTS

RESULT 1
ID Q75926 standard; DNA; 1410 BP.

AC Q75926; 17-AUG-1995 (first entry)
DE Mouse kappa opioid receptor MOR1 cDNA.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeric; assay; probe; ss.
OS Mus musculus.
FH Key location/Qualifiers
FT CDS 185..1328
FT /*tag= a
FT /product= mouse kappa opioid receptor
PN W09428132-A.
PD 08-DEC-1994.
PR 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR P-PSDB; R67669.
PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 10; Page 207-211; 300pp; English.
CC The nucleotide sequence of the novel mouse kappa opioid receptor gene
CC MOR1. The gene was isolated from a mouse brain cDNA library using a
CC fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRI) receptor
CC subtypes SSTR1, SSTR2 and SSTR3. The 1.2 kb PstI fragment from the mouse

CC kappa opioid receptor clone, lambda msl-1, was subcloned into the CMV
CC promoter-based expression vector PCMV-6b. The resultant construct
CC PCMV-msl-1 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete,
CC truncated or chimeric opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 1410 BP; 322 A; 360 C; 337 G; 391 T;

Query Match 100.0%; Score 1410; DB 13; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 1410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	1	gcgcaccttgctgattcccaacagcagcagctctctccagtcttggaagcacaattga	60
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Db	61	gcacacggaacgtggaccatcagcagctgtaacacgactaactaagatctaaagtgtgact	120
QY	61	GCATCAGGAACGTGGACCATCAGGGCTGAACAGCTACTCAGATCTAAAGTGTGACTT	120
Db	121	ggaaagctgacggtgacttgggaagggaggtcgccaatcagcgatctgagctgcaagcgc	180
QY	121	GGAAGCTGACGGTGACTTGGGAAGGAGGTCCGCAATCAGCGATCTGAGCTGACGCGC	180
Db	181	tcacacatgagtcaccccatcagatcttcagagagatccagcgcctactcgtctccca	240
QY	181	TCACCATGAGTCCCCCATCAGATCTTCCGAGGAGATCCAGGCCCTACTGCTTCCCA	240
Db	241	gtgcttcctctcccaacagcagctcttggttcccaactgggcagaaatccgacagta	300
QY	241	GTGCTTCCTCTCCCAACAGCAGCTCTTGGTTCCTCCCACTGGGCAAGATCCGACAGTA	300
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QY	361	CTGTATATCATCACCGCTGTCTACTCTGTGTATTTGTGTGGGCTTGTGGCAATTCTC	420
Db	421	tggtcatgtttgtcatcatcaccgatacaggaagatgaagaccgcaaccacatctacatat	480
QY	421	TGTCATGTTTGTATCATCCGATACAGCATGAAGACCCGACACATCTACATAT	480
Db	481	ttaacctgcttggcagatgcttggtaactaaccactatgccccttcaagtgctgtct	540
QY	481	TTAACCTGGCTTGGCAGATGCTTGGTTACTACCACTATGCCCTTTCAGAGTGTCT	540
Db	541	acttgatgaattcttggccttggagatgtgataagaagtgtcatcttccattgact	600
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QY	661	CTGTGTGCCACCCGTGTGAAGCTTGGACTTCCGAACACCTTGAAGCAAGATCATCA	720
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QY	781	CCAAAGTCAGGAAGATGTGATGATGATGAATGCTCCTTGCAAGTTTCTGATGATGAAT	840
Db	841	atccctggtggtatctcttcatgaagatctgtgtctgcttgccttgccttgccttgcct	900


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QY      841 ATTCTGGTGGATCTCTTCATGAAGATCTGTCTTCGTCTTTGCCCTTTGTGATCCAG  900
Db      901 tectcatcatcatgtctgtctacacacctgatgatccctgcgcctgaagagtgtccggtcc  960
QY      901 TCTTCATCATCATGTCTGTCTACACCCCTGATGATCTGCGCCTGAAGAGTGTCCGCTCC  960
Db      961 tgtctgctcccgagagaaggaaccgaaatctccgcgcacatcaaccaagctgtgtgtag  1020
QY      961 TGTCTGGCTCCCGAGAGAGGACCGAATCTCCGCCGATCACCAAGCTGTGCTGTAG  1020
Db      1021 tagttgcagctctcatcatctgttggaccccatcacatcttatactctgtgtgaggtc  1080
QY      1021 TAGTTGCAGTCTTCATCATCTGTGTGACCCCATTCACATCTTATCCCTGGTGGAGGCTC  1080
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QY      1081 TGGGAAGCACCTCCACACAGCAGCTGCCCTCTCCAGCTATTATTCTGTATTCCTTGG  1140
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QY      1141 GTTATACCAACAGCAGCCTGAATCCTGTCTCTAIGCCTTCTGATGAAAACTTCAAGC  1200
Db      1201 ggtgttttagggacttctgtctccctattaagatgcaatggagcgccagagcaccata  1260
QY      1201 GGTGTTTAGGACTCTCTGCTCCCTATTAAAGATGCGAATGAGCGCCAGACCAATA  1260
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QY      1381 ATCTTGTTTAAACCAAGATTACAACCTGCAG  1410

RESULT  2
ID      Q86725 standard; cDNA; 2481 BP.
AC      Q86725;
DT      01-DEC-1995 (first entry)
DE      Mammalian kappa opioid receptor protein cDNA.
KW      Mammalian kappa opioid receptor; mouse delta opioid receptor; analgesic;
KW      amplification; primer; rat; probe; E.coli; RT-PCR; hypnotic compound; ds.
OS      Rattus rattus.
FH      Key
FH      CDS          Location/Qualifiers
FT      CDS          111..1253
FT      CDS          /product= kappa opioid receptor
PN      J07070191-A.
PD      14-MAR-1995.
PE      30-JUL-1993; 190261.
PR      09-JUL-1993; JP-170591.
PA      (TAKE ) TAKEDA CHEM IND LTD.
DR      WPI; 95-144857/19.
DR      P-PSDB; R72591.
PT      Kappa opioid receptor protein and cells expressing it - useful
PT      for the screening of compounds for analgesic and hypnotic
PT      properties
PS      Claim 2; Page 9-10; 15pp; Japanese.
CC      The nucleotide sequence of the novel mammalian kappa opioid receptor
CC      cDNA. The gene was isolated by amplifying a fragment from rat brain mRNA
CC      by reverse transcriptase-PCR (RT-PCR) using primers Q86726-7 derived from
CC      the mouse delta-opioid receptor gene. This fragment was cloned into the
CC      plasmid pCR11 to produce pR11. The plasmid pR11 was used to probe a rat
CC      brain DNA library in lambda ZAPII to obtain a clone of the rat kappa
CC      opioid receptor gene, designated pKOPR2. This clone was introduced into
CC      E.coli JM109 for production of the receptor protein. The receptor protein
CC      is useful for screening of analgesic and hypnotic compounds including
CC      peptides and proteins.
SQ      Sequence      2481 BP;          629 A;          588 C;          544 G;          720 T;
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Query Match      16.2%; Score 229; DB 15; Length 2481;
Best Local Similarity 98.1%; Pred. No. 8.00e-228;
Matches 529; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db      279 gccatccctgtatcatcaaccgctgtctactctgtgtgttgtgtgtggttagtggc  338
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QY      414 AATTCTCTGTCAATGTTGTCAATCATCCGATACGAAAGATGAAGACCGCAACCATC  473
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QY      534 GCTGTCTACTTGAATGATTTCTTGCCCTTTGGAGATGTGCTATGCAAGATTGTCAATTCC  593
Db      519 attgactctacaacaatgtttacacagcatattcaacctgacacatgatgagtgtgacgcg  578
QY      594 ATTGACTACTACAACATGTTTACCGCATATTCACTTGACCATGATGAGTGTGACCCGC  653
Db      579 tacattgcctgtgtgccaccctgtgaaagcttggatttccgaacaccttgaagcaag  638
QY      654 TACATTGCTGTGTGCCACCCTGTGAAGCTTTGGACTTCCGAACACCTTTGAAGCAAG  713
Db      639 atcatcaaatctgtcatttggctactgtgcacatcatctgtgtgtatatacagcgtatgctt  698
QY      714 ATCATCAACATCTGCATTTGGCTCTTGCAATCATCTGTTGTATATCAGCGATAGTCCCT  773
Db      699 gagggcaccaaagtcaaggagaatgtgatatcatatgaatgctccttgcagtttccgtat  758
QY      774 GGAGGCCAACCAAGTCAGGGAAGATGTGATGTCAATTGAATGCTCCTTGCACTTCCAT  833
Db      759 gatgaatatctcgtgtggacctcttcatatgaagatcgtgtcttcttcttgcctttgt  817
QY      834 GATGAATATTCTCTGTGGTGGATCTCTTCATGAAGAATCTGTCTTCTTGTGCTTTGT  892

RESULT  3
ID      Q75931 standard; DNA; 1000 BP.
AC      Q75931;
DT      18-AUG-1995 (first entry)
DE      Human kappa opioid receptor partial cDNA fragment.
KW      Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW      transmembrane domain; somatostatin; receptor; human; expression vector;
OS      Homo sapiens.
FH      Key
FH      CDS          Location/Qualifiers
FT      CDS          102..989
FT      CDS          /product= partial human kappa opioid receptor
PN      W09428132-A.
PD      08-DEC-1994.
PE      20-MAY-1994; U05747.
PR      20-MAY-1993; US-066296.
PR      30-JUL-1993; US-100694.
PR      05-NOV-1993; US-147592.
PA      (ARCH-) ARCH DEV CORP.
PI      Bell GI, Reisine T, Yasuda K;
DR      WPI; 95-022804/03.
DR      P-PSDB; R67672.
PT      Polynucleotides and peptides derived from opioid receptor
PT      polypeptides - for use in therapeutic compositions and in
PT      screening assays for useful drug substances.
PS      Claim 10; Page 236-239; 300pp; English.
CC      The partial nucleotide sequence of the novel human kappa opioid receptor
CC      gene. The gene was isolated from a human brain hippocampus cDNA library
CC      using a probe from the mouse kappa opioid receptor gene (Q75926). The
CC      gene is missing the N-terminal sequence. The C-terminal sequence is
```



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CC very similar to the mouse kappa opioid receptor sequence. Of the
CC C-terminal 293 amino acids, 281 residues are identical and 6 residues
CC have conservative substitutions. The gene encoding the human opioid
CC receptor can be placed in a suitable expression vector for production of
CC the protein in a cell. The opioid receptors thus produced are useful for
CC the development of novel assays designed to select or improve substances,
CC capable of interacting with the opioid receptor proteins, for use in
CC diagnosis, drug design and therapeutic applications.
SQ Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T;

Query Match
Best Local Similarity 100.0%; Pred. No. 4.01e-12;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 132 tacatatttaacctgcttggcagatgctt 163
   |||||
QY 474 TACATATTTAACCTGCTTGGCAGATGCTTT 505

RESULT 4
ID T12550 standard; cDNA; 1142 BP.
AC T12550;
DT 03-SEP-1996 (first entry)
DE Human kappa opioid receptor cDNA.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
   neurology; diagnosis; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..1142
FT /*tag= a
FT /product= kappa-opioid receptor
FT /note= "incomplete termination codon"
PN WO9601898-A1.
PD 25-JAN-1996.
PF 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B, Simonin F;
PI WPI; 96-097628/10.
DR P-PSDB; R88722.
PT New nucleic acid encoding the human Kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 3; Page 13-15; 30pp; French.
CC This sequence codes for the human kappa opioid receptor and was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

Query Match
Best Local Similarity 100.0%; Pred. No. 4.01e-12;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 289 tacatatttaacctgcttggcagatgctt 320
   |||||
QY 474 TACATATTTAACCTGCTTGGCAGATGCTTT 505

RESULT 5
ID Q56702 standard; DNA; 2447 BP.
AC Q56702;
DT 15-SEP-1994 (first entry)
DE Partial sequence of the human kappa opioid receptor
DE genomic clone H14 (KORA).
KW Opioid receptor; morphine; opiate; ss.
OS Homo sapiens.
PN WO9404552-A.
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PD 03-MAR-1994.
PF 13-AUG-1993; U07665.
PR 13-AUG-1992; US-929200.
PA (REGC ) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
PI WPI; 94-083099/10.
DR DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpds. for opioid (ant)agonist activity
PS Example; Fig 8b; 74pp; English.
CC To isolate opiate receptor genomic clones, 300,000 human genomic
CC clones and a similar number of mouse genomic clones were probed
CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI
CC fragment. One mouse clone and three human genomic clones were
CC isolated. The 3 human clones had very different EcoRI patterns
CC which indicated that three different genes were represented by the
CC human genomic clones which were designated H3, H14 and H20. H14 maps
CC to chromosome 8. It encodes the human kappa opioid receptor.
SQ Sequence 2447 BP; 683 A; 512 C; 498 G; 747 T;

Query Match
Best Local Similarity 100.0%; Pred. No. 3.20e-11;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 213 atagtccttgagcgaccaaagtcagggaag 243
   |||||
QY 765 ATAGTCCTTGAGGACCAAGTCAGGGAAG 795

RESULT 6
ID Q29156 standard; DNA; 822 BP.
AC Q29156;
DT 08-MAR-1993 (first entry)
DE Brain somatostatin receptor 5' DNA.
KW SR; antibodies; tumours; glycoprotein; pancreatic somatostatinoma;
   Rat; ss.
OS Rattus rattus.
FH Key Location/Qualifiers
FT CDS 1..822
FT /*tag= a
FT /product= a
FT /note= "incomplete termination codon"
PN EP-508221-A.
PD 14-OCT-1992.
PF 25-MAR-1992; 105164.
PR 28-MAR-1991; US-677009.
PR 07-JAN-1992; US-817921.
PA (AMCY ) AMERICAN CYANAMID CO.
PI Corbett MJ, Eppler CM, Hadcock J, Hulmes JD, Shieh H;
PI Strnad J, Zysklyr, Cecil ME;
PI WPI; 92-341551/42.
DR P-PSDB; R27505.
PT New somatostatin receptor, active fragments and antibodies -
PT prevents somatostatin binding to its receptor, useful for
PT treating and detecting tumours e.g. pancreatic somatostatinoma
PS Claim 18; Fig 10; 50pp; English.
CC A partial clone of purified pituitary somatostatin was used to design
CC PCR primers for amplification of somatostatin receptor DNA i.e.
CC primers ICII and TM VII. Rat genomic DNA was subjected to PCR and
CC from the deduced location of the receptor cDNA was obtd. This sequence
CC ICII, a 501 bp fragment of the receptor cDNA was obtd. This sequence
CC was used in PCR to obtain the 5' rat brain SR sequence (some bases
CC undefined and having a gap in the sequence). The receptor may be
CC used to raise antibodies for detection and treatment of tumours in
CC patients, and to treat e.g. pancreatic somatostatinoma, and to
CC regulate the action of somatostatin in vivo.
CC See also Q29154-7 and Q35865-6.
SQ Sequence 822 BP; 158 A; 245 C; 220 G; 194 T;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.92e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 262 aagatgaagaccgacacacatcatcat 290
   |||||
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QY 450 AAGATGAGACCGCAACCAACATCTACAT 478

```

RESULT 7
ID Q75928 standard; DNA; 1330 BP.
AC Q75928;
DT 17-AUG-1995 (first entry)
DE Mouse opioid receptor-like receptor MOP2 cDNA.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimaeric; assay; probe; ss.
OS Mus musculus.
FH Key
FT CDS Location/Qualifiers
FT CDS /*tag= a
FT /product= mouse opioid receptor-like receptor
PN WO9428132-A.
PD 08-DEC-1994.
PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR P-PSDB; R67671.
PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 28; Page 225-229; 300pp; English.
CC The nucleotide sequence of the novel mouse opioid receptor-like receptor
CC gene MOP2. MOP2 is a mouse receptor with pharmacological properties which
CC are dissimilar to the properties of classic opioid receptors such kappa,
CC delta, mu or sigma. It has been found that drug of high abuse potential
CC or analgesic potency bind selectively to this receptor. This suggests
CC that this receptor could be important in the development of drugs to
CC treat addiction. Other opioid receptors isolated and produced such as the
CC novel mouse kappa and delta opioid receptors (Q75926-7) are useful for
CC the development of novel assays designed to select or improve substances,
CC capable of interacting with the opioid receptor proteins, for use in
CC diagnosis, drug design and therapeutic applications.
SQ Sequence 1330 BP; 250 A; 368 C; 350 G; 362 T;

Query Match
Best Local Similarity 1.8%; Score 25; DB 13; Length 1330;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 539 gactactacaacatgtttaccagca 563
QY 597 GACTACTACACATGTTTACCAGCA 621

RESULT 8
ID Q89233 standard; cDNA; 1567 BP.
AC Q89233;
DT 20-OCT-1995 (first entry)
DE Rat opioid receptor cDNA.
KW Opioid receptor; MOR-1; gene therapy; diagnostic; ss.
OS Rattus sp.
FH Key
FT CDS Location/Qualifiers
FT CDS /*tag= a
FT /product= a
PN WO9507983-A.
PD 23-MAR-1995.
PF 13-SEP-1994; U10358.
PR 13-SEP-1993; US-120601.
PA (INDV ) UNIV INDIANA FOUND.
PI Yu L;
DR WPI; 95-131351/17.
DR P-PSDB; R71968.
PT New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.
```

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PS Example 9; Page 218-222; 266pp; English.
CC The cDNA given in Q89233 was isolated from a rat brain library by
CC low stringency hybridization with rat mu opioid receptor cDNA
CC (Q89222). The clone encoded a 367-amino acid protein (R71968)
CC that showed high homology with mu, kappa and delta opioid receptors
CC but lacked affinity for their ligands, suggesting it to be
CC a novel member of the opioid receptor family.
SQ Sequence 1567 BP; 313 A; 440 C; 402 G; 412 T;

Query Match
Best Local Similarity 1.8%; Score 25; DB 14; Length 1567;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 551 gactactacaacatgtttaccagca 575
QY 597 GACTACTACACATGTTTACCAGCA 621

RESULT 9
ID Q90096 standard; cDNA; 2600 BP.
AC Q90096;
DT 03-NOV-1995 (first entry)
DE Mouse kappa-3 opioid receptor.
KW Kappa-3 opioid receptor; analgesia; ss.
OS Mus sp.
FH Key
FT CDS Location/Qualifiers
FT CDS /*tag= a
FT /product= a
PN WO9512616-A.
PD 11-MAY-1995.
PF 03-NOV-1994; U12728.
PR 05-NOV-1993; US-147949.
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
PI Pan Y, Pasternak GW;
DR WPI; 95-193814/25.
DR P-PSDB; R74298.
PT Nucleic acid molecule(s) encoding a kappa-3 opioid receptor, and
PT antibody against the receptor - used to detect the receptor, and to
PT image cell membrane-bound receptor in a subject
PS Disclosure; Fig.1; 68pp; English.
CC Degenerate primers based on conserved sequences of the mouse delta
CC opioid receptor were used in PCR to amplify mouse kappa-3 opioid
CC receptor cDNA from a mouse brain lambda ZAP cDNA library.
SQ Sequence 2600 BP; 536 A; 680 C; 663 G; 721 T;

Query Match
Best Local Similarity 1.8%; Score 25; DB 14; Length 2600;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 677 gactactacaacatgtttaccagca 701
QY 597 GACTACTACACATGTTTACCAGCA 621

RESULT 10
ID Q92972 standard; DNA; 2706 BP.
AC Q92972;
DT 22-DEC-1995 (first entry)
DE Rat opiorph receptor OR7 DNA.
KW Opiorph receptor; opioid; ss.
OS Rattus sp.
PN WO9519986-A1.
PD 27-JUL-1995.
PF 20-JAN-1995; U00939.
PR 21-JAN-1994; US-185360.
PA (AMCY ) AMERICAN CYANAMID CO.
PI Epler CM, Hulmes JD, Ozenberger BA;
DR WPI; 95-269412/35.
DR P-PSDB; R76638.
PT New isolated DNA encoding an opiorph receptor - used to develop
PT prods. for identifying opioid agonists and antagonists and for
PT detection and manipulation
PS Disclosure; Fig.1; 35pp; English.
```


CC Primers based on rodent opiod receptors were used to amplify rat
CC genomic DNA. Products were re-amplified and subcloned into pCR-II
CC vector and amplified in E. coli. Plasmid DNAs were isolated, and
CC an unspliced sequence was obt'd. (Q92972) encoding the transmembrane
CC domain opiorph receptor protein OR7.
SQ Sequence 2706 BP; 569 A; 675 C; 704 G; 758 T;

Query Match 1.8%; Score 25; DB 15; Length 2706;

Best Local Similarity 100.0%; Pred. No. 5.12e-06;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 485 gactactacaacatgttaccagca 509
|||||

QY 597 GACTACTACACATGTTACCAGCA 621

RESULT 11
ID Q56700 standard; cDNA; 1821 BP.

AC Q56700;

DT 15-SEP-1994 (first entry)

DE Sequence of murine delta opiod receptor in the DOR-1 cDNA clone.

KW Opioid receptor; morphine; opiate; ss.

OS Mus musculus.

FH Key Location/Qualifiers

FT CDS 29..1139

PI /*tag= a

PN W09404552-A.

PD 03-MAR-1994.

PE 13-AUG-1993; U07665.

PR 13-AUG-1992; US-929200.

PA (REGC) UNIV CALIFORNIA.

PI Edwards RH, Evans CJ, Kaufman D, Keith DE;

DR WPI; 94-083099/10.

DR P-PSDB; R48629.

PT DNA encoding opiod receptors and antibodies against this

PT receptor - used to express and locate these receptors, and screen

PT cpds. for opiod (ant)agonist activity

PS Claim 1; Fig 5; 74pp; English.

CC A cDNA library was constructed using mRNA isolated from the NG109-15

CC cell line. A single clone, named the DOR-1 clone was isolated.

CC Comparisons with known sequences in GenBank showed highest homology

CC between DOR-1 and the G-protein-coupled somatostatin receptor. Other

CC features of the DOR-1 clone AA sequence deduced from the cDNA

CC sequence include 3 consensus glycosylation sites at residues 18 and

CC 33 (predicted to be in the extracellular N-terminal domain), and at

CC residue 310 (close to the C-terminus and predicted to be

CC intracellular). Phosphokinase C consensus sites are present within

CC predicted intracellular domains, at residues 242,255, 344 & 352.

CC Seven putative membrane-spanning regions were identified. The DOR-1

CC clone produces a delta receptor with a predicted mol. wt. of 40,558

CC kaltens prior to post-translational modifications.

SQ Sequence 1821 BP; 339 A; 559 C; 541 G; 382 T;

Query Match 1.6%; Score 23; DB 10; Length 1821;

Best Local Similarity 100.0%; Pred. No. 2.20e-04;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 404 tccattgactactacaacatgtt 426
|||||

QY 591 TCCATTGACTACTACACATGTT 613

RESULT 12
ID Q66556 standard; cDNA; 2216 BP.

AC Q66556;

DT 19-JAN-1995 (first entry)

DE Murine delta opiod receptor coding sequence.

KW delta opiod; enkephalin; receptor; mouse; murine; analgesic; pain;

KW drug addiction; neurological disorder; psychiatric; disorder;

KW cardiovascular disorder; ds.

OS Mus musculus.

FH Key Location/Qualifiers

FT CDS 59..1174

/*tag= a
/product= opiod_receptor

FN FR2697850-A.

PN 13-MAY-1994.

PD 10-NOV-1992; 013526.

PR 10-NOV-1992; FR-013526.

PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.

PI Kieffer B;

DR WPI; 94-178255/22.

DR P-PSDB; R66503.

PT New nucleic acid encoding opiod receptor - and related

PT polypeptide, antisense nucleic acid, probes, recombinant cells

PT and ligands, useful in diagnosis and treatment of e.g.

PT neurological disorders

PS Claim 3; Page 16-18; 29pp; French.

CC A cDNA bank constructed from hybridoma NG108-15, was used to

CC transfect COS-1 cells. The cells were tested for ability to bind

CC tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or

CC absence of the opiod antagonist naloxone. Clone K56 was isolated

CC from a positive colony and found to contain a 2216bp insert. This

CC cDNA encodes a delta opiod (enkephalin) receptor with apparent

CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.

SQ Sequence 2216 BP; 460 A; 647 C; 649 G; 460 T;

Query Match 1.6%; Score 23; DB 11; Length 2216;

Best Local Similarity 100.0%; Pred. No. 2.20e-04;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 434 tccattgactactacaacatgtt 456
|||||

QY 591 TCCATTGACTACTACACATGTT 613

RESULT 13

ID Q75927 standard; DNA; 2272 BP.

AC Q75927;

DT 17-AUG-1995 (first entry)

DE Mouse delta opiod receptor MOR1 cDNA.

KW Mouse; kappa; delta; mu; opiod receptor; brain; primer; PCR; amplify;

KW transmembrane domain; somatostatin; receptor; human; expression vector;

KW truncate; chimeric; assay; probe; ss.

OS Mus musculus.

FH Key Location/Qualifiers

FT CDS 12..1130

PI /*tag= a

FT /product= mouse delta opiod receptor

PN W09428132-A.

PD 08-DEC-1994.

PE 20-MAY-1994; U05747.

PR 20-MAY-1993; US-066296.

PR 30-JUL-1993; US-100694.

PR 05-NOV-1993; US-147592.

PA (ARCH-) ARCH DEV CORP.

PI Bell GI, Reisine T, Yasuda K;

DR WPI; 95-022804/03.

DR P-PSDB; R67670.

PT Polynucleotides and peptides derived from opiod receptor

PT polypeptides - for use in therapeutic compositions and in

PT screening assays for useful drug substances.

PS Claim 6; Page 215-221; 300pp; English.

CC The nucleotide sequence of the novel mouse delta opiod receptor gene

CC MOR1. The gene was isolated from a mouse brain cDNA library using a

CC fragment (amplified from the cDNA library with primers Q75929-30) as a

CC probe. The primers are based on the conserved sequences present in the

CC second and third transmembrane domains of somatostatin (SRIF) receptor

CC subtypes SSR1, SSR2 and SSR3. The 1.3 kb EcoRI-SacI fragment from the

CC mouse delta opiod receptor clone, lambda msl-2, was subcloned into the

CC CMV promoter-based expression vector PCMV-6c. The resultant construct

CC PCMV-msl-2 was transfected into COS-1 cells for protein production. The

CC gene encoding the opiod receptor can be used to produce complete,

CC truncated or chimeric opiod receptor proteins. The opiod receptors

CC thus produced are useful for the development of novel assays designed to

CC select or improve substances, capable of interacting with the opiod


```
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 2272 BP; 485 A; 665 C; 650 G; 472 T;

Query Match
Best Local Similarity 100.0%; Score 23; DB 13; Length 2272;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 387 tccattgactactacacatgtt 409
   |||||
QY 591 TCCATTGACTACTACACATGTT 613

RESULT 14
ID T12551 standard; cDNA; 36 BP.
AC T12551;
DT 04-SEP-1996 (first entry)
DE Human kappa opioid receptor partial 5'-cDNA PCR primer RP69.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis; polymerase chain reaction; ss.
OS Synthetic.
PN WO9601898-A1.
PD 25-JAN-1996.
PF 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B; Simonin F;
DR WPI; 96-097628/10.
PT New nucleic acid encoding the human Kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Example 2; Page 9; 30pp; French.
CC The sequence coding for the human kappa opioid receptor was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Specifically, primers RP69 and RH84 (T12551 and T12552)
CC amplified a 508 bp fragment comprising the 5'-region of the coding
CC sequence; primers RN6 and RP70 (T12553 and T12554) amplified a
CC 760 bp fragment comprising the 3'-region of the coding sequence.
CC The fragments were ligated via an EcoRI site at position 365.
CC Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 36 BP; 6 A; 13 C; 13 G; 4 T;

Query Match
Best Local Similarity 100.0%; Score 20; DB 20; Length 36;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 17 gagctgcagcgtcaccatg 36
   |||||
QY 169 GAGCTGCAGCGCTCACCATG 188

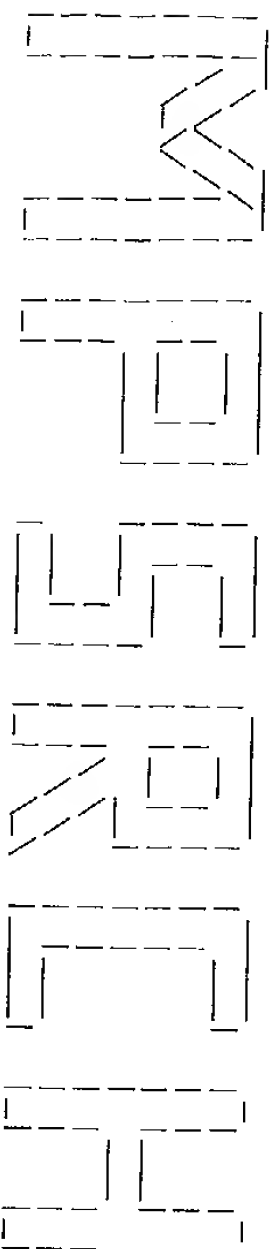
RESULT 15
ID T12554 standard; cDNA; 39 BP.
AC T12554;
DT 04-SEP-1996 (first entry)
DE Human kappa opioid receptor partial 3'-cDNA PCR primer RP70.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis; polymerase chain reaction; ss.
OS Synthetic.
PN WO9601898-A1.
PD 25-JAN-1996.
PF 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B; Simonin F;
DR WPI; 96-097628/10.
PT New nucleic acid encoding the human Kappa opioid receptor - useful
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PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Example 2; Page 9; 30pp; French.
CC The sequence coding for the human kappa opioid receptor was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Specifically, primers RP69 and RH84 (T12551 and T12552)
CC amplified a 508 bp fragment comprising the 5'-region of the coding
CC sequence; primers RN6 and RP70 (T12553 and T12554) amplified a
CC 760 bp fragment comprising the 3'-region of the coding sequence.
CC The fragments were ligated via an EcoRI site at position 365.
CC Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 39 BP; 9 A; 13 C; 10 G; 7 T;

Query Match
Best Local Similarity 100.0%; Score 20; DB 20; Length 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 20 tccacgactagtcatactg 39
   |||||
Cp 1339 TCCACGACTAGTCATACTGG 1320
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Mpsrch_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 21 00:27:25 1998; MasPar time 994.34 Seconds

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Gap 60

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Post-processing: Minimum Match 0%
Listing first 1000 summaries

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14:gb_est6 15:gb_est7 16:gb_est8 17:gb_est9 18:gb_est10
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Statistics: Mean 9.434; Variance 1.217; scale 7.749

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
	1	26	1.8	153	10	R31984	Yh62c10.r1	Homo sapien	1.61e-19
	2	24	1.7	183	10	R81583	Yj04b04.r1	Homo sapien	2.83e-15
	3	18	1.3	206	18	AA317847	EST19840	Retina II Hom	5.42e-04
	4	18	1.3	349	14	AA000300	mg32a09.r1	Soares mous	5.42e-04
	5	18	1.3	352	10	R04688	pk27e08.r1	Caenorhabdi	5.42e-04
	6	18	1.3	364	19	AA366615	EST77582	Pancreas tumo	5.42e-04
	7	18	1.3	374	22	C15712	Human fetal	brain cDNA	5.42e-04
	8	18	1.3	384	16	N57941	Yv61g04.s1	Soares feta	5.42e-04
	9	18	1.3	414	13	M62652	za14d10.s1	Homo sapien	5.42e-04
	10	18	1.3	433	11	H41020	YP72d11.s1	Homo sapien	5.42e-04
	11	18	1.3	433	10	R81332	Yj04b04.s1	Homo sapien	5.42e-04
	12	18	1.3	448	13	N78731	zb05a11.s1	Homo sapien	5.42e-04
	13	18	1.3	466	17	AA218901	zq15e05.s1	Stratagene	5.42e-04
	14	18	1.3	477	19	AA407460	EST00811	Mouse 7.5 dpc	5.42e-04
	15	18	1.3	491	21	B35459	HS-1029-A1-E02-MR.ab1		5.42e-04

C	16	18	1.3	492	21	B50064	CIT978SK-2206.TV	CIT97	5.42e-04	
	17	18	1.3	521	23	AA447244	zw93c04.r1	Soares tota	5.42e-04	
	18	18	1.3	523	22	C15915	Human fetal brain cDNA	RPC111-10M22.TP	RPC111	5.42e-04
	19	19	1.3	616	21	B72980	65H12 Human retina	CDN	1.10e-05	
	20	18	1.3	630	13	W22330	RPC111-15D7.TV	RPC111	5.42e-04	
	21	18	1.3	643	21	B75300	zn62e11.r1	Stratagene	5.42e-04	
	22	18	1.3	651	15	AA130056	zp92g04.s1	Stratagene	5.42e-04	
	23	18	1.3	680	16	AA196290	F3459 Fetal heart	Homo	5.42e-04	
	24	17	1.2	150	13	R57540	ze76f06.r1	Soares feta	2.17e-02	
	25	17	1.2	153	16	AA024669	human STS	WI-5445.	2.17e-02	
	26	17	1.2	169	20	G03281	Mouse 3'-directed	CDN	2.17e-02	
	27	17	1.2	173	23	MUSGS00777	EST55465	Homo sapiens	2.17e-02	
	28	17	1.2	191	11	T32888	EST38189	Homo sapiens	2.17e-02	
	29	17	1.2	196	11	T31750	human STS	SHGC-17378.	2.17e-02	
	30	17	1.2	209	20	G29153	EST13269	Thymus tumor	2.17e-02	
	31	17	1.2	239	18	AA303018	za44h04.r1	Soares feta	2.17e-02	
	32	17	1.2	241	13	W04435	HS-1046-B2-A08-MR.abi		2.17e-02	
	33	17	1.2	242	21	B37984	EST60579	Activated T-c	2.17e-02	
	34	17	1.2	245	19	AA352568	K4840F Fetal heart,	La	2.17e-02	
	35	17	1.2	254	14	N83261	za90e02.r1	Soares feta	2.17e-02	
	36	17	1.2	272	13	W05635	EST63142	Jurkat T-cell	2.17e-02	
	37	17	1.2	274	19	AA354599	EST90083	Synovial memb	2.17e-02	
	38	17	1.2	280	19	AA377442	ml174h04.r1	Stratagene	2.17e-02	
	39	17	1.2	287	16	AA066604	EST76830	Pineal gland	2.17e-02	
	40	17	1.2	288	19	AA365953	Yf38c12.s1	Homo sapien	2.17e-02	
	41	17	1.2	292	10	R10994	zn44d08.s1	Stratagene	2.17e-02	
	42	17	1.2	294	23	AA098808	Yd02h03.s1	Homo sapien	2.17e-02	
	43	17	1.2	299	10	R39367	Yj60d04.r1	Homo sapien	2.17e-02	
	44	17	1.2	300	10	R50578	zo53g12.s1	Stratagene	2.17e-02	
	45	17	1.2	302	15	AA148241	mg42e09.r1	Soares mous	2.17e-02	
	46	17	1.2	307	14	AA002486	zf04h04.s1	Soares feta	2.17e-02	
	47	17	1.2	308	16	AA057134	F.rubripes	GSS sequenc	2.17e-02	
	48	17	1.2	311	21	FR0017736	YP24c07.s1	Homo sapien	2.17e-02	
	49	17	1.2	312	11	H43643	EST99944	Pancreas tumo	2.17e-02	
	50	17	1.2	316	19	AA386021	z176b04.s1	Stratagene	2.17e-02	
	51	17	1.2	317	22	AA055802	ye45e04.s1	Homo sapien	2.17e-02	
	52	17	1.2	321	9	T95662	human STS	SHGC-11563.	2.17e-02	
	53	17	1.2	322	20	G14595	Yb45h03.s1	Homo sapien	2.17e-02	
	54	17	1.2	322	9	T55007	zd26e06.s1	Soares feta	2.17e-02	
	55	17	1.2	324	15	W60490	EST82365	Prostate glan	2.17e-02	
	56	17	1.2	326	19	AA370666	rs07b05.r1	Sommer Pris	2.17e-02	
	57	17	1.2	327	16	AA191999	Yx70h10.s1	Homo sapien	2.17e-02	
	58	17	1.2	327	12	N23227	H. sapiens	Partial CDN	2.17e-02	
	59	17	1.2	330	13	HSC20A072	EST70628	T-cell lympho	2.17e-02	
	60	17	1.2	337	19	AA361360	Yv72e02.r1	Soares feta	2.17e-02	
	61	17	1.2	338	16	N78089	mm55c09.r1	Stratagene	2.17e-02	
	62	17	1.2	340	16	AA068348	z176g12.s1	Stratagene	2.17e-02	
	63	17	1.2	344	22	AA057756	rs08a03.r1	Sommer Pris	2.17e-02	
	64	17	1.2	350	16	AA191834	ze94c10.s1	Soares feta	2.17e-02	
	65	17	1.2	351	16	AA029632	EST176920	Jurkat T-cel	2.17e-02	
	66	17	1.2	353	18	AA305758	NIBT072A07	Infant brai	2.17e-02	
	67	17	1.2	359	14	T26986	C.elegans	CDNA clone	Y	2.17e-02
	68	17	1.2	360	22	C13142	Yy74c05.s1	Homo sapien	2.17e-02	
	69	17	1.2	361	12	N48588	mw97f03.r1	Soares mous	2.17e-02	
	70	17	1.2	365	17	AA238039	Human colon	3'directed		2.17e-02
	71	17	1.2	376	23	HUMGS04037	zp87b04.r1	Stratagene	2.17e-02	
	72	17	1.2	378	16	AA190363	rs06g04.r1	Sommer Pris	2.17e-02	
	73	17	1.2	379	16	AA191964	vf81g06.r1	Soares mous	2.17e-02	
	74	17	1.2	381	23	AA451453	mh41d03.r1	Soares mous	2.17e-02	
	75	17	1.2	384	16	AA016810	EST100701	Pancreas tum	2.17e-02	
	76	17	1.2	385	18	AA295532	Y127f05.s1	Homo sapien	2.17e-02	
	77	17	1.2	386	11	H15927	zrl8g11.s1	Stratagene	2.17e-02	
	78	17	1.2	387	17	AA226981	Yj69c05.r1	Homo sapien	2.17e-02	
	79	17	1.2	389	10	R48882	md75a05.r1	Soares mous	2.17e-02	
	80	17	1.2	391	14	W59166	zh48f10.r1	Soares feta	2.17e-02	
	81	17	1.2	393	16	W92171	zd26e06.r1	Soares feta	2.17e-02	
	82	17	1.2	395	15	W60776	EST101891	Mouse 7.5 dpc	2.17e-02	
	83	17	1.2	396	19	AA410146	Yv46e04.s1	Homo sapien	2.17e-02	
	84	17	1.2	396	9	T95347	z190f02.s1	Stratagene	2.17e-02	
	85	17	1.2	399	23	AA088856	z180g03.r1	Stratagene	2.17e-02	
	86	17	1.2	401	15	AA102189	zd26g06.s1	Soares feta	2.17e-02	
	87	17	1.2	401	15	W60663	Yj59e04.s1	Homo sapien	2.17e-02	
	88	17	1.2	403	10	R50362			2.17e-02	

C	89	17	1.2	403	11	H02609	yj41d06.s1	Homo sapien	2.17e-02	C	162	15	1.1	142	12	N47b51	yy34e08.r1	Homo sapien	1.65e+01				
C	90	17	1.2	406	15	W61054	z629h11.r1	Soares feta	2.17e-02	C	163	15	1.1	143	16	AA066237	zm14h02.r1	Stratagene	1.65e+01				
C	91	17	1.2	406	14	W76826	me73g11.r1	Soares mous	2.17e-02	C	164	15	1.1	148	17	AA223624	zr11g08.r1	Stratagene	1.65e+01				
C	92	17	1.2	407	23	AA454617	zx96d11.s1	Soares ovar	2.17e-02	C	165	16	1.1	152	15	N97330	0019M7_gmbpFHB3.1,	G.	6.84e-01				
C	93	17	1.2	409	21	B72394	RPC111-8K24.TV	RPC111	2.17e-02	C	166	16	1.1	154	16	AA062813	ze89c06.s1	Soares feta	1.65e+01				
C	94	17	1.2	410	9	T62761	yc70h03.r1	Homo sapien	2.17e-02	C	167	15	1.1	158	14	AA013030	ze28b05.s1	Soares reti	1.65e+01				
C	95	17	1.2	413	11	H02076	yj34f01.r1	Homo sapien	2.17e-02	C	168	15	1.1	163	14	N89052	k7549F	Fetal heart, La	1.65e+01				
C	96	17	1.2	413	15	W60914	zd29h11.s1	Soares feta	2.17e-02	C	169	15	1.1	167	11	T34757	EST74708	Homo sapiens	1.65e+01				
C	97	17	1.2	417	17	AA117889	mo65b09.r1	Stratagene	2.17e-02	C	170	16	1.1	169	14	HSB97D042	H. sapiens partial	CDN	6.84e-01				
C	98	17	1.2	418	11	HI7419	ym40d11.s1	Homo sapien	2.17e-02	C	171	16	1.1	169	14	W98597	ng14b07.r1	Soares mous	1.65e+01				
C	99	17	1.2	418	22	CI8527	Human placenta	CDNA 5'	2.17e-02	C	172	15	1.1	171	18	AA310414	EST18145	Heart I	Homo	1.65e+01			
C	100	17	1.2	422	10	R67051	yi30b07.s1	Homo sapien	2.17e-02	C	173	15	1.1	173	21	B23155	F2503TF	IGF Arabidopsi	1.65e+01				
C	101	17	1.2	424	18	AA305523	ESM176509	Colon carcina	2.17e-02	C	174	15	1.1	174	20	HUMSWS1616	human chromosome 7	STS	1.65e+01				
C	102	17	1.2	424	15	W92279	ze15c03.s1	Soares feta	2.17e-02	C	175	16	1.1	176	18	AA297905	EST113467	Jurkat T-cell	1.65e+01				
C	103	17	1.2	425	12	H56992	yr07c04.r1	Homo sapien	2.17e-02	C	176	15	1.1	177	15	W89440	mfr80a07.r1	Soares mous	6.84e-01				
C	104	17	1.2	426	16	N71798	yz29a10.r1	Soares mult	2.17e-02	C	177	16	1.1	185	14	N93668	zb50e03.s1	Soares feta	1.65e+01				
C	105	17	1.2	429	14	AA004914	zh90h05.s1	Soares feta	2.17e-02	C	178	15	1.1	188	13	N93674	zb50f01.s1	Homo sapien	6.84e-01				
C	106	17	1.2	438	15	AA130357	zo19h12.s1	Stratagene	2.17e-02	C	179	16	1.1	190	10	R70920	Y150a08.s1	Homo sapien	6.84e-01				
C	107	17	1.2	440	15	W76111	zd65c03.r1	Soares feta	2.17e-02	C	180	16	1.1	197	9	AA364691	EST75579	Pineal gland	6.84e-01				
C	108	17	1.2	440	21	B44853	HS-1060-A1-F06-MF.ab1		2.17e-02	C	181	16	1.1	201	19	TA86314	Y684a10.s1	Homo sapien	6.84e-01				
C	109	17	1.2	440	14	R94145	yt74b09.s1	Soares feta	2.17e-02	C	182	16	1.1	203	20	G07077	human	STS	WI-9013.	6.84e-01			
C	110	17	1.2	446	11	H02711	yt41d06.r1	Homo sapien	2.17e-02	C	183	15	1.1	203	14	N93043	zb59g02.s1	Soares feta	1.65e+01				
C	111	17	1.2	446	13	W47848	mc82g09.r1	Soares mous	2.17e-02	C	184	16	1.1	204	19	W87340	zh66b09.r1	Soares feta	6.84e-01				
C	112	17	1.2	448	15	W94327	zd77f03.r1	Soares feta	2.17e-02	C	185	15	1.1	204	19	AA351852	EST59798	Infant brain	1.65e+01				
C	113	17	1.2	452	16	W86834	zh64h08.s1	Soares feta	2.17e-02	C	186	15	1.1	204	17	AA144132	mq54a12.r1	Soares 2NbM	1.65e+01				
C	114	17	1.2	454	11	H23991	ym49c03.s1	Homo sapien	2.17e-02	C	187	15	1.1	205	12	N55949	U4535F	Homo sapiens	CD	1.65e+01			
C	115	17	1.2	455	16	N43253	SM31CA689SK	Brugia mal	2.17e-02	C	188	15	1.1	205	11	H25472	Y147d08.r1	Homo sapien	1.65e+01				
C	116	17	1.2	457	19	AA037803	zk38b11.s1	Soares preg	2.17e-02	C	189	15	1.1	208	11	H06683	Y182f12.s1	Homo sapien	1.65e+01				
C	117	17	1.2	458	21	FR0022448	F. rubripes	GSS sequenc	2.17e-02	C	190	16	1.1	209	17	AA153538	ms15b02.r1	Stratagene	6.84e-01				
C	118	17	1.2	459	9	T77292	yc95h06.r1	Homo sapien	2.17e-02	C	191	15	1.1	209	22	C03524	Human	Heart	CDNA, clon	1.65e+01			
C	119	17	1.2	469	10	R24080	yh33h07.s1	Soares preg	2.17e-02	C	192	15	1.1	214	11	T34758	EST74735	Homo sapiens	1.65e+01				
C	120	17	1.2	471	19	AA134117	zh129f07.s1	Soares preg	2.17e-02	C	193	15	1.1	215	18	AA323179	EST25921	Cerebellum	IT	1.65e+01			
C	121	17	1.2	473	23	RICC0524A	Rice	CDNA, partial	seq	2.17e-02	C	194	15	1.1	215	13	W03702	za74c03.r1	Soares feta	1.65e+01			
C	122	17	1.2	477	15	W74623	yg20g07.r1	Homo sapien	2.17e-02	C	195	15	1.1	217	16	AA019688	ze61h07.r1	Soares reti	1.65e+01				
C	123	17	1.2	477	15	W69263	zd77f03.s1	Soares feta	2.17e-02	C	196	16	1.1	218	13	HST1H025	H. sapiens	partial	CDN	1.65e+01			
C	124	17	1.2	482	15	W69263	zd45h05.s1	Soares feta	2.17e-02	C	197	15	1.1	221	15	W45227	zc23c11.r1	Soares sene	1.65e+01				
C	125	17	1.2	484	17	AA152660	mr88d05.r1	Stratagene	2.17e-02	C	198	15	1.1	224	19	AA368477	EST79880	Placenta	I	Ho	1.65e+01		
C	126	17	1.2	486	11	H38947	yp48g10.r1	Homo sapien	2.17e-02	C	199	15	1.1	225	20	HUMSWX402	Human	chromosome X	STS	1.65e+01			
C	127	17	1.2	487	15	W52368	zc47g06.r1	Soares sene	2.17e-02	C	200	15	1.1	227	13	HSC3GE042	H. sapiens	partial	CDN	1.65e+01			
C	128	17	1.2	489	23	AA500746	vf96e12.r1	Soares mous	2.17e-02	C	201	15	1.1	229	18	AA303984	EST16674	Aorta	endothe	1.65e+01			
C	129	17	1.2	494	19	AA115516	zi03a09.r1	Soares preg	2.17e-02	C	202	15	1.1	231	15	AA090947	Yy1465	seq.	F	Petal	hea	1.65e+01	
C	130	17	1.2	498	18	AA286114	vc33h08.r1	Barstead	MP	2.17e-02	C	203	15	1.1	233	23	RICG1441A	Rice	CDNA, partial	seq	1.65e+01		
C	131	17	1.2	502	11	H43453	yo64b04.r1	Homo sapien	2.17e-02	C	204	15	1.1	233	17	AA169010	ms33h04.r1	Stratagene		1.65e+01			
C	132	17	1.2	504	12	N41606	yw67b02.r1	Homo sapien	2.17e-02	C	205	16	1.1	234	18	AA347931	EST54310	Fetal heart	I	6.84e-01			
C	133	17	1.2	504	14	AA017033	ze37c09.s1	Soares reti	2.17e-02	C	206	15	1.1	235	12	H74939	527	Brassica napus	CDN	6.84e-01			
C	134	17	1.2	505	21	B01901	csRL-142H10-u	CSRL	flo	2.17e-02	C	207	16	1.1	236	12	N53996	yy99c05.r1	Homo sapien		6.84e-01		
C	135	17	1.2	506	14	R93265	yt69c06.r1	Soares feta	2.17e-02	C	208	16	1.1	237	20	DM61F10T	D. melanogaster	STS	STS	de	6.84e-01		
C	136	17	1.2	513	21	B53657	CIT-HSP-201104	TR	CIT	2.17e-02	C	209	16	1.1	237	20	G05485	human	STS	WT-9956.		6.84e-01	
C	137	17	1.2	514	22	HUM421E11B	Human fetal	brain	CDNA	2.17e-02	C	210	16	1.1	240	15	AA091515	113716	seq.	F	Petal	hea	6.84e-01
C	138	17	1.2	518	18	AA310332	ESR181175	Jurkat	T-cell	2.17e-02	C	211	15	1.1	241	19	AA350961	EST58517	Infant	brain		1.65e+01	
C	139	17	1.2	533	23	AA541932	vj58c02.r1	Knowles	Sol	2.17e-02	C	212	16	1.1	246	19	AA367208	EST78255	Pancreas	tumo		6.84e-01	
C	140	17	1.2	533	21	FR0010690	F. rubripes	GSS sequenc		2.17e-02	C	213	15	1.1	246	18	AA294935	EST100316	Pancreas	tum		1.65e+01	
C	141	17	1.2	566	16	AA167745	zg40g03.s1	Stratagene		2.17e-02	C	214	15	1.1	247	13	HSC2AF082	H. sapiens	partial	CDN		1.65e+01	
C	142	17	1.2	577	21	FR0022410	F. rubripes	GSS sequenc		2.17e-02	C	215	15	1.1	248	11	R88057	ym87b10.r1	Homo sapien		1.65e+01		
C	143	17	1.2	581	23	AA445665	vf62f03.r1	Barstead	MP	2.17e-02	C	216	15	1.1	249	18	AA301278	EST14201	Testis	tumor		1.65e+01	
C	144	17	1.2	592	21	B64863	CIT-HSP-201104	TRB	CIT	2.17e-02	C	217	16	1.1	250	18	AA301155	EST14133	Testis	tumor		6.84e-01	
C	145	17	1.2	604	16	AA044960	zf52h09.r1	Soares reti		2.17e-02	C	218	16	1.1	250	20	G14803	human	STS	SHGC-13575.		6.84e-01	
C	146	17	1.2	613	16	AA191666	zq43d04.s1	Stratagene		2.17e-02	C	219	15	1.1	251	19	AA361886	EST71211	T-cell	lympho		1.65e+01	
C	147	17	1.2	618	21	FR0022405	F. rubripes	GSS sequenc		2.17e-02	C	220	16	1.1	253	21	FR0002637	F. rubripes	GSS	sequenc		6.84e-01	
C	148	17	1.2	619	21	FR0019372	F. rubripes	GSS sequenc		2.17e-02	C	221	16	1.1	254	13	HSC34G112	H. sapiens	partial	CDN		6.84e-01	
C	149	17	1.2	636	22	AA195013	zr35a07.s1	Soares NHHM		2.17e-02	C	222	16	1.1	258	15	AA081960	zn21f11.r1	Stratagene		6.84e-01		
C	150	17	1.2	672	22	AA195119	zr35a07.r1	Soares NHHM		2.17e-02	C	223	16	1.1	258	19	AA371042	EST82779	Prostate	gland		1.65e+01	
C	151	17	1.2	884	16	AA203299	zx55a01.r1	Soares feta		2.17e-02	C	224	15	1.1	259	21	FR0021983	F. rubripes	GSS	sequenc		6.84e-01	
C	152	17	1.2	925	20	G26659	human	STS	STS_X82240.	2.17e-02	C	225	16	1.1	261	19	AA362870	EST72724	Ovary	II	Homo	1.65e+01	
C	153	17	1.2	1163	21	B10623	T6G11-Sp6	TAMU	Arabido	2.17e-02	C	226	15	1.1	261	23	RICG2108A	Rice	CDNA, partial	seq		6.84e-01	
C	154	16	1.1	57	14	W98987	mf86f12.r1	Soares mous		6.84e-01	C	227	16	1.1	263	17	AA076755	7B01F12	Chromosome	7	F	6.84e-01	
C	155	15	1.1	85	9	T49517	ya76e08.r1	Homo sapien		1.65e+01	C	228	15	1.1	263	18	AA297076	EST112626	Cerebellum	I		1.65e+01	
C																							

235	16	1.1	269 15	AA073507	mj98b09.r1 Soares mous	6.84e-01	308	15	1.1	323 18	AA326668	EST29878 Cerebellum II	1.65e+01
236	16	1.1	269 15	W08605	mb46c01.r1 Soares mous	6.84e-01	309	16	1.1	324 16	AA185649	mus0g01.r1 Soares mous	6.84e-01
237	15	1.1	269 11	H28672	y168g12.s1 Homo sapien	1.65e+01	310	16	1.1	326 11	M85601	EST02117 Homo sapien	6.84e-01
238	15	1.1	272 15	AA052103	mt50h01.r1 Soares mous	1.65e+01	311	15	1.1	326 9	T54088	ya92b07.s1 Homo sapien	1.65e+01
239	15	1.1	273 11	T31686	EST37070 Homo sapiens	1.65e+01	312	16	1.1	327 19	AA376864	EST89338 Small Intesti	6.84e-01
240	16	1.1	274 13	ATRS4985	A. thaliana transcribe	6.84e-01	313	15	1.1	327 19	AA115628	zk96c08.s1 Soares preg	1.65e+01
241	16	1.1	275 22	HUM233E05B	Human aorta CDNA 5'-en	6.84e-01	314	16	1.1	329 16	AA107623	ml60c09.r1 Stratagene	6.84e-01
242	15	1.1	275 19	AA366973	EST77990 Pancreas tumo	1.65e+01	315	15	1.1	329 12	H84490	yy02c11.r1 Homo sapien	1.65e+01
243	15	1.1	276 10	R65722	Y126b09.r1 Homo sapien	1.65e+01	316	15	1.1	330 18	AA271340	va71b07.r1 Soares mous	1.65e+01
244	15	1.1	276 9	T06272	EST04161 Homo sapiens	1.65e+01	317	15	1.1	330 23	RICG11239A	Rice CDNA, partial seq	1.65e+01
245	15	1.1	277 13	HSC3C052	H. sapiens partial CDN	1.65e+01	318	16	1.1	331 17	AA220908	23 Pinus radiata somat	6.84e-01
246	16	1.1	277 19	AA373670	EST85713 HSC172 cells	6.84e-01	319	16	1.1	331 16	AA196766	Yy95e11.r1 Homo sapien	1.65e+01
247	16	1.1	282 14	C06509	LL3581F Fetal heart, L	6.84e-01	320	15	1.1	331 12	N51131	EST03981 Homo sapiens	6.84e-01
248	15	1.1	282 22	C06509	similar to none.	1.65e+01	321	16	1.1	332 9	T06092	ms87g03.r1 Soares mous	1.65e+01
249	16	1.1	283 13	N80275	za96f04.s1 Homo sapien	6.84e-01	322	15	1.1	332 17	AA175451	C.elegans CDNA clone Y	1.65e+01
250	15	1.1	283 18	AA319093	EST1258 Adrenal gland	1.65e+01	323	15	1.1	332 22	CELK056FLR	Yr59e09.s1 Homo sapien	6.84e-01
251	16	1.1	287 9	T07937	EST05828 Homo sapiens	6.84e-01	324	16	1.1	332 11	R98649	Yr59e09.s1 Homo sapien	6.84e-01
252	16	1.1	289 9	T59763	Yc13b12.r1 Homo sapien	6.84e-01	325	16	1.1	333 9	T91903	Yr59e09.s1 Homo sapien	6.84e-01
253	16	1.1	289 10	HSC13E041	H. sapiens partial CDN	6.84e-01	326	15	1.1	333 9	T73934	Yc54g12.s1 Homo sapien	1.65e+01
254	16	1.1	289 13	HSC34C041	H. sapiens partial CDN	6.84e-01	327	15	1.1	334 9	T96050	Yc42e10.s1 Homo sapien	1.65e+01
255	16	1.1	289 16	AA057340	zf58h09.r1 Soares reti	6.84e-01	328	15	1.1	334 18	AA345864	EST52203 Greater oment	1.65e+01
256	16	1.1	290 9	R02410	ye82a06.r1 Homo sapien	6.84e-01	329	15	1.1	335 15	AA095630	EST92546 Skin tumor I	6.84e-01
257	16	1.1	292 18	AA325123	EST70959 T-cell lympho	6.84e-01	330	16	1.1	335 19	AA379676	EST92546 Skin tumor I	6.84e-01
258	16	1.1	293 19	AA361581	EST70959 T-cell lympho	6.84e-01	331	15	1.1	336 9	T74982	Yc85d04.r1 Homo sapien	6.84e-01
259	15	1.1	293 10	R23656	Yh35g05.r1 Homo sapien	1.65e+01	332	16	1.1	336 9	R00603	Yc74c05.r1 Homo sapien	1.65e+01
260	16	1.1	294 9	T79088	Yd69d01.r1 Homo sapien	6.84e-01	333	16	1.1	337 18	AA332005	EST35974 Embryo, 8 wee	6.84e-01
261	16	1.1	294 12	H86153	similar to insulin 1.	6.84e-01	334	15	1.1	337 14	W64490	me04c02.r1 Soares mous	1.65e+01
262	15	1.1	294 9	T00683	Ys97g07.r1 Homo sapien	1.65e+01	335	15	1.1	337 9	T06583	EST04272 Homo sapiens	6.84e-01
263	15	1.1	294 12	H86153	WEST01404 Caenorhabdit	1.65e+01	336	16	1.1	337 15	AA097387	mk09d12.r1 Soares mous	6.84e-01
264	15	1.1	295 16	AA196698	zq59c11.r1 Stratagene	1.65e+01	337	16	1.1	337 22	CEMK071BYR	C.elegans CDNA clone Y	6.84e-01
265	15	1.1	295 19	AA374651	EST86818 HSC172 cells	1.65e+01	338	16	1.1	337 22	C06608	similar to insulin 1.	6.84e-01
266	15	1.1	296 18	AA307835	EST17869 Aorta endothe	1.65e+01	339	16	1.1	338 10	R35292	Yg62c10.r1 Homo sapien	1.65e+01
267	15	1.1	296 16	AA159039	zo57e01.s1 Stratagene	1.65e+01	340	15	1.1	339 18	AA327941	EST31374 Embryo, 12 we	6.84e-01
268	15	1.1	296 19	AA360788	EST69986 T-cell lympho	1.65e+01	341	15	1.1	339 16	AA194003	rs10g11.r1 Sommer Pris	1.65e+01
269	16	1.1	297 13	HSC3GA041	H. sapiens partial CDN	6.84e-01	342	15	1.1	339 12	H56449	Yq98g10.s1 Homo sapien	1.65e+01
270	16	1.1	297 18	HA333428	EST11371 Uterus Homo s	6.84e-01	343	15	1.1	339 9	T07190	EST05079 Homo sapiens	1.65e+01
271	16	1.1	298 12	H84296	ys95d12.r1 Homo sapien	6.84e-01	344	15	1.1	339 22	AA438069	ve48f06.r1 Beddington	6.84e-01
272	16	1.1	298 18	AA298142	mb40a07.r1 Soares mous	6.84e-01	345	15	1.1	340 23	AA518591	vh94h06.r1 Barstead mo	1.65e+01
273	16	1.1	298 14	W08119	C.elegans CDNA clone Y	6.84e-01	346	16	1.1	340 22	AA442600	zv57h02.r1 Soares test	1.65e+01
274	16	1.1	300 22	C08313	C.elegans CDNA clone Y	1.65e+01	347	16	1.1	341 20	HUMSWS3352	human chromosome 7 STS	1.65e-01
275	15	1.1	300 10	R08512	ye95h06.r1 Homo sapien	1.65e+01	348	15	1.1	341 21	B23035	F24N8TR IGF Arabidopsis	1.65e+01
276	15	1.1	302 22	C15349	Human fetal brain CDNA	6.84e-01	349	15	1.1	343 23	RICSI1805A	Rice CDNA, partial seq	6.84e-01
277	15	1.1	304 10	R26732	yh51f01.s1 Homo sapien	1.65e+01	350	16	1.1	343 12	AA354608	EST62897 Jurkat T-cell	1.65e+01
278	15	1.1	304 13	HSE20E012	H. sapiens partial CDN	1.65e+01	351	16	1.1	344 11	G05527	human STS WI-6040.	6.84e-01
279	15	1.1	304 18	AA312960	EST183820 Pancreas tum	1.65e+01	352	16	1.1	344 20	T27939	EST20790 Homo sapiens	1.65e+01
280	15	1.1	305 11	H51043	YP84d10.s1 Homo sapien	1.65e+01	353	15	1.1	344 9	T93787	ye05d07.s1 Homo sapien	1.65e+01
281	15	1.1	305 16	AA055893	yf43h12.r1 Homo sapien	1.65e+01	354	15	1.1	344 21	B69737	CIT-HSP-228K3.TF CIT-H	6.84e-01
282	15	1.1	307 12	N36917	mm29e07.r1 Stratagene	6.84e-01	355	16	1.1	345 15	AA097679	EST53717 Fetal heart I	1.65e+01
283	16	1.1	307 14	W76723	me66b09.r1 Soares mous	6.84e-01	356	15	1.1	347 18	AA347422	C.elegans CDNA clone Y	6.84e-01
284	16	1.1	307 12	N36917	YY38c07.s1 Homo sapien	1.65e+01	357	16	1.1	347 22	C10007	va65h10.r1 Soares mous	6.84e-01
285	15	1.1	307 23	AA464189	zx83g05.s1 Soares ovar	1.65e+01	358	15	1.1	347 19	AA270513	Citrus CDNA, partial s	1.65e+01
286	15	1.1	308 16	AA001137	EST85569 HSC172 cells	6.84e-01	359	15	1.1	348 10	R68402	Yh99h08.r1 Homo sapien	1.65e+01
287	15	1.1	308 19	AA373501	ze48a02.r1 Soares reti	1.65e+01	360	16	1.1	349 13	HSC1FH091	H. sapiens partial CDN	6.84e-01
288	15	1.1	308 17	AA248148	csq0618.seq.F Human fe	1.65e+01	361	15	1.1	349 16	AA057139	zf60a07.r1 Soares reti	1.65e+01
289	15	1.1	309 13	HSC2FH072	H. sapiens partial CDN	1.65e+01	362	15	1.1	350 22	AA435026	ve06b05.r1 Soares mous	6.84e-01
290	15	1.1	309 17	HSC1IH011	mw23d03.r1 Soares mous	1.65e+01	363	15	1.1	351 13	FR0021096	F. rubripes GSS sequenc	1.65e+01
291	15	1.1	310 19	AA361579	EST70954 T-cell lympho	6.84e-01	364	15	1.1	351 13	ATRS2521	A. thaliana transcribe	1.65e+01
292	15	1.1	310 17	AA174960	ms88d07.r1 Soares mous	6.84e-01	365	15	1.1	352 9	R03086	pk03f11.r1 Caenorhabdi	1.65e+01
293	15	1.1	311 22	C15673	Human fetal brain CDNA	6.84e-01	366	16	1.1	352 12	N44209	YY52d11.r1 Homo sapien	6.84e-01
294	16	1.1	315 18	AA344780	EST37843 Embryo, 9 wee	1.65e+01	367	15	1.1	353 20	G03535	STS hl4a618 5.	1.65e+01
295	16	1.1	318 10	R06620	EST50701 Gall bladder	6.84e-01	368	15	1.1	353 16	AA057798	human STS WI-2058.	6.84e-01
296	15	1.1	319 23	RICCI0064A	Rice CDNA, partial seq	1.65e+01	369	15	1.1	353 9	T37407	EST102524 Saccharomyce	1.65e+01
297	15	1.1	320 22	AA438188	ve63c11.r1 Beddington	6.84e-01	370	15	1.1	353 17	AA117492	mp84f09.r1 Soares feta	1.65e+01
298	16	1.1	321 13	HSC1MH031	H. sapiens partial CDN	6.84e-01	371	15	1.1	354 12	H85911	z671e06.s1 Soares feta	1.65e+01
299	16	1.1	322 13	W33740	mc54h08.r1 Soares mous	6.84e-01	372	15	1.1	355 12	H71307	Ys95b08.r1 Homo sapien	6.84e-01
300	15	1.1	323 20	G17561	human STS SHGC-6690 cl	1.65e+01	373	15	1.1	355 18	AA298268	EST114123 Prostate gla	1.65e+01
301	15	1.1	323 12	H90195	YU85d05.r1 Homo sapien	1.65e+01	374	15	1.1	356 14	AA008503	mg86b07.r1 Soares mous	6.84e-01
302	15	1.1					375	15	1.1				
303	16	1.1					376	16	1.1				
304	16	1.1					377	15	1.1				
305	16	1.1					378	15	1.1				
306	15	1.1					379	16	1.1				
307	15	1.1					380	15	1.1				

C	381	16	1.1	356 10	R76032	Yi60a07.r1 Homo sapien	6.84e-01	454	16	1.1	383 14	AA050766	mj16c06.r1 Soares mous	6.84e-01
C	382	16	1.1	356 19	AA033705	zk20a07.s1 Soares preg	6.84e-01	455	15	1.1	383 10	R49981	Yj56f06.s1 Homo sapien	1.65e+01
C	383	16	1.1	357 13	W33525	mc52b05.r1 Soares mous	6.84e-01	456	15	1.1	383 11	H08432	Yl89a06.r1 Homo sapien	1.65e+01
C	384	16	1.1	357 18	AA332236	EST36146 Embryo, 8 wee	6.84e-01	457	15	1.1	384 23	AA451108	Yf87f12.r1 Soares mous	1.65e+01
C	385	15	1.1	357 11	H19765	yn55e10.s1 Homo sapien	1.65e+01	458	15	1.1	384 9	T09604	0194m3 Plasmodium falc	1.65e+01
C	386	15	1.1	357 15	AA094643	cp0942.seq.F Fetal hea	1.65e+01	459	15	1.1	384 15	W477412	zc35e01.s1 Soares sene	1.65e+01
C	387	16	1.1	359 22	C06950	similar fo insulin 1.	6.84e-01	460	15	1.1	384 10	R54118	Yg98a03.r1 Homo sapien	1.65e+01
C	388	15	1.1	359 11	M77933	EST01517 Homo sapiens	1.65e+01	461	15	1.1	385 15	R89879	mf77e02.r1 Soares mous	1.65e+01
C	389	15	1.1	359 9	T79619	Yd71e09.s1 Homo sapien	1.65e+01	462	16	1.1	385 11	R83917	Yp06g09.s1 Homo sapien	6.84e-01
C	390	15	1.1	359 14	AA050307	mj12b07.r1 Soares mous	1.65e+01	463	15	1.1	385 21	FR0005835	F.rubripes GSS sequenc	1.65e+01
C	391	16	1.1	360 18	AA324493	EST27612 Cerebellum II	6.84e-01	464	15	1.1	385 11	H43433	Yp09f10.r1 Homo sapien	1.65e+01
C	392	15	1.1	360 18	AA302095	EST15206 Aorta endothe	1.65e+01	465	15	1.1	385 17	AA243300	zr26h03.r1 Stratagene	1.65e+01
C	393	15	1.1	360 22	CEIK094B1F	C.elegans CDNA clone Y	1.65e+01	466	15	1.1	385 22	HUM079A05A	Human fetal brain cDNA	1.65e+01
C	394	15	1.1	360 22	CEIK051E6F	C.elegans CDNA clone Y	1.65e+01	467	16	1.1	386 15	W83783	zn68h10.s1 Stratagene	6.84e-01
C	395	16	1.1	360 22	CEIK103H2F	C.elegans CDNA clone Y	6.84e-01	468	16	1.1	386 15	W83783	mf33a03.r1 Soares mous	6.84e-01
C	396	16	1.1	360 22	CEIK090H2F	C.elegans CDNA clone Y	6.84e-01	469	16	1.1	386 11	H20456	yn61c11.r1 Homo sapien	6.84e-01
C	397	16	1.1	360 22	CEIK052B6F	C.elegans CDNA clone Y	6.84e-01	470	16	1.1	387 19	AA148882	z127a09.r1 Soares preg	6.84e-01
C	398	16	1.1	360 22	CEIK116E9F	C.elegans CDNA clone Y	6.84e-01	471	15	1.1	387 10	R40685	Yf79h12.s1 Homo sapien	1.65e+01
C	399	16	1.1	360 9	T60831	Yb70f06.r1 Homo sapien	6.84e-01	472	15	1.1	388 15	AA120307	mn16h08.r1 Beddington	1.65e+01
C	400	16	1.1	360 22	CEIK103G3F	C.elegans CDNA clone Y	6.84e-01	473	16	1.1	389 22	CEIK027C2R	C.elegans CDNA clone Y	6.84e-01
C	401	15	1.1	360 22	CEIK035A4F	C.elegans CDNA clone Y	1.65e+01	474	15	1.1	389 10	R41283	Yf85e04.s1 Homo sapien	1.65e+01
C	402	15	1.1	361 10	R80207	Yi92g06.s1 Homo sapien	1.65e+01	475	15	1.1	389 21	B53168	CIT-HSP-2009B6.TF CIT-	1.65e+01
C	403	15	1.1	361 13	N78825	zb17a01.s1 Homo sapien	1.65e+01	476	16	1.1	390 13	W33605	mc53h01.r1 Soares mous	6.84e-01
C	404	15	1.1	361 23	AA455186	zx79e02.r1 Soares ovar	1.65e+01	477	15	1.1	390 17	AA144490	mr17d10.r1 Soares mous	1.65e+01
C	405	16	1.1	362 17	AA250510	mw99e01.r1 Soares mous	6.84e-01	478	15	1.1	390 12	N51734	Yz01a01.s1 Homo sapien	1.65e+01
C	406	15	1.1	362 14	AA051444	mj51a09.r1 Soares mous	1.65e+01	479	15	1.1	391 9	T81054	Yd26c04.r1 Homo sapien	1.65e+01
C	407	16	1.1	363 11	AA346307	EST52430 Greater oment	6.84e-01	480	15	1.1	391 13	W39059	zb34c02.r1 Soares para	1.65e+01
C	408	16	1.1	363 18	H42280	yo63d01.r1 Homo sapien	6.84e-01	481	16	1.1	392 18	AA273695	va23b07.r1 GuayWoodfor	6.84e-01
C	409	15	1.1	364 9	T83653	Yd67b09.s1 Homo sapien	1.65e+01	482	16	1.1	392 10	R30916	Yh59g03.r1 Homo sapien	6.84e-01
C	410	15	1.1	364 11	T36285	EST99724 Homo sapiens	1.65e+01	483	15	1.1	392 10	R30916	Yg66a06.r1 Homo sapien	1.65e+01
C	411	16	1.1	365 19	AA376939	EST89427 Small intesti	6.84e-01	484	15	1.1	392 16	AA064541	ml40e06.r1 Stratagene	6.84e-01
C	412	16	1.1	365 14	W64980	me04a06.r1 Soares mous	6.84e-01	485	16	1.1	393 20	HS247ZD9	H.sapiens (D6S1581) DN	6.84e-01
C	413	16	1.1	365 11	R83526	Yp15h01.r1 Homo sapien	6.84e-01	486	16	1.1	393 11	H53447	Yt86d11.s1 Homo sapien	6.84e-01
C	414	16	1.1	367 14	W35018	mc35a06.r1 Soares mous	6.84e-01	487	16	1.1	394 15	W60572	zd26g06.r1 Soares feta	6.84e-01
C	415	15	1.1	367 9	T83643	Yd67a07.s1 Homo sapien	1.65e+01	488	16	1.1	394 15	AA119687	mo27g02.r1 Life Tech m	6.84e-01
C	416	16	1.1	368 15	AA093070	mm0450.seq.F Fetal hea	6.84e-01	489	15	1.1	394 12	H82534	Ys69f12.s1 Homo sapien	1.65e+01
C	417	16	1.1	368 9	T60780	Yb70f06.s1 Homo sapien	6.84e-01	490	16	1.1	395 20	HUMSWS3726	human chromosome 7 STS	6.84e-01
C	418	15	1.1	368 23	AA530207	Vj46g07.r1 Stratagene	1.65e+01	491	16	1.1	395 18	AA270719	va67d01.r1 Soares mous	6.84e-01
C	419	16	1.1	370 9	T82209	Yd95g09.r1 Homo sapien	6.84e-01	492	16	1.1	395 22	HS269XG5	C.elegans CDNA clone Y	6.84e-01
C	420	16	1.1	370 14	W66652	me25e09.r1 Soares mous	6.84e-01	493	16	1.1	395 20	HS269XG5	H.sapiens (D19S409) D	6.84e-01
C	421	15	1.1	370 16	AA199576	zq75e07.s1 Stratagene	1.65e+01	494	15	1.1	395 11	H16694	Ym26e10.s1 Homo sapien	1.65e+01
C	422	15	1.1	370 23	AA474477	vd55d09.r1 Knowles SOL	1.65e+01	495	15	1.1	395 11	H40890	Yn93d06.s1 Homo sapien	1.65e+01
C	423	16	1.1	371 11	T33074	EST56584 Homo sapiens	6.84e-01	496	16	1.1	395 13	N68339	za67a12.s1 Homo sapien	6.84e-01
C	424	16	1.1	371 17	AA235733	zt32b06.s1 Soares ovar	6.84e-01	497	16	1.1	396 22	C06974	similar to insulin 1.	6.84e-01
C	425	16	1.1	372 22	T18830	Human placenta CDNA 5'	6.84e-01	498	16	1.1	396 16	AA018660	ze53f10.r1 Soares reti	6.84e-01
C	426	16	1.1	372 19	T25336	EST191R BL29 Burkitt's	6.84e-01	499	16	1.1	396 10	R51527	Yg72e12.r1 Homo sapien	6.84e-01
C	427	16	1.1	373 14	W55652	mc07d04.r1 Soares mous	6.84e-01	500	15	1.1	396 9	T08896	EST06788 Homo sapiens	1.65e+01
C	428	15	1.1	373 15	AA115597	z105h09.s1 Soares preg	1.65e+01	501	16	1.1	397 16	C06806	zh48c07.r1 Soares feta	6.84e-01
C	429	16	1.1	373 10	R76810	Y162f02.s1 Homo sapien	6.84e-01	502	15	1.1	397 22	C06806	similar to insulin1.	6.84e-01
C	430	15	1.1	374 23	AA386975	Rice CDNA, partial seq	1.65e+01	503	16	1.1	398 14	W08066	mb39d11.r1 Soares mous	6.84e-01
C	431	15	1.1	374 19	AA445247	vc81f05.r1 Ko mouse em	1.65e+01	504	16	1.1	398 9	T78615	Yd69d11.s1 Homo sapien	6.84e-01
C	432	15	1.1	374 23	AA445247	vf62c11.r1 Barstead MP	1.65e+01	505	15	1.1	398 13	W52257	zc46c12.s1 Soares sene	1.65e+01
C	433	16	1.1	374 11	H50445	Y029g12.s1 Homo sapien	6.84e-01	506	16	1.1	399 19	AA351232	EST58927 Infant brain	6.84e-01
C	434	16	1.1	375 19	HSPD04451	H.sapiens EST sequence	6.84e-01	507	16	1.1	399 17	AA105818	mp47d12.r1 Barstead MP	6.84e-01
C	435	15	1.1	375 14	W80291	me90c02.r1 Soares mous	1.65e+01	508	15	1.1	399 14	W33970	mb57b06.r1 Soares mous	1.65e+01
C	436	15	1.1	375 9	T01972	WEST02693 Caenorhabdit	1.65e+01	509	15	1.1	399 19	HSPD06803	H.sapiens EST sequence	1.65e+01
C	437	16	1.1	376 22	C09096	C.elegans CDNA clone Y	6.84e-01	510	15	1.1	399 19	AA031841	zk17a04.r1 Soares preg	1.65e+01
C	438	16	1.1	376 17	AA253984	va10a04.r1 Soares mous	6.84e-01	511	15	1.1	399 19	AA407230	EST02225 Mouse 7.5 dpc	1.65e+01
C	439	16	1.1	377 16	AA212155	mu80h08.r1 Stratagene	6.84e-01	512	15	1.1	400 20	G14303	human STS SHGC-8334 cl	6.84e-01
C	440	16	1.1	377 15	AA188617	zp78c10.s1 Stratagene	6.84e-01	513	15	1.1	400 23	AA471241	PMY2235 KGIa Lambda za	1.65e+01
C	441	15	1.1	377 10	R80304	Y192f05.r1 Homo sapien	1.65e+01	514	15	1.1	400 20	G18186	Yh52b01.s1 Homo sapien	1.65e+01
C	442	15	1.1	378 11	H09467	Y197g05.r1 Homo sapien	1.65e+01	515	15	1.1	400 16	AA021500	human STS SHGC-14358 c	1.65e+01
C	443	15	1.1	378 10	R26425	Yh47d09.r1 Homo sapien	1.65e+01	516	15	1.1	400 16	AA181109	zp67c12.s1 Stratagene	1.65e+01
C	444	16	1.1	379 9	M89353	CEIK21F12 Caenorhabditi	6.84e-01	517	15	1.1	401 10	R34187	Yh84c08.r1 Homo sapien	1.65e+01
C	445	16	1.1	380 22	CEIK039D8R	C.elegans CDNA clone Y	6.84e-01	518	15	1.1	401 20	HUMSWX740	human chromosome X STS	1.65e+01
C	446	15	1.1	380 14	R58865	NIB2056 Normalized inf	1.65e+01	519	15	1.1	401 9	R01195	Ye77e02.s1 Homo sapien	6.84e-01
C	447	15	1.1	381 10	R78640	Yi74f07.s1 Homo sapien	1.65e+01	520	16	1.1	402 18	AA271231	Yb73e03.r1 Soares mous	1.65e+01
C	448	15	1.1	381 10	R44401	Yg36h08.s1 Homo sapien	1.65e+01	521	16	1.1	403 14	AA002772	mg45e10.r1 Soares mous	6.84e-01
C	449	16	1.1	382 14	AA002809	mg56e05.r1 Soares mous	6.84e-01	522	16	1.1	403 14	AA002772	zw68b11.s1 Soares test	1.65e+01
C	450	15	1.1	382 21	FR0018699	F.rubripes GSS sequenc	1.65e+01	523	15	1.1	403 23	AA448396	Yz91e07.r1 Homo sapien	6.84e-01
C	451	15	1.1	382 13	N75409	za82d02.s1 Homo sapien	1.65e+01	524	16	1.1	404 12	N80324	Yx48c05.r1 Homo sapien	1.65e+01
C	452	16	1.1	382 12	H58757	EST00052 Homo sapiens	6.84e-01	525	15	1.1	404 13	N30465	Yg88b09.r1 Homo sapien	6.84e-01
C	453	15	1.1	382 16	W86590	zh62e10.s1 Soares feta	1.65e+01	526	16	1.1	405 10	R55659		

C	527	15	1.1	405	19	AA354702	EST62999 Jurkat T-cell	1.65e+01	600	16	1.1	428	22	C06536	similar to insulin 1.	6.84e-01
C	528	15	1.1	405	11	R86003	yp12c03.r1 Homo sapien	1.65e+01	601	15	1.1	428	15	AA113269	zn69c03.s1 Stratagene	1.65e+01
C	529	16	1.1	406	19	AA413038	ve52b03.r1 Beddington	6.84e-01	602	15	1.1	428	15	AA130034	zo40h12.s1 Stratagene	1.65e+01
C	530	16	1.1	406	11	T24171	crs159 Ricinus communi	6.84e-01	603	15	1.1	428	14	AA050793	mg73b07.r1 Soares mous	1.65e+01
C	531	16	1.1	406	23	AA448007	zw82h05.s1 Soares test	6.84e-01	604	15	1.1	428	15	AA037104	zc51a10.r1 Soares sene	1.65e+01
C	532	16	1.1	406	15	AA146711	zo35e10.r1 Stratagene	6.84e-01	605	15	1.1	429	10	R06278	yf08f01.s1 Homo sapien	1.65e+01
C	533	15	1.1	406	15	w72390	zd66h05.s1 Soares feta	1.65e+01	606	15	1.1	429	15	w39735	zc19e12.r1 Soares para	1.65e+01
C	534	15	1.1	407	16	AA160391	zo64b03.r1 Stratagene	1.65e+01	607	16	1.1	429	22	C06642	similar to insulin 1.	6.84e-01
C	535	16	1.1	407	13	M69887	za68c05.s1 Homo sapien	6.84e-01	608	16	1.1	430	15	AA084480	zf77f06.r1 Soares pine	6.84e-01
C	536	15	1.1	408	10	T94350	ye35b12.s1 Homo sapien	1.65e+01	609	15	1.1	430	22	AA147619	z152d01.s1 Soares preg	1.65e+01
C	537	15	1.1	408	15	R33804	yh78c10.r1 Homo sapien	1.65e+01	610	15	1.1	431	16	AA121792	zn72e06.s1 Stratagene	1.65e+01
C	538	16	1.1	409	15	AA127416	zn90h12.r1 Stratagene	6.84e-01	611	16	1.1	431	17	AA224285	zr15a12.r1 Stratagene	6.84e-01
C	539	16	1.1	409	18	AA274499	vb02b08.r1 Soares mous	6.84e-01	612	15	1.1	431	12	N35598	yy25d06.s1 Homo sapien	1.65e+01
C	540	16	1.1	409	11	H50024	yo26c03.r1 Homo sapien	6.84e-01	613	15	1.1	431	12	H66715	yr83b12.r1 Homo sapien	1.65e+01
C	541	15	1.1	409	20	G22920	human STS WI-13765.	1.65e+01	614	15	1.1	431	21	B51074	CIT978SK-40N21.TV CIT9	1.65e+01
C	542	16	1.1	410	16	AA097319	mm36b08.r1 Stratagene	6.84e-01	615	15	1.1	431	15	w69734	zc51a05.r1 Soares feta	1.65e+01
C	543	16	1.1	410	23	AA466189	vg88c12.r1 Barstead mo	6.84e-01	616	15	1.1	431	23	AA452105	zx15b01.s1 Soares tota	1.65e+01
C	544	15	1.1	410	23	AA112687	zn70c09.r1 Stratagene	1.65e+01	617	16	1.1	432	21	B53450	CIT-HSP-2010K3.TR CIT-	6.84e-01
C	545	16	1.1	411	23	AA499144	vi84h02.r1 Stratagene	6.84e-01	618	15	1.1	432	13	N70611	za77g10.s1 Homo sapien	1.65e+01
C	546	16	1.1	411	12	NA9281	yv23a12.s1 Homo sapien	6.84e-01	619	15	1.1	433	22	C07008	similar to insulin 1.	1.65e+01
C	547	15	1.1	411	14	w98762	mg09b09.r1 Soares mous	1.65e+01	620	16	1.1	434	22	C06831	similar to insulin 1.	6.84e-01
C	548	16	1.1	411	10	R07241	yl14e04.r1 Homo sapien	6.84e-01	621	16	1.1	434	11	H47100	yp77c03.s1 Homo sapien	6.84e-01
C	549	16	1.1	412	23	AA472305	vh01d03.r1 Soares mous	6.84e-01	622	15	1.1	435	22	CELK006C7R	C.elegans cDNA clone Y	1.65e+01
C	550	16	1.1	412	22	C06600	similar to insulin 1.	6.84e-01	623	15	1.1	435	12	N49098	yy79f02.s1 Homo sapien	1.65e+01
C	551	15	1.1	412	12	H63392	yr53b04.s1 Homo sapien	1.65e+01	624	16	1.1	435	19	AA047333	zk69c10.s1 Soares preg	6.84e-01
C	552	16	1.1	412	13	N77808	zb16a05.s1 Homo sapien	6.84e-01	625	15	1.1	435	15	AA104532	mc046d12.r1 Life Tech m	1.65e+01
C	553	15	1.1	412	14	AA051775	mj54h12.r1 Soares mous	1.65e+01	626	15	1.1	435	10	R64253	yl21c03.r1 Homo sapien	1.65e+01
C	554	15	1.1	413	11	R94945	yq44b02.s1 Homo sapien	1.65e+01	627	15	1.1	435	10	R62422	yg52b12.s1 Homo sapien	1.65e+01
C	555	16	1.1	414	22	AA405645	zw39e10.r1 Soares tota	6.84e-01	628	15	1.1	435	15	w39223	zc16c05.r1 Soares para	1.65e+01
C	556	15	1.1	414	21	B58980	CIT-HSP-2014123.TR CIT	1.65e+01	629	16	1.1	436	21	FR0004011	F.rubripes GSS sequenc	6.84e-01
C	557	15	1.1	414	14	N91428	za16f04.r1 Soares feta	1.65e+01	630	15	1.1	436	19	AA029151	zk09e08.r1 Soares preg	1.65e+01
C	558	15	1.1	414	14	w24110	zb48h02.r1 Soares feta	1.65e+01	631	15	1.1	438	15	w37585	zc10e05.r1 Soares para	1.65e+01
C	559	15	1.1	415	20	G21242	human STS WI-16237.	1.65e+01	632	15	1.1	438	16	AA199554	zg67h11.r1 Stratagene	1.65e+01
C	560	16	1.1	415	22	C06513	similar to insulin 1.	6.84e-01	633	15	1.1	438	16	AA205620	mu41h10.r1 Soares sene	1.65e+01
C	561	15	1.1	415	14	AA000503	mg23e03.r1 Soares mous	1.65e+01	634	16	1.1	439	17	AA210355	zb37d02.r1 Soares para	6.84e-01
C	562	16	1.1	415	14	w18514	mb88e08.r1 Soares mous	1.65e+01	635	16	1.1	439	13	w19610	yl88b10.r1 Homo sapien	1.65e+01
C	563	16	1.1	415	14	N90190	za65h12.s1 Soares feta	6.84e-01	636	15	1.1	439	11	H08631	yl15d04.s1 Homo sapien	1.65e+01
C	564	16	1.1	416	21	B40238	HS-1051-A1-F12-MF.abi	6.84e-01	637	15	1.1	439	11	H26296	yp20g09.r1 Homo sapien	6.84e-01
C	565	16	1.1	416	10	R79893	yi85d01.r1 Homo sapien	6.84e-01	638	16	1.1	440	11	H44781	Human STS UT5170.	6.84e-01
C	566	15	1.1	416	13	w35967	mc58a12.r1 Soares mous	1.65e+01	639	16	1.1	440	20	wuMUT5170	za73b08.r1 Soares feta	1.65e+01
C	567	16	1.1	416	15	AA082169	zn42g03.r1 Stratagene	6.84e-01	640	15	1.1	440	13	H01434	zb86d06.s1 Soares sene	1.65e+01
C	568	15	1.1	416	15	AA408602	EST03072 Mouse 7.5 dpc	1.65e+01	641	15	1.1	440	14	N98497	zg94d06.r1 Stratagene	1.65e+01
C	569	15	1.1	417	17	AA110977	mp57d09.r1 Soares 2NbM	1.65e+01	642	15	1.1	440	16	AA216544	mw34b02.r1 GuyWoodfor	6.84e-01
C	570	15	1.1	417	10	R56445	yg90h11.s1 Homo sapien	1.65e+01	643	16	1.1	441	17	AA2140361	CELI18B Caenorhabditis	6.84e-01
C	571	16	1.1	417	13	w44127	mc74b01.r1 Soares mous	1.65e+01	644	16	1.1	441	9	M89173	zc32b02.s1 Soares sene	1.65e+01
C	572	16	1.1	417	16	AA061149	ml39g10.r1 Stratagene	6.84e-01	645	15	1.1	441	15	w46436	zk02c03.s1 Soares preg	6.84e-01
C	573	16	1.1	418	22	C06840	similar to insulin 1.	6.84e-01	646	16	1.1	441	19	AA026958	CIT978SK-A-240E10.TPC	6.84e-01
C	574	16	1.1	419	19	AA010275	zi08g07.r1 Soares feta	6.84e-01	647	16	1.1	442	14	AA038405	mi90g11.r1 Soares mous	6.84e-01
C	575	16	1.1	419	23	AA444179	ve34a12.r1 Ko mouse em	6.84e-01	648	16	1.1	442	14	AA038405	A. thaliana transcribe	6.84e-01
C	576	16	1.1	420	15	AA015788	ze30a09.r1 Soares reti	6.84e-01	649	16	1.1	442	13	ATTS1730	za68c05.r1 Homo sapien	6.84e-01
C	577	15	1.1	420	10	R31674	yh63b09.s1 Homo sapien	1.65e+01	650	16	1.1	442	13	N98860	zt24c07.s1 Soares ovar	1.65e+01
C	578	15	1.1	420	23	AA443069	aa83g03.r1 Homo sapien	1.65e+01	651	16	1.1	442	10	W98469	yg90b04.r1 Homo sapien	6.84e-01
C	579	16	1.1	420	12	H89808	yu82g03.r1 Homo sapien	6.84e-01	652	15	1.1	442	11	H20953	yn66a03.s1 Homo sapien	1.65e+01
C	580	16	1.1	421	22	C07149	similar to insulin 1.	6.84e-01	653	16	1.1	442	10	AA284783	zl14e12.r1 Soares preg	6.84e-01
C	581	15	1.1	421	12	H89348	yw28c02.s1 Homo sapien	1.65e+01	654	15	1.1	442	14	w98469	zm19h04.r1 Soares mous	6.84e-01
C	582	15	1.1	421	20	G29779	human STS SHGC-35222.	1.65e+01	655	15	1.1	442	11	H20953	yn66a03.s1 Homo sapien	1.65e+01
C	583	15	1.1	421	12	H90900	yu89d02.s1 Homo sapien	1.65e+01	656	16	1.1	443	13	w05113	za82d05.r1 Soares feta	6.84e-01
C	584	15	1.1	421	10	R18056	yg15c09.r1 Homo sapien	1.65e+01	657	16	1.1	443	10	R49625	yg61f03.s1 Homo sapien	1.65e+01
C	585	15	1.1	422	10	R69218	yi39h02.r1 Homo sapien	1.65e+01	658	15	1.1	443	10	R67171	yh08c07.r2 Homo sapien	6.84e-01
C	586	16	1.1	423	23	AA512051	vj43b02.r1 Stratagene	6.84e-01	659	16	1.1	443	10	AA136777	zk99d05.r1 Soares preg	6.84e-01
C	587	16	1.1	423	12	N45385	yw97c07.r1 Homo sapien	1.65e+01	660	16	1.1	444	19	w62614	md58d03.r1 Soares mous	1.65e+01
C	588	15	1.1	423	16	AA189120	zi04c03.s1 Soares feta	6.84e-01	661	16	1.1	445	14	w36380	mb83d09.r1 Soares preg	6.84e-01
C	589	16	1.1	423	19	AA009768	zo40h12.r1 Stratagene	1.65e+01	662	15	1.1	446	14	AA040355	zk45f09.s1 Soares mous	1.65e+01
C	590	15	1.1	423	15	AA130033	zc19e12.s1 Soares para	6.84e-01	663	15	1.1	446	17	AA267883	va18h05.r1 Soares mous	6.84e-01
C	591	16	1.1	424	15	w15307	mc47g02.r1 Soares mous	6.84e-01	664	16	1.1	447	13	w16766	zb16a05.r1 Soares feta	6.84e-01
C	592	16	1.1	425	14	w41315	similar to insulin 1.	6.84e-01	665	15	1.1	447	14	w35782	mc15b06.r1 Soares mous	1.65e+01
C	593	16	1.1	425	22	C06514	mh96b12.r1 Soares mous	1.65e+01	666	15	1.1	447	12	N25314	yz52g11.s1 Homo sapien	1.65e+01
C	594	16	1.1	425	16	AA024089	EST02433 Mouse 7.5 dpc	1.65e+01	667	15	1.1	447	19	AA042972	zk56d06.r1 Soares preg	6.84e-01
C	595	15	1.1	426	19	AA407759	mjl0f09.r1 Soares mous	1.65e+01	668	15	1.1	447	23	AA463306	zx77d04.r1 Soares tota	6.84e-01
C	596	15	1.1	427	14	AA050122	H.sapiens EST sequence	1.65e+01	669	16	1.1	447	23	AA389197	mp18g09.r1 Life Tech m	1.65e+01
C	597	15	1.1	427	19	HSPD05187	zp75d02.s1 Stratagene	1.65e+01	670	15	1.1	448	13	N56728	yp76f06.r1 Homo sapien	1.65e+01
C	598	15	1.1	427	16	AA187949	HS-1017-A1-D02-MF.abi	6.84e-01	671	15	1.1	448	13	H39840	yp01g09.r1 Homo sapien	1.65e+01
C	599	16	1.1	427	21	B33306			672	15	1.1	448	11			

673	15	1.1	448 17	AA237687	mx29e04.r1	Soares	mous	1.65e+01	746	15	1.1	467 13	N75449	za83a07.s1	Homo sapien	1.65e+01	
674	15	1.1	448 12	N34960	yy50c12.s1	Homo sapien		1.65e+01	747	16	1.1	468 17	AA265813	mz71d08.r1	Soares	mous	6.84e-01
675	16	1.1	448 9	T98279	ye59f02.s1	Homo sapien		6.84e-01	748	15	1.1	468 12	H80390	yu59g01.r1	Homo sapien		1.65e+01
676	16	1.1	448 17	AA170275	ms82e11.r1	Soares	mous	6.84e-01	749	15	1.1	468 15	W79682	zd73g04.r1	Soares	feta	1.65e+01
677	16	1.1	448 18	AA312749	EST183435	Jurkat T-ce1		6.84e-01	750	16	1.1	468 16	AA026394	ze92d04.s1	Soares	feta	6.84e-01
678	15	1.1	448 21	B23356	F28J3TR	IGF Arabidopsi		1.65e+01	751	15	1.1	468 13	ATTS1725	A. thaliana	transcribe		1.65e+01
679	15	1.1	448 11	R93056	yq13b08.s1	Homo sapien		1.65e+01	752	16	1.1	469 13	N74136	za76a01.s1	Homo sapien		6.84e-01
680	15	1.1	448 14	AA034623	mi53g05.r1	Soares	mous	1.65e+01	753	16	1.1	469 20	G30645	human STS	SHGC-37694.		6.84e-01
681	16	1.1	449 23	AA469742	vi70b04.r1	Barstead mo		6.84e-01	754	16	1.1	470 17	AA261657	mz87f11.r1	Soares	mous	6.84e-01
682	16	1.1	449 9	T81634	yd34b07.r1	Homo sapien		6.84e-01	755	16	1.1	470 17	AA123438	mp91d07.r1	Soares	2NbM	6.84e-01
683	16	1.1	449 12	H85673	ys68a03.r1	Homo sapien		6.84e-01	756	15	1.1	470 14	N94350	zb75g08.s1	Soares	sene	1.65e+01
684	15	1.1	449 10	R61344	yh15a02.s1	Homo sapien		1.65e+01	757	15	1.1	470 14	AA015158	mi63b05.r1	Soares	mous	1.65e+01
685	15	1.1	450 12	N40785	yw62a07.r1	Homo sapien		1.65e+01	758	15	1.1	470 23	R1CS2523A	rice cDNA,	partial seq		1.65e+01
686	15	1.1	450 22	AA436147	zd49g05.s1	Soares	NhHM	6.84e-01	759	15	1.1	471 17	AA250039	mx21b04.r1	Soares	mous	1.65e+01
687	16	1.1	450 15	W70094	yb27h01.s1	Homo sapien		6.84e-01	760	16	1.1	472 11	H49315	yo21e09.r1	Homo sapien		6.84e-01
688	16	1.1	450 9	T51613	ESR48706	Homo sapiens		1.65e+01	761	16	1.1	473 12	H98810	yx17h09.s1	Homo sapien		6.84e-01
689	15	1.1	450 11	T28595	zf06e09.s1	Soares	feta	1.65e+01	762	16	1.1	473 10	R54715	yj78e10.r1	Homo sapien		6.84e-01
690	15	1.1	450 16	AA039477	CTF-HSP-469G4.TPB	CTF-		1.65e+01	763	15	1.1	473 22	AA442062	zw63a04.s1	Soares	tota	1.65e+01
691	15	1.1	450 21	B47562	mp39h02.r1	Barstead MP		6.84e-01	764	16	1.1	474 15	AA061554	mj91g07.r1	Soares	mous	1.65e+01
692	16	1.1	451 17	AA108823	yu11b08.s1	Homo sapien		6.84e-01	765	15	1.1	474 12	H98761	yx13b10.s1	Homo sapien		1.65e+01
693	16	1.1	451 12	H80132	ys11b08.s1	Homo sapien		6.84e-01	766	15	1.1	475 11	R94422	yg42e08.r1	Homo sapien		1.65e+01
694	15	1.1	451 15	AA016257	ze33d01.s1	Soares	retl	1.65e+01	767	15	1.1	475 17	AA232419	zf23d08.r1	Homo sapien		1.65e+01
695	16	1.1	452 22	C06788	similar to	insulin 1.		6.84e-01	768	15	1.1	476 11	H48370	yg69e05.r1	Homo sapien		1.65e+01
696	15	1.1	452 23	AA500137	vp08d08.r1	Homo sapien		6.84e-01	769	15	1.1	476 15	W84467	zd89g09.r1	Soares	feta	1.65e+01
697	16	1.1	452 11	R88121	zo22g04.s1	Stratagene		1.65e+01	770	15	1.1	476 11	H10253	ym02d01.r1	Homo sapien		1.65e+01
698	15	1.1	453 15	AA132935	me84e06.r1	Soares	mous	1.65e+01	771	16	1.1	477 13	W07358	za98g07.r1	Soares	feta	6.84e-01
699	15	1.1	453 14	W76773	mi24c11.r1	Soares	mous	1.65e+01	772	16	1.1	477 14	W61737	md63d11.r1	Soares	mous	6.84e-01
700	15	1.1	453 14	AA030436	yv75a05.r1	Homo sapien		1.65e+01	773	16	1.1	477 21	B43196	HS-1057-A2	A02-MR.abi		6.84e-01
701	15	1.1	453 13	N78217	ys10f02.r1	Homo sapien		1.65e+01	774	15	1.1	477 10	R31488	yh75e09.r1	Homo sapien		1.65e+01
702	15	1.1	453 12	H73247	zk69c10.r1	Soares	preg	6.84e-01	775	16	1.1	478 22	C05299	Human Heart	cDNA, c1on		6.84e-01
703	16	1.1	454 19	AA047332	va49b08.r1	Soares	mous	1.65e+01	776	15	1.1	478 9	T87522	yg89d09.r1	Homo sapien		1.65e+01
704	15	1.1	454 17	AA261641	zb95e04.s1	Soares	para	6.84e-01	777	15	1.1	479 21	B58726	CTF-HSP-2013N10.TP	CTF		1.65e+01
705	16	1.1	455 15	W31375	SW3ICA692SK	Brugia mal		6.84e-01	778	15	1.1	480 15	W89417	mf80a04.r1	Soares	mous	1.65e+01
706	16	1.1	455 16	N43256	va53c04.r1	Soares	mous	1.65e+01	779	15	1.1	481 12	N34475	yx13e07.s1	Homo sapien		1.65e+01
707	15	1.1	455 17	AA259932	EST187589	Colon carc1n		1.65e+01	780	15	1.1	481 19	AA114890	vb12c09.r1	Soares	preg	1.65e+01
708	15	1.1	455 18	AA315609	zk38a09.s1	Soares	preg	1.65e+01	781	15	1.1	482 18	AA288288	ze70e07.s1	Soares	feta	1.65e+01
709	15	1.1	457 14	AA037796	vall1a08.r1	Soares	mous	6.84e-01	782	15	1.1	482 16	AA022498	zo83a11.s1	Stratagene		1.65e+01
710	16	1.1	457 17	AA260573	z114e12.s1	Soares	preg	6.84e-01	783	15	1.1	482 16	AA159821	T22E19TR	TAMU Arabidop		6.84e-01
711	16	1.1	457 19	AA129931	yd12a02.s1	Homo sapien		1.65e+01	784	16	1.1	482 21	B62572	ym19c04.r1	Homo sapien		6.84e-01
712	15	1.1	457 9	T67438	RPu1401CG	Rat myometri		1.65e+01	785	15	1.1	482 21	B28488	T10A11TR	TAMU Arabidop		1.65e+01
713	15	1.1	457 14	AA012703	zo94g02.s1	Stratagene		6.84e-01	786	15	1.1	482 21	B34573	HS-1024-B2	G10-MR.abi		1.65e+01
714	15	1.1	458 22	AA433857	mj34h10.r1	Soares	mous	6.84e-01	787	15	1.1	482 13	W04965	mi44e02.r1	Soares	mous	1.65e+01
715	16	1.1	459 16	AA169305	zh85a02.s1	Soares	feta	6.84e-01	788	15	1.1	483 14	N76361	yz39h06.r1	Soares	feta	1.65e+01
716	16	1.1	460 14	AA049506	z137d04.s1	Soares	preg	1.65e+01	789	16	1.1	483 16	N933309	zb69d04.s1	Soares	feta	1.65e+01
717	16	1.1	460 14	AA002058	ze30f12.r1	Soares	retl	1.65e+01	790	15	1.1	484 14	N933309	mm56b07.r1	Stratagene		1.65e+01
718	15	1.1	460 19	AA131876	mq40a06.r1	Barstead MP		1.65e+01	791	15	1.1	484 15	AA059664	mx05a11.r1	Soares	2NbM	1.65e+01
719	15	1.1	460 15	AA015969	zh62b03.s1	Soares	feta	1.65e+01	792	16	1.1	484 15	AA051739	mf53b02.r1	Soares	mous	6.84e-01
720	15	1.1	460 17	AA139618	vb07b05.r1	Soares	mous	1.65e+01	793	16	1.1	485 16	AA067637	mw81c04.r1	Homo sapien		6.84e-01
721	15	1.1	460 16	W86627	mi44c02.r1	Soares	mous	6.84e-01	794	15	1.1	485 23	AA448943	mh30c11.r1	Soares	mous	6.84e-01
722	15	1.1	461 18	AA274968	yn68f10.r1	Homo sapien		6.84e-01	795	15	1.1	485 21	B58809	Human placenta	cDNA 5'		6.84e-01
723	16	1.1	462 14	AA033501	CTF-HSP-228M10.TPB	CTF		1.65e+01	796	15	1.1	485 17	AA116221	mf05b04.r1	Soares	mous	6.84e-01
724	16	1.1	462 11	H22426	zx63c01.s1	Soares	tota	1.65e+01	797	16	1.1	486 16	AA021966	mi11f07.r1	Soares	mous	6.84e-01
725	15	1.1	462 21	B71196	zc44g04.r1	Soares	sene	6.84e-01	798	16	1.1	487 13	AA051739	mf53b02.r1	Soares	mous	6.84e-01
726	15	1.1	462 23	AA460966	me79d07.r1	Soares	mous	6.84e-01	799	15	1.1	487 14	N57311	mw82458	similar to	insulin 1.	6.84e-01
727	15	1.1	463 15	W48828	me79d07.r1	Soares	mous	6.84e-01	800	16	1.1	488 22	C18868	yo04g10.s1	Homo sapien		1.65e+01
728	16	1.1	463 14	W78544	vg36c02.r1	Soares	mous	1.65e+01	801	16	1.1	489 14	AA049900	ze94c10.r1	Soares	feta	1.65e+01
729	15	1.1	463 23	AA510362	mi64b12.r1	Soares	mous	6.84e-01	802	15	1.1	489 16	W96940	zk61c06.r1	Soares	preg	1.65e+01
730	16	1.1	463 17	AA014539	ms96c07.r1	Soares	mous	6.84e-01	803	15	1.1	490 19	AA287222	mx21b04.r1	Soares	mous	1.65e+01
731	16	1.1	464 11	AA175581	crs377	R1c1nus communi		6.84e-01	804	15	1.1	491 15	W82458	yo21e09.r1	Homo sapien		6.84e-01
732	16	1.1	464 12	N30457	yx48b05.r1	Homo sapien		6.84e-01	805	16	1.1	491 12	C07167	mx21b04.r1	Soares	mous	1.65e+01
733	16	1.1	464 12	N30457	yp42e08.r1	Homo sapien		1.65e+01	806	16	1.1	491 12	H72771	yo04g10.s1	Homo sapien		1.65e+01
734	15	1.1	465 11	H30337	mb74c02.r1	Soares	mous	1.65e+01	807	15	1.1	492 16	AA029631	ze94c10.r1	Soares	feta	1.65e+01
735	15	1.1	465 14	W17565	zl96c06.r1	Stratagene		1.65e+01	808	15	1.1	492 12	N35193	zk61c06.r1	Soares	preg	1.65e+01
736	15	1.1	465 15	AA059402	vg18e10.r1	Soares	mous	1.65e+01	809	15	1.1	492 19	AA040610	mx21b04.r1	Soares	mous	1.65e+01
737	15	1.1	465 23	AA509397	yo78c09.r1	Homo sapien		6.84e-01	810	15	1.1	493 14	AA049168	zk61c06.r1	Soares	preg	1.65e+01
738	15	1.1	465 11	H30840	vg65a03.r1	Soares	mous	6.84e-01	811	16	1.1	493 16	AA181154	zk61c06.r1	Soares	preg	1.65e+01
739	16	1.1	466 23	AA461985	yy52d11.s1	Homo sapien		6.84e-01	812	15	1.1	493 15	AA097917	zk61c06.r1	Soares	preg	1.65e+01
740	16	1.1	466 12	N34316	zd37e01.r1	Soares	feta	1.65e+01	813	15	1.1	493 22	AA193287	zk61c06.r1	Soares	preg	1.65e+01
741	15	1.1	466 15	W68813	yh12b04.s1	Homo sapien		1.65e+01	814	15	1.1	493 9	T81695	zk61c06.r1	Soares	preg	1.65e+01
742	15	1.1	466 10	R60021	yl76f11.r1	Homo sapien		1.65e+01	815	15	1.1	493 21	AA306692	zk61c06.r1	Soares	preg	1.65e+01
743	15	1.1	466 11	H05709	zh78c03.r1	Soares	feta	1.65e+01	816	15	1.1	494 18	AA306692	zk61c06.r1	Soares	preg	1.65e+01
744	15	1.1	466 16	W90230	yl35e12.r1	Homo sapien											

819	16	1.1	496	11	T14940	crs426 Ricinus communi	6.84e-01	892	15	1.1	540	18	AA272928	va41a05.r1 Soares mous	1.65e+01
820	16	1.1	497	14	W30797	zb77f04.r1 Soares sene	6.84e-01	893	15	1.1	541	16	AA191442	zp84g03.s1 Stratagene	1.65e+01
821	15	1.1	497	14	W66857	mel5h10.r1 Soares mous	1.65e+01	894	15	1.1	544	16	AA160477	zq49b10.s1 Stratagene	1.65e+01
822	15	1.1	497	10	R35324	yg65b03.r1 Homo sapien	1.65e+01	895	15	1.1	544	11	W45170	843 Arabidopsis thali	1.65e+01
823	15	1.1	498	14	N94451	zb77f04.s1 Soares sene	6.84e-01	896	15	1.1	545	23	AA529101	vi32f02.r1 Barstead mo	1.65e+01
824	16	1.1	499	12	N46890	yy58b05.r1 Homo sapien	6.84e-01	897	15	1.1	546	23	AA445571	vf61c09.r1 Barstead MP	1.65e+01
825	15	1.1	500	14	AA015039	mi63h06.r1 Homo sapien	1.65e+01	898	16	1.1	546	12	N40419	yx89f03.r1 Homo sapien	6.84e-01
826	15	1.1	501	12	N32510	yy11c06.r1 Homo sapien	1.65e+01	899	16	1.1	546	21	B59720	CIT-HSP-344C22.TVD CIT	6.84e-01
827	16	1.1	502	11	H12032	ym16g06.r1 Homo sapien	6.84e-01	900	15	1.1	547	18	AA277272	vb68e02.r1 Barstead mo	1.65e+01
828	15	1.1	503	23	AA518507	vi01e02.r1 Barstead mo	1.65e+01	901	15	1.1	550	21	B61300	nm38c11.r1 Stratagene	1.65e+01
829	15	1.1	504	16	H91914	ys81h03.r1 Homo sapien	1.65e+01	902	15	1.1	551	16	AA067191	24 Pinus radiata somat	6.84e-01
830	16	1.1	504	22	AA441819	nm31c10.r1 Stratagene	1.65e+01	903	16	1.1	551	17	AA220909	ze24e12.r1 Soares feta	1.65e+01
831	15	1.1	504	17	AA267062	zw62f02.s1 Soares tota	1.65e+01	904	15	1.1	552	15	AA056359	vi35c02.r1 Beddington	1.65e+01
832	16	1.1	504	19	AA267095	mz95e09.r1 Soares mous	6.84e-01	905	15	1.1	553	23	AA529285	vi35c02.r1 Beddington	1.65e+01
833	15	1.1	505	12	NS1369	zt93g12.r1 Soares test	1.65e+01	906	16	1.1	553	10	R76883	yi64a07.s1 Homo sapien	6.84e-01
834	15	1.1	505	9	T74180	yz16c07.s1 Soares test	1.65e+01	907	16	1.1	553	16	AA181352	zp42b06.s1 Stratagene	6.84e-01
835	15	1.1	506	23	AA538298	yc60d09.r1 Homo sapien	1.65e+01	908	16	1.1	554	15	W82320	mf04f12.r1 Soares mous	6.84e-01
836	16	1.1	507	22	AA435128	vi98e10.r1 Barstead mo	6.84e-01	909	16	1.1	554	22	AA436968	zv72g05.r1 Soares tota	6.84e-01
837	16	1.1	508	20	G24367	ve16d10.r1 Soares mous	6.84e-01	910	15	1.1	554	15	AA001385	ze45c12.r1 Soares reti	1.65e+01
838	16	1.1	508	22	AA435128	human STS WI-14184.	6.84e-01	911	16	1.1	555	22	C07148	similar to insulin 1.	6.84e-01
839	16	1.1	508	9	T90448	yd42e12.s1 Homo sapien	6.84e-01	912	15	1.1	556	15	W44367	zc27e07.r1 Soares sene	1.65e+01
840	15	1.1	508	11	H09248	yl98b10.r1 Homo sapien	1.65e+01	913	16	1.1	558	18	AA276068	vc30c10.r1 Barstead MP	6.84e-01
841	15	1.1	508	10	R32324	yh68e06.s1 Homo sapien	1.65e+01	914	15	1.1	558	9	T69001	yc31d09.s1 Homo sapien	1.65e+01
842	15	1.1	509	15	AA151935	zc02a08.s1 Stratagene	1.65e+01	915	15	1.1	559	17	AA108437	mp33b06.r1 Barstead MP	6.84e-01
843	15	1.1	509	19	AA400624	zu70d08.r1 Soares test	1.65e+01	916	15	1.1	563	13	W26936	19a6 Human	1.65e+01
844	15	1.1	509	14	AA014532	mg84f11.r1 Soares mous	1.65e+01	917	16	1.1	564	22	C06914	similar to insulin 1.	6.84e-01
845	16	1.1	509	16	AA027547	mi06b03.r1 Soares mous	6.84e-01	918	15	1.1	565	9	T80256	yd03e07.r1 Homo sapien	1.65e+01
846	15	1.1	509	11	H15003	yl26c09.r1 Soares sapien	1.65e+01	919	15	1.1	565	23	AA455763	zx73a05.r1 Soares ovar	1.65e+01
847	16	1.1	510	13	W46095	mc78c03.r1 Soares mous	6.84e-01	920	15	1.1	566	23	AA452664	zx35a08.r1 Soares tota	1.65e+01
848	16	1.1	511	16	AA165058	zc09f10.r1 Stratagene	6.84e-01	921	15	1.1	568	23	AA519939	TgESTTz257f10.r1 TgME49	1.65e+01
849	15	1.1	512	15	W93978	zd97h09.s1 Soares feta	1.65e+01	922	15	1.1	569	21	B58209	CIT-HSP-2012C12.TR CIT	1.65e+01
850	16	1.1	513	14	W62070	md84e06.r1 Soares mous	6.84e-01	923	16	1.1	570	17	AA224681	CpEST.151 PSKlImInuScp	6.84e-01
851	15	1.1	513	14	W89020	zh72d11.s1 Soares feta	1.65e+01	924	16	1.1	570	23	AA537116	Vk45a11.r1 Soares mous	6.84e-01
852	15	1.1	514	17	AA213013	mw86e06.r1 Soares mous	1.65e+01	925	16	1.1	574	23	AA472478	vh07b01.r1 Soares mous	6.84e-01
853	15	1.1	514	17	AA234013	zr50c08.r1 Soares NHM	1.65e+01	926	16	1.1	574	15	W73276	zd54h09.s1 Soares feta	6.84e-01
854	15	1.1	515	14	AA028291	mi20d07.r1 Soares mous	1.65e+01	927	16	1.1	575	23	AA530694	vf50b08.r1 Stratagene	6.84e-01
855	15	1.1	515	15	W92769	zd93e03.s1 Soares feta	1.65e+01	928	16	1.1	575	23	AA537037	vj87a05.r1 Knowles Sol	6.84e-01
856	15	1.1	517	13	N57266	yw93h10.r1 Homo sapien	1.65e+01	929	16	1.1	587	13	W28120	42c5 Human	6.84e-01
857	16	1.1	518	18	AA315135	EST187139 Colon carcIn	6.84e-01	930	15	1.1	587	15	AA372287	zc52g01.r1 Soares sene	1.65e+01
858	16	1.1	519	16	N76183	yz30e05.r1 Soares mult	6.84e-01	931	16	1.1	588	9	T67929	yc28c08.s1 Homo sapien	6.84e-01
859	16	1.1	519	15	AA082832	zn21f11.s1 Stratagene	6.84e-01	932	15	1.1	589	21	FR0024761	F.rubripes GSS sequenc	1.65e+01
860	15	1.1	520	16	AA161339	zq40b09.r1 Homo sapien	1.65e+01	933	16	1.1	590	21	FR0024652	F.rubripes GSS sequenc	6.84e-01
861	15	1.1	521	12	H90995	yu89a07.r1 Homo sapien	1.65e+01	934	16	1.1	592	21	FR0020362	F.rubripes GSS sequenc	6.84e-01
862	15	1.1	521	22	AA442263	zv61h05.s1 Soares test	1.65e+01	935	15	1.1	593	10	R77187	yi65e07.r1 Homo sapien	1.65e+01
863	15	1.1	521	12	N29718	yw78f06.s1 Homo sapien	1.65e+01	936	15	1.1	594	6	HS292336	zc15b09.s1 Soares para	1.65e+01
864	16	1.1	522	17	AA116574	mp98h09.r1 Soares 2NDM	6.84e-01	937	15	1.1	595	15	W84344	zd89e07.s1 Soares feta	1.65e+01
865	15	1.1	522	13	W05742	za88d02.r1 Soares feta	1.65e+01	938	16	1.1	595	15	AA104002	mo45h08.r1 Life Tech m	6.84e-01
866	15	1.1	523	23	AA530058	vj15e07.r1 Barstead mo	1.65e+01	939	15	1.1	596	16	AA065652	nm43h03.r1 Stratagene	1.65e+01
867	16	1.1	524	21	B14852	343D12.TV CIT978SKA1 H	6.84e-01	940	15	1.1	597	21	FR0022365	F.rubripes GSS sequenc	1.65e+01
868	15	1.1	524	17	AA253596	CpEST.178 PSKlImInuScp	1.65e+01	941	15	1.1	597	16	N78013	yv71a02.r1 Soares feta	1.65e+01
869	15	1.1	525	23	C24391	zd19e12.s1 Soares feta	1.65e+01	942	15	1.1	599	17	AA116268	me88b11.r1 Soares mous	1.65e+01
870	16	1.1	525	18	AA318256	Dictyostelium discoide	6.84e-01	943	15	1.1	606	16	AA160643	mp95g12.r1 Soares 2NDM	1.65e+01
871	15	1.1	525	18	AA318256	EST20319 Retina II Hom	1.65e+01	944	16	1.1	606	21	FR0021611	zq49b11.r1 Stratagene	6.84e-01
872	16	1.1	527	14	AA050619	mj15h04.r1 Soares mous	6.84e-01	945	16	1.1	606	21	FR0021611	F.rubripes GSS sequenc	6.84e-01
873	15	1.1	527	16	AA065516	ml71a07.r1 Stratagene	1.65e+01	946	16	1.1	607	17	AA163412	F.rubripes GSS sequenc	6.84e-01
874	15	1.1	527	19	AA058525	zk82e02.s1 Soares preg	6.84e-01	947	16	1.1	608	21	B30222	F.rubripes GSS sequenc	6.84e-01
875	16	1.1	529	15	W89561	mf71h12.r1 Soares mous	6.84e-01	948	16	1.1	610	18	AA273431	vc01a09.r1 Soares mous	6.84e-01
876	16	1.1	530	23	AA456283	zx99h06.r1 Soares NhHM	6.84e-01	949	16	1.1	610	18	AA036175	mi70c12.r1 Soares mous	6.84e-01
877	15	1.1	530	15	AA104640	mo55c06.r1 Life Tech m	1.65e+01	950	16	1.1	612	14	AA036175	mr43g07.r1 Life Tech m	1.65e+01
878	16	1.1	531	14	W98519	vb83g01.r1 Soares mous	6.84e-01	951	15	1.1	612	18	AA288875	zd54g10.s1 Soares feta	1.65e+01
879	16	1.1	531	14	W97647	mg09e03.r1 Soares mous	6.84e-01	952	15	1.1	614	15	W73273	mf87b07.r1 Soares mous	1.65e+01
880	16	1.1	531	14	W97647	mf99f09.r1 Soares mous	6.84e-01	953	15	1.1	614	15	AA065953	z67h10.r1 Stratagene	6.84e-01
881	16	1.1	531	23	AA448150	zw82h05.r1 Soares test	6.84e-01	954	16	1.1	615	21	B68319	CIT978SK-A-752B10.TV.1	6.84e-01
882	15	1.1	531	20	G06748	human STS WI-7894.	1.65e+01	955	16	1.1	618	16	AA205618	zq67h10.r1 Stratagene	6.84e-01
883	16	1.1	532	23	AA462086	vg72c12.r1 Soares mous	6.84e-01	956	16	1.1	619	21	FR0005950	F.rubripes GSS sequenc	6.84e-01
884	16	1.1	534	14	AA050554	mj20f06.r1 Soares mous	6.84e-01	957	15	1.1	619	21	FR0005950	F.rubripes GSS sequenc	6.84e-01
885	15	1.1	534	9	T62804	yb99h05.r1 Homo sapien	1.65e+01	958	15	1.1	620	16	AA068448	mm46c02.r1 Stratagene	1.65e+01
886	15	1.1	536	12	N24430	yx26a09.r1 Homo sapien	1.65e+01	959	16	1.1	621	15	W84522	zd90f10.s1 Soares feta	6.84e-01
887	16	1.1	537	23	AA473279	vd44d09.r1 Barstead MP	6.84e-01	960	16	1.1	625	17	AA218341	mv74c11.r1 Soares mous	6.84e-01
888	15	1.1	537	20	G22422	human STS WT-30011.	1.65e+01	961	15	1.1	627	14	AA029645	ze95f03.r1 Soares feta	1.65e+01
889	16	1.1	538	14	W97422	mf95h06.r1 Soares mous	6.84e-01	962	15	1.1	629	23	AA518262	vi27d07.r1 Barstead mo	6.84e-01
890	15	1.1	539	9	T63495	yc22g02.s1 Homo sapien	1.65e+01	963	16	1.1	632	18	AA270382	va63d10.r1 Soares mous	6.84e-01
891	16	1.1	540	9	T79223	yd70a01.r1 Homo sapien	6.84e-01	964	15	1.1	634	15	AA012956	ze27b02.r1 Soares reti	1.65e+01


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968 15 1.1 662 17 AA230770 mw07h12.r1 Soares mous 1.65e+01
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970 15 1.1 668 21 B72185 RPCI11-7K18.TV RPCI11 1.65e+01
971 16 1.1 675 20 HUMUT6491 Human STS UT6491. 6.84e-01
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974 15 1.1 688 21 AG003232 Homo sapiens genomic D 1.65e+01
975 16 1.1 693 13 W23295 82G8 Human retina cDNA 6.84e-01
976 16 1.1 711 14 AA032646 m134f12.r1 Soares mous 6.84e-01
977 15 1.1 726 13 W23260 81H2 Human retina cDNA 1.65e+01
978 15 1.1 772 21 B06959 CSRL-88H6-u CSRL flow 1.65e+01
979 16 1.1 817 21 B11106 T4K8-T7.1 TAMU Arabido 6.84e-01
980 16 1.1 843 21 B08135 F8A5-T7.1 IGF Arabidop 6.84e-01
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982 15 1.1 866 13 W28838 52d4 Human retina cDNA 1.65e+01
983 15 1.1 872 16 AA203178 2x55c07.r1 Soares feta 1.65e+01
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985 16 1.1 878 13 W27918 39g1 Human retina cDNA 6.84e-01
986 16 1.1 898 14 W97050 m188g09.r1 Soares mous 6.84e-01
987 16 1.1 917 21 B10294 F11019-T7 IGF Arabidop 6.84e-01
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990 16 1.1 982 21 B12894 T17011-Sp6 TAMU Arabid 6.84e-01
991 16 1.1 991 21 B09028 T4K8-T7 TAMU Arabidops 6.84e-01
992 15 1.1 1008 21 B10023 F5F1-T7.1 IGF Arabidop 1.65e+01
993 16 1.1 1018 21 B11248 T2905-T7 TAMU Arabidop 6.84e-01
994 16 1.1 1044 21 B11025 F8A5-T7.3 IGF Arabidop 6.84e-01
995 15 1.1 1047 21 AB005980 Mouse genomic DNA, chr 1.65e+01
996 15 1.1 1198 21 B09428 F20F11-T7 IGF Arabidop 1.65e+01
997 15 1.1 1272 14 W29398 mb98a09.r1 Soares mous 1.65e+01
998 15 1.1 1297 21 B10695 T21N1-Sp6.2 TAMU Arabi 1.65e+01
999 15 1.1 1487 21 B13396 jd164 Trypanosome Shot 1.65e+01
1000 16 1.1 3076 23 HUMSUPY030 Human brain cDNA, comp 6.84e-01
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ALIGNMENTS

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RESULT 1
LOCUS R31984 153 bp mRNA EST 28-APR-1995
DEFINITION yh62c10.r1 Homo sapiens cDNA clone 134322 5' similar to gb:L25119
MO-TYPE OPIOID RECEPTOR (HUMAN);.
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ACCESSION R31984
NID 6787827

KEYWORDS EST.
SOURCE human clone=134322 library=Soares placenta Nb2HP vector=PT7T3D
(pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a

Not I - oligo(dT) primer [5'
AACTGGAAGAAATTCGGCGCCGACGAGAAATTTTCTTTTCTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified PT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo. .
Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 153)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

```
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 120
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
    source
        1..153
        /organism="Homo sapiens"
        /clone="134322"
BASE COUNT 25 a 49 c 37 g 42 t
ORIGIN
    Query Match 1.8%; Score 26; DB 10; Length 153;
    Best Local Similarity 100.0%; Pred. No. 1.61e-19;
    Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 45 GTCTGTACACCCGTGATGATCCTGGC 70
QY 915 GTCTGTACACCCGTGATGATCCTGGC 940
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RESULT 2
LOCUS R81583 183 bp mRNA EST 12-JUN-1995
DEFINITION yf04b04.r1 Homo sapiens cDNA clone 147727 5' similar to gb:L25119
MO-TYPE OPIOID RECEPTOR (HUMAN);.
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ACCESSION R81583
NID 9858186

KEYWORDS EST.
SOURCE human clone=147727 library=Soares placenta Nb2HP vector=PT7T3D
(pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5'
AACTGGAAGAAATTCGGCGCCGACGAGAAATTTTCTTTTCTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified PT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo. .
Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 183)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality.
FEATURES
 source
 1..183
 /organism="Homo sapiens"
 /clone="147727"

BASE COUNT 31 a 56 c 40 g 46 t 10 others
ORIGIN

RESULT 5
LOCUS R04688 352 bp mRNA EST 31-MAR-1995
DEFINITION pk27e08.r1 Caenorhabditis briggsae cDNA.
ACCESSION R04688
NID 9754424
KEYWORDS EST.
SOURCE Caenorhabditis briggsae library=Kuwabara Mixed stage C. briggsae strain=g6 Gujarat vector=Lambda gt10 primer=Commercially available M13 reverse dye primer Rsitel=EcORI Rsite2=EcORI Stage:mixed, Sex:hermaphrodite. Library construction: First strand oligo(dT) primed. Second strand was as per Gubler/Hoffman. Ligated to EcORI adaptors. Library is non-directional. Library is non-normalized. Library constructed by P.F. Kuwabara. Additional details on construction of the library are described in P.F. Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor sequence: GAATTC CGTGTGTCG.

ORGANISM
Caenorhabditis briggsae
Eukaryotae; mitochondrial eukaryotes; eukaryote crown group; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Pseudocoelomata; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Caenorhabditis.

REFERENCE
AUTHORS 1 (bases 1 to 352)
Hillier,L., Chiapelli,B., Chissoe,S., Clark,N., Couch,J., Dubuque,T., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Kuwabara,P., Le,M., Mardis,E., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Wohlmann,P. and Wilson,R.
TITLE Washington University Caenorhabditis briggsae EST project
JOURNAL Unpublished (1995)
COMMENT Other_ESTs: pk27e08.s1
Contact: Marra MA
Washington University Genome Sequencing Center
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1455
Fax: 314 286 1810
Email: mmarra@watson.wustl.edu
PCR_F: TGTAAACGACGGCCAGTGAGCAAGTTCAGCCTGG
PCR_B: CAGGAACAGCTATGACCTTATGATTTCTTCAGGGTA
Source: Washington University Genome Sequencing Center
PCR amplified DNA is available from Washington University Genome Sequencing Center. Aliquots of the library may be requested from P. Kuwabara (pekemrc-lmb.cam.ac.uk).

FEATURES
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Location/Qualifiers
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/organism="Caenorhabditis briggsae"
/strain="G16 Gujarat"

BASE COUNT 126 a 58 c 86 g 82 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.42e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 161 AGACAATGATGATGAGGA 178
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Cp 918 AGACAATGATGATGAGGA 901

RESULT 6
LOCUS AA366615 364 bp mRNA EST 21-APR-1997
DEFINITION EST77582 Pancreas tumor III Homo sapiens cDNA 5' end.
ACCESSION AA366615
NID 92018933
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 364)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,

TITLE
JOURNAL MEDLINE
COMMENT Other_ESTs: THC148243
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
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Location/Qualifiers
1..364
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/note="Organ: pancreas; Vector: pBluescript SK-; Site_1: EcORI; Site_2: XhoI"
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/db_xref="taxon:9606"
/clone_lib="Pancreas tumor III"
/dev_stage="adult"
<1..>364

BASE COUNT 90 a 92 c 65 g 111 t 6 others
ORIGIN

Query Match 1.3%; Score 18; DB 19; Length 364;
Best Local Similarity 100.0%; Pred. No. 5.42e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 228 CAGCTGCCCTCTCCAGCT 245
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QY 1102 CAGCTGCCCTCTCCAGCT 1119

RESULT 7
LOCUS C15712 374 bp mRNA EST 03-SEP-1996
DEFINITION Human fetal brain cDNA 5'-end GEN-159G10.
ACCESSION C15712
NID 91570419
KEYWORDS EST; EST(expressed sequence tag); Human fetal brain.
SOURCE Homo sapiens fetus brain cDNA to mRNA, clone:159G10.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)
AUTHORS Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimada,Y., Shinomiya,H., Suzuki,M., Takaichi,A., Takeda,S., Watanabe,T., Maekawa,H., Nakamura,Y. and Takahashi,E.
TITLE Otsuka cDNA project
JOURNAL Unpublished (1996)
REFERENCE 2 (bases 1 to 374)


```

AUTHORS      Fujiwara,T.
TITLE        Direct Submission
JOURNAL      Submitted (13-MAY-1996) to the DDBJ/EMBL/GenBank databases. Tsutomu
              Fujiwara, Otsuka GEN Research Institute,Otsuka Pharmaceutical
              Co.,Ltd; 463-10 Kagasuno Kawauchi-cho, Tokushima, Tokushima 771-01,
              Japan (Tel:+81-886-65-2888, Fax:+81-886-37-1035)
FEATURES
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      /db_xref="taxon:9606"
      /clone="159G10"
      /dev_stage="fetus"
      /tissue_type="brain"
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Best Local Similarity 100.0%;   Pred. No. 5.42e-04;
Matches 18;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Db      330 GCTGACACAGCTACTCAGG 347
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QY      85 GCTGACACAGCTACTCAGG 103

RESULT      8
LOCUS       N57941              384 bp      mRNA
DEFINITION  yw6lg04.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone
            247254 3'.
ACCESSION   N57941
NID         g1201831
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE   1 (bases 1 to 384)
AUTHORS     Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E.,
            Waterston,R., Williamson,A., Wohlmann,P. and Wilson,R.
            WashU-Merck EST project
            Unpublished (1995)
TITLE       Contact: Wilson RK
JOURNAL
COMMENT     WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through INL; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 944   Std Error: 0.00
            Seq primer: ml3 -40 forward
            High quality sequence stop: 258.
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                /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                1st strand cDNA was primed with a Pac I - oligo(dT) primer
                [5' AACTGAGAGAAATTAATTAAGATCCTTTTCTTTTCTTTTCTTTT 3'],
                double-stranded cDNA was ligated to Eco RI adaptors
                (Pharmacia), digested with Pac I and cloned into the Pac I
                and Eco RI sites of the modified pT7T3 vector. Library
                went through one round of normalization. Library
                constructed by Bento Soares and M.Fatima Bonaldo."
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                /clone="247254"
                /clone_lib="Soares fetal liver spleen 1NFLS"
                /sex="male"
                /dev_stage="20 week-post conception fetus"

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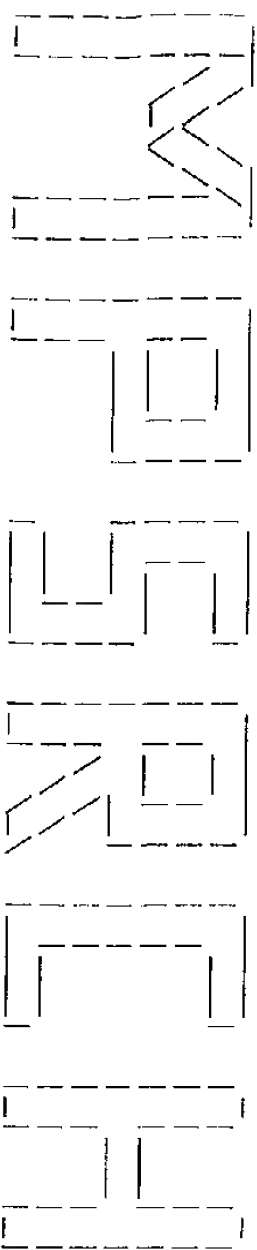
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ORIGIN						
Query Match						
Best Local Similarity		1.3%;		Score 18;		DB 15; Length 384;
Matches		18; Conservative		0; Mismatches		0; Indels 0; Gaps 0;
Db	292 AGCTGGAGAGGGCAGCTG	309				
Cp	1119 AGCTGGAGAGGGCAGCTG	1102				
RESULT 9						
LOCUS	N62652	414 bp	mRNA	EST	01-MAR-1996	
DEFINITION	zai4d10.s1 Homo sapiens cDNA clone 292531 3'.					
ACCESSION	N62652					
NID	g1210481					
KEYWORDS	EST.					
SOURCE	human clone=292531 primer=m13 -40 forward library=Soares fetal liver spleen INFLS vector=PT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5' AACTGGAAGATTATTAAGATCTTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homiidae; Homo. 1 (bases 1 to 414)					
AUTHORS	Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasaki,E., Waterston,R., Williamson,A., Woldmann,P. and Wilson,R.					
TITLE	The WashU-Merck EST Project					
JOURNAL	Unpublished (1995)					
COMMENT	Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High quality sequence stops: 248 Source: IMAGE Consortium, LNL This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Location/Qualifiers 1..414 /organism="Homo sapiens" /clone="292531" <1..>414					
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ORIGIN						
Query Match						
Best Local Similarity		1.3%;		Score 18; DB 13; Length 414;		
Matches		18; Conservative		0; Mismatches		0; Indels 0; Gaps 0;
Db	291 AGCTGGAGAGGGCAGCTG	308				
Cp	1119 AGCTGGAGAGGGCAGCTG	1102				

RESULT 10
LOCUS H41020 433 bp mRNA EST 16-AUG-1995
DEFINITION XP72d11.s1 Homo sapiens cDNA clone 192981 3'.
ACCESSION H41020
NID 9917072
KEYWORDS EST.
SOURCE human clone=192981 library=Soares adult brain N2b4HB55Y
vector=PT7T3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=Promega -21ml3 Rsite1=Not I
Rsite2=Eco RI 55-year old male. 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5',
TGTACCAATCTGAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified PT7T3 vector (Pharmacia). Library went
through one round of normalization to a Cot = 53. Library
constructed by Bento Soares and M.Fatima Bonaldo. The adult brain
RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18
hours after death which occurred in consequence of a ruptured
aortic aneurysm. RNA was prepared from a pool of tissues
representing the following areas of the brain: frontal, parietal,
temporal and occipital cortex from the left and right hemispheres,
subcortical white matter, basal ganglia, thalamus, cerebellum,
midbrain, pons and medulla.
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 433)
REFERENCE
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 305
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
source location/Qualifiers
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/clone="192981"
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Best Local Similarity 100.0%; Pred. No. 5.42e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 372 AACTGGGCAGATCCGAC 389
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QY 279 AACTGGGCAGATCCGAC 296
RESULT 11
LOCUS R81332 433 bp mRNA EST 12-JUN-1995
DEFINITION YJ04b04.s1 Homo sapiens cDNA clone 147727 3'.
ACCESSION R81332
NID 9857935
KEYWORDS EST.
SOURCE human clone=147727 library=Soares placenta Nb2HP vector=PT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin

resistant) primer=Promega -21ml3 Rsite1=Not I Rsite2=Eco RI female
placenta obtained at birth (full term). 1st strand cDNA was primed
with a Not I - oligo(dT) primer [5',
AACTGAAGATTCGCGCGCAGAGAAATTTTCTTTTCTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified PT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 433)
REFERENCE
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 241
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
source location/Qualifiers
1..433
/organism="Homo sapiens"
/clone="147727"
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Best Local Similarity 90.0%; Pred. No. 5.42e-04;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 333 TNCACGNCATGTCATCTGG 352
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Cp 1339 TCCACGACTAGTCATCTGG 1320
RESULT 12
LOCUS N78731 448 bp mRNA EST 29-MAR-1996
DEFINITION zb05a11.s1 Homo sapiens cDNA clone 301148 3'.
ACCESSION N78731
NID 91241432
KEYWORDS EST.
SOURCE human clone=301148 primer=m13 -40 forward library=Soares fetal lung
NbHL19W vector=PT7T3D (Pharmacia) with a modified polylinker
host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI 19
week fetus. 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'-TGTACCAATCTGAGTGGAGCGCGCATTTTCTTTTCTTTT-3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified PT7T3 vector (Pharmacia). Library went
through one round of normalization to a Cot = 5. Library
constructed by Bento Soares and M.Fatima Bonaldo.
Homo sapiens
ORGANISM
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 448)
REFERENCE
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

RESULT 15
LOCUS B35459 491 bp DNA GSS 16-OCT-1997
DEFINITION HS-1029-A1-E02-MR.abi CIT Human Genomic Sperm Library C Homo
sapiens genomic clone Plate=CT808 Col=3 Row=1.
ACCESSION B35459
NTD g2534828
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 491)
AUTHORS Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
Tralcoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
TITLE Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
JOURNAL Unpublished (1997)
COMMENT
Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackrone@u.washington.edu
Sequence Tagged Connector
Plate: CT808 row: 1 column: 3
Class: BAC ends
High quality sequence stop: 491.
FEATURES
source
Location/Qualifiers
1..491
/organism="Homo sapiens"
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BASE COUNT 129 a 107 c 106 g 149 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.42e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 209 ACCAAGTCAGGGAAGAT 226
|||
QY 780 ACCAAGTCAGGGAAGAT 797

Search completed: Tue Apr 21 00:47:07 1998
Job time : 1182 secs.



(TM)

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MPsrch_nu n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 21 00:53:02 1998; MasPar time 888.78 Seconds

Tabular output not generated. 1330.411 Million cell updates/sec

Title: >US-08-292-694A-11
Description: (1-1000) from US08292694A.seq
Perfect Score: 994

N.A. Sequence: 1 AAGAAGCAAAATCAGTAATC.....CCAGTATGACTAGTCGTGA 1000
Comp: TTCTTCGTTTGTAGTCATTAG.....GGTCATTAAGTATGATCAGACACCT

Scoring table: TABLE fmetric
Gap 60

Nmatch STD : Dbase 0; Query 0

Searched: 354530 seqs, 591221332 bases x 2

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database:

emb153

1:em_in 2:em_or 3:em_cm 4:em_ov 5:em_pl 6:em_htg
7:em_hum1 8:em_hum2 9:em_ba 10:em_ro 11:em_un 12:em_vi
13:em_pat
genbank105

Database: 14:gb_ro 15:gb_cm 16:gb_ov 17:gb_in 18:gb_pl 19:gb_ba
20:gb_st 21:gb_vi 22:gb_ph 23:gb_sy 24:gb_un 25:gb_pat
26:gb_htg

Statistics: Mean 9.127; Variance 3.194; scale 2.858

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
			%						
1	729	73.3	1142	25	A48343			Sequence 1 from Patent	0.00e+00
2	47	4.7	1733	14	CPT04092			Cavia porcellus Hartle	4.79e-25
3	33	3.3	432	14	NM016998			Mus musculus kappa opi	1.76e-11
4	33	3.3	488	14	MUSMORGD			Mouse MORGD gene for k	1.76e-11
5	33	3.3	658	14	RNKR2			Rattus norvegicus kapp	1.76e-11
6	33	3.3	1109	14	S77868S2			kappa opiod receptor	1.44e-10
7	32	3.2	1273	14	RATROD			Rat mRNA for opiod re	1.44e-10
8	32	3.2	1288	14	S81111			kappa-opioid receptor	1.44e-10
9	32	3.2	1358	14	RATKOR1A			Rat kappa opiod recep	1.44e-10
10	32	3.2	1410	14	MUSKAFOPRE			Mouse kappa opiod rec	1.44e-10
11	32	3.2	2094	14	RATKOR1B			Rattus norvegicus kapp	1.44e-10
12	32	3.2	2481	25	E08874			CDNA coding rat kappa-	1.44e-10
13	32	3.2	2481	14	RATKOR			Rattus norvegicus mRNA	1.44e-10
14	32	3.2	4048	14	RNKR3			Rattus norvegicus kapp	1.44e-10

15	32	3.2	4742	14	RN000442			Rattus norvegicus kapp	1.44e-10
16	29	2.9	356	14	S81965			delta opiod receptor/	6.67e-08
17	29	2.9	686	15	SSU71149			Sus scrofa delta opioi	6.67e-08
18	29	2.9	1366	14	RN000475			Rattus norvegicus Spra	6.67e-08
19	29	2.9	1418	14	RATROA			Rat mRNA for rat opioi	6.67e-08
20	29	2.9	1834	14	S65335			delta opiod receptor	6.67e-08
21	29	2.9	1835	14	MUSDOPRCP			Mouse delta-opioid rec	6.67e-08
22	29	2.9	2203	14	S66181			delta opiate receptor	6.67e-08
23	29	2.9	2219	14	MUSDELTO			Mus musculus delta-opi	6.67e-08
24	29	2.9	2219	25	A38528			Sequence 1 from Patent	6.67e-08
25	29	2.9	2272	14	MUSDLOPRE			Mouse delta opiod rec	6.67e-08
26	26	2.6	638	14	MUSMORGD			Mouse MORGD gene for k	2.40e-05
27	26	2.6	720	14	S77863			kappa opiod receptor MOR	2.40e-05
28	26	2.6	1186	14	S77868S3			Rattus norvegicus mu o	2.40e-05
29	26	2.6	1367	14	RN035424			Rattus norvegicus mu o	2.40e-05
30	26	2.6	1401	14	RATMOPIOD			Rat mu opiod receptor	2.40e-05
31	26	2.6	1448	14	RN002083			Rattus norvegicus mu-o	2.40e-05
32	26	2.6	1586	14	RATMORA			Rattus norvegicus mu o	2.40e-05
33	26	2.6	2135	14	RATMOR1A			Rattus norvegicus mu o	2.40e-05
34	26	2.6	2397	14	RATROB			Rat mRNA for rat opioi	2.40e-05
35	23	2.3	1231	16	CCMUOPI			C.commersoni mRNA for	6.24e-03
36	23	2.3	1881	15	PIGMUOPR			Sus scrofa mu opiod r	6.24e-03
37	21	2.1	21	25	A48346			Sequence 4 from Patent	2.04e-01
38	21	2.1	2205	15	SSU72758			Sus scrofa orphanin FQ	2.04e-01
39	20	2.0	20	25	A48345			Sequence 3 from Patent	1.08e+00
40	20	2.0	39	25	A48347			Sequence 5 from Patent	1.08e+00
41	20	2.0	356	14	NMKOR3S06			Mus musculus opiod re	1.08e+00
42	20	2.0	371	14	NMKOR2			Mus musculus mu opiod	1.08e+00
43	20	2.0	998	25	A38530			Sequence 3 from Patent	1.08e+00
44	20	2.0	1079	14	NM014165			Mus musculus orphan op	1.08e+00
45	20	2.0	1083	14	MUSMORGPC2			Mouse MORGC gene for o	1.08e+00
46	20	2.0	1253	14	RATOPRE			Rattus norvegicus opio	1.08e+00
47	20	2.0	1265	25	I13403			Sequence 3 from patent	1.08e+00
48	20	2.0	1265	14	MUSSR1A			Mus musculus somatosta	1.08e+00
49	20	2.0	1304	14	RN005239			Rattus norvegicus opio	1.08e+00
50	20	2.0	1338	14	NM004952			Mus musculus C57Bl/6N	1.08e+00
51	20	2.0	1452	25	I62296			Sequence 3 from patent	1.08e+00
52	20	2.0	1452	14	RN01913			Rattus norvegicus Spra	1.08e+00
53	20	2.0	1461	14	RATSR			Rat somatostatlin recep	1.08e+00
54	20	2.0	1567	14	RATOPRCEP			Rat opiod receptor fa	1.08e+00
55	20	2.0	1610	14	NM026915			Mus musculus mu opiod	1.08e+00
56	20	2.0	1634	25	I13402			Sequence 1 from patent	1.08e+00
57	20	2.0	1699	14	RATSCM			Rattus norvegicus mRNA	1.08e+00
58	20	2.0	1817	14	RATRORC			Rat mRNA for opiod re	1.08e+00
59	20	2.0	2024	14	NMOP1RECP			M.musculus mRNA for op	1.08e+00
60	20	2.0	2229	14	NM019380			Mus musculus mu opiod	1.08e+00
61	20	2.0	2354	14	RN007871			Rattus norvegicus Spra	1.08e+00
62	20	2.0	2600	14	NM009421			Mus musculus K3 opiate	1.08e+00
63	20	2.0	2706	14	RATXOR1A			Rattus norvegicus alte	1.08e+00
64	20	2.0	3615	14	RNGPCRMA			R.norvegicus mRNA for	1.08e+00
65	20	2.0	148534	26	HS11703			Human DNA sequence ***	1.08e+00
66	19	1.9	1763	19	CTU83196			Chlamydia trachomatis	5.41e+00
67	19	1.9	1832	15	HRSADHS			Horse alcohoh dehydros	5.41e+00
68	19	1.9	5745	19	CPIROXIAB			C.perfringens DNA for	5.41e+00
69	19	1.9	7628	18	SCYUL222W			S.cerevisiae chromosom	5.41e+00
70	19	1.9	10510	19	HITU32761			R.cerevisiae chromoso	5.41e+00
71	19	1.9	14102	19	AE001117			Haemophilus influenzae	5.41e+00
72	19	1.9	28650	18	SPAC2267			Borrelia burgdorferi (5.41e+00
73	19	1.9	38779	17	CET24B8			S.pombe chromosome I c	5.41e+00
74	19	1.9	38990	18	SC9402			Caenorhabditis elegans	5.41e+00
75	19	1.9	40257	18	SCXLET			S.cerevisiae chromosom	5.41e+00
76	19	1.9	110000	18	SCCHRIX			S.cerevisiae chromoso	5.41e+00
77	18	1.8	261	14	NM084153			Mus musculus ca repeat	2.54e+01
78	18	1.8	770	15	S67315			cholesterol 7 alpha-hy	2.54e+01
79	18	1.8	822	14	MUSGNRHA03			Mus musculus gonadotro	2.54e+01
80	18	1.8	921	15	MUSGRHC			Equus caballus pituita	2.54e+01
81	18	1.8	921	15	AF018072			Monkeypox virus tumor	2.54e+01
82	18	1.8	1207	21	MYU08543			Monkeypox virus strain	2.54e+01
83	18	1.8	1207	21	MYU087841			Mouse gonadotropin-rel	2.54e+01
84	18	1.8	1227	14	MUSGRHR			Mus musculus (strain C	2.54e+01
85	18	1.8	1227	14	MUSGORHOR			Sequence 9 from patent	2.54e+01
86	18	1.8	1296	25	I13406			Monkeypox virus	2.54e+01
87	18	1.8	1316	21	MYU88142			Monkeypox virus tumor	2.54e+01

C	88	18	1.8	1317	21	MVU87847	Monkeypox virus strain	2.54e+01	C	161	17	1.7	6041	18	SCSPA2G	S. cerevisiae SPA2 gen	1.11e+02
C	89	18	1.8	1320	21	MVU87845	Monkeypox virus strain	2.54e+01	C	162	17	1.7	6450	19	TTNARZTWV	T. thermophilus narg, n	1.11e+02
C	90	18	1.8	1416	18	VVGS1	V. vinifera mRNA for cy	2.54e+01	C	163	17	1.7	11391	19	MPAE000037	Mycoplasma pneumoniae	1.11e+02
C	91	18	1.8	1801	18	SCYGL223C	S. cerevisiae chromsom	2.54e+01	C	164	17	1.7	11725	25	I05479	Sequence 13 from Paten	1.11e+02
C	92	18	1.8	1805	14	MUSLD2	Mus musculus Id gene,	2.54e+01	C	165	17	1.7	11725	25	I07993	Sequence 1 from Paten	1.11e+02
C	93	18	1.8	2051	15	CEGPCR1	Canis familiaris RDC1	2.54e+01	C	166	17	1.7	14293	17	PFSC03052	Plasmodium falciparum	1.11e+02
C	94	18	1.8	2180	15	S73493	heparin cofactor II-p1	2.54e+01	C	167	17	1.7	17267	18	SCU43834	Saccharomyces cerevisi	1.11e+02
C	95	18	1.8	2238	15	RABNANUCOT	Oryctolagus cuniculus	2.54e+01	C	168	17	1.7	20108	17	CEZC443	Caenorhabditis elegans	1.11e+02
C	96	18	1.8	2238	25	II1726	Sequence 1 from Patent	2.54e+01	C	169	17	1.7	22700	17	CEFF36G3	Caenorhabditis elegans	1.11e+02
C	97	18	1.8	2267	14	MUSGRHRA	Mouse gonadotropin-rel	2.54e+01	C	170	17	1.7	24709	17	CEC26H9A	Caenorhabditis elegans	1.11e+02
C	98	18	1.8	2346	15	CFU91844	Canis familiaris gluco	2.54e+01	C	171	17	1.7	25402	17	CELT28H11	Caenorhabditis elegans	1.11e+02
C	99	18	1.8	2443	16	XLNUCLEOL	X. laevis mRNA for nucl	2.54e+01	C	172	17	1.7	25934	17	CELT05B11	Caenorhabditis elegans	1.11e+02
C	100	18	1.8	2497	14	RRATBP2	Rat mRNA for zinc fing	2.54e+01	C	173	17	1.7	30190	17	CEZK524	Caenorhabditis elegans	1.11e+02
C	101	18	1.8	3002	15	RABCP7A	Rabbit cholesterol-7-a	2.54e+01	C	174	17	1.7	30190	17	CEZK524	Caenorhabditis elegans	1.11e+02
C	102	18	1.8	3154	17	LMGCR2	L. migratoria gcr1 mRNA	2.54e+01	C	175	17	1.7	30563	17	CEZK524	Caenorhabditis elegans	1.11e+02
C	103	18	1.8	3154	17	LMGCR1	L. migratoria gcr1 mRNA	2.54e+01	C	176	17	1.7	31628	17	CELT27F6	Caenorhabditis elegans	1.11e+02
C	104	18	1.8	3706	14	MUSGNRHA01	Mus musculus gonadotro	2.54e+01	C	177	17	1.7	32088	18	SC32KBF	S. cerevisiae 32kb DNA	1.11e+02
C	105	18	1.8	8809	17	DRODISABIE	Drosophila melanogaste	2.54e+01	C	178	17	1.7	33490	17	CEZK20	Caenorhabditis elegans	1.11e+02
C	106	18	1.8	9470	19	PDU34346	Paracoccus denitrifica	2.54e+01	C	179	17	1.7	34576	26	CEZK1A9	Caenorhabditis elegans	1.11e+02
C	107	18	1.8	22847	18	SPAC18B11	S. pombe chromosome I c	2.54e+01	C	180	17	1.7	35959	17	CELT0A9	Caenorhabditis elegans	1.11e+02
C	108	18	1.8	27016	17	CEF40E10	Caenorhabditis elegans	2.54e+01	C	181	17	1.7	36640	26	CELT02D3	Caenorhabditis elegans	1.11e+02
C	109	18	1.8	34197	17	CELT28F2	Caenorhabditis elegans	2.54e+01	C	182	17	1.7	36640	26	CEW02B4	Caenorhabditis elegans	1.11e+02
C	110	18	1.8	39187	17	CELC01F1	Caenorhabditis elegans	2.54e+01	C	183	17	1.7	37049	19	MLACEA	M. leprae acea gene for	1.11e+02
C	111	18	1.8	41452	17	CER06F6	Caenorhabditis elegans	2.54e+01	C	184	17	1.7	38734	19	SC10A5	Streptomyces coelicolo	1.11e+02
C	112	18	1.8	44082	18	SPAC29A4	S. pombe chromosome I c	2.54e+01	C	185	17	1.7	41000	26	AC002085	S. cerevisiae chromsom	1.11e+02
C	113	18	1.8	91979	18	ATAC002510	Arabidopsis thaliana c	2.54e+01	C	186	17	1.7	43661	18	SCXCOSM83	Caenorhabditis elegans	1.11e+02
C	114	18	1.8	187647	26	CEY16B4	Caenorhabditis elegans	2.54e+01	C	187	17	1.7	43661	18	CEZK524	Caenorhabditis elegans	1.11e+02
C	115	18	1.8	202028	26	CEY19D2	Caenorhabditis elegans	2.54e+01	C	188	17	1.7	44512	26	HS367G8	Human DNA sequence ***	1.11e+02
C	116	17	1.7	27	25	I33193	Sequence 5 from patent	1.11e+02	C	189	17	1.7	48297	17	AC003701	Drosophila melanogaste	1.11e+02
C	117	17	1.7	351	19	MYCTGS	Mycoplasma pneumoniae	1.11e+02	C	190	17	1.7	49790	26	HS415C1	Human DNA sequence ***	1.11e+02
C	118	17	1.7	354	14	CP067928	Cavia porcellus mu-opi	1.11e+02	C	191	17	1.7	78844	18	AB006708	Arabidopsis thaliana g	1.11e+02
C	119	17	1.7	489	25	E04057	CDNA encoding human ce	1.11e+02	C	192	17	1.7	81701	18	AB006706	Arabidopsis thaliana g	1.11e+02
C	120	17	1.7	678	18	SCU26257	Saccharomyces cerevisi	1.11e+02	C	193	17	1.7	89779	18	AB005234	Arabidopsis thaliana g	1.11e+02
C	121	17	1.7	708	18	OSU17900	Orpinomyces sp. cyclop	1.11e+02	C	194	17	1.7	100145	26	AC003104	Caenorhabditis elegans	1.11e+02
C	122	17	1.7	851	17	ICTORDE	Lucilia cuprina chymot	1.11e+02	C	195	17	1.7	100177	26	CEY55D9	Caenorhabditis elegans	1.11e+02
C	123	17	1.7	954	16	ICP03760	Ictalurus punctatus DN	1.11e+02	C	196	17	1.7	114747	26	HS422H11	Human DNA sequence ***	1.11e+02
C	124	17	1.7	1084	19	TPPSAZURN	T. pantotropha mRNA for	1.11e+02	C	197	17	1.7	128000	26	AC004046	Caenorhabditis elegans	1.11e+02
C	125	17	1.7	1154	19	ACCAA6IG	Actinobacter haemolyt	1.11e+02	C	198	17	1.7	137357	26	AC003003	Caenorhabditis elegans	1.11e+02
C	126	17	1.7	1215	15	OCPP1A	Rabbit mRNA for type-1	1.11e+02	C	199	17	1.7	137404	26	AC002375	Homo sapiens; HTGS pha	1.11e+02
C	127	17	1.7	1252	15	BTNTLK6P	B. taurus DNA for inter	1.11e+02	C	200	17	1.7	140000	26	AC004047	Human DNA sequence ***	1.11e+02
C	128	17	1.7	1291	16	XICALR	X. laevis mRNA for calr	1.11e+02	C	201	17	1.7	159877	26	HS217C2	Human DNA sequence ***	1.11e+02
C	129	17	1.7	1293	18	ATHCK2B	Arabidopsis thaliana m	1.11e+02	C	202	17	1.7	169646	26	AC004019	Human DNA sequence ***	1.11e+02
C	130	17	1.7	1346	18	AGGLN1	A. glutinosa mRNA for g	1.11e+02	C	203	17	1.7	171097	26	HS471M13	Human DNA sequence ***	1.11e+02
C	131	17	1.7	1349	15	OCPP1A	Rabbit mRNA for type-1	1.11e+02	C	204	17	1.7	176781	26	AC002989	Human DNA sequence ***	1.11e+02
C	132	17	1.7	1353	18	PVGSR2	Phaseolus vulgaris mRN	1.11e+02	C	205	17	1.7	188833	26	AC004125	Human DNA sequence ***	1.11e+02
C	133	17	1.7	1369	18	ATU12858	Arabidopsis thaliana c	1.11e+02	C	206	17	1.7	216371	26	AC002549	Homo sapiens; HTGS pha	1.11e+02
C	134	17	1.7	1458	16	DRAJ1596	Danio rerio mRNA for c	1.11e+02	C	207	17	1.7	220709	26	AC002288	Caenorhabditis elegans	1.11e+02
C	135	17	1.7	1492	15	OCPP1	Rabbit mRNA for protei	1.11e+02	C	208	17	1.7	250611	14	MAAE000653	Mus musculus TCR beta	1.11e+02
C	136	17	1.7	1532	14	MMSM2G09	Mus musculus single-mi	1.11e+02	C	209	17	1.7	252128	26	CEY18D10	Caenorhabditis elegans	1.11e+02
C	137	17	1.7	1538	14	RNU36898	Rattus norvegicus puta	1.11e+02	C	210	17	1.7	261012	26	HS343C1	Human DNA sequence ***	1.11e+02
C	138	17	1.7	1861	14	AF000236	Mus musculus RDC1 orph	1.11e+02	C	211	16	1.6	320751	26	AC003978	Homo sapiens; HTGS pha	1.11e+02
C	139	17	1.7	2012	14	MMAJ2271	Mus musculus mRNA for	1.11e+02	C	212	16	1.6	31	25	I62294	Sequence 1 from patent	4.48e+02
C	140	17	1.7	2020	18	SCYJR01IC	S. cerevisiae chromsom	1.11e+02	C	213	16	1.6	54	25	A12990	Nucleotide sequence 6	4.48e+02
C	141	17	1.7	2399	18	CCU25129	Cochliobolus carbonum	1.11e+02	C	214	16	1.6	75	23	SYNINSPNI	Nucleotide sequence 5	4.48e+02
C	142	17	1.7	2564	15	SSU22108	Sus scrofa g protein-c	1.11e+02	C	215	16	1.6	84	25	I49638	Rat insulin-I gene sig	4.48e+02
C	143	17	1.7	2664	16	AF026039	Xenopus laevis EphB2-t	1.11e+02	C	216	16	1.6	90	25	E00026	Sequence 5 from patent	4.48e+02
C	144	17	1.7	2837	26	AC003913	*** SEQUENCING IN PROG	1.11e+02	C	217	16	1.6	112	21	ACBERB2	DNA coding of insulin	4.48e+02
C	145	17	1.7	2914	14	MUSMSIM6J	Mouse mRNA for mSim, c	1.11e+02	C	218	16	1.6	128	25	A07535	avian erythroblastosis	4.48e+02
C	146	17	1.7	2987	14	RATLYSHY	Rattus norvegicus lysz	1.11e+02	C	219	16	1.6	171	23	SYNHUMINA	Nucleotide sequence 16	4.48e+02
C	147	17	1.7	3071	14	MMU42554	Mus musculus sim trans	1.11e+02	C	220	16	1.6	176	13	E09184	Synthetic human insuli	4.48e+02
C	148	17	1.7	3113	19	MESARG	M. barkeri argininosucc	1.11e+02	C	221	16	1.6	181	16	SAVFOK3	Synthetic DNA sequence	4.48e+02
C	149	17	1.7	3120	14	MMJ000262	Mus musculus mRNA for	1.11e+02	C	222	16	1.6	187	16	SAVFOK10	S. leucomaenis leucomae	4.48e+02
C	150	17	1.7	3213	18	ATHHSP81	A. thaliana HSP81-1 gen	1.11e+02	C	223	16	1.6	191	16	SAVFOK6	S. leucomaenis leucomae	4.48e+02
C	151	17	1.7	3314	21	U23770	Murine adenovirus type	1.11e+02	C	224	16	1.6	206	16	SAVEOK1	S. leucomaenis leucomae	4.48e+02
C	152	17	1.7	3336	17	LCU75355	Lucilia cuprina ecdyst	1.11e+02	C	225	16	1.6	221	18	SCU21484	Schizophyllum commune	4.48e+02
C	153	17	1.7	3565	1	DMAC544	Drosophila melanogaste	1.11e+02	C	226	16	1.6	221	18	SCU21483	Schizophyllum commune	4.48e+02
C	154	17	1.7	3614	14	D64135	Mus musculus sim2 mRNA	1.11e+02	C	227	16	1.6	222	18	SCU21485	Schizophyllum commune	4.48e+02
C	155	17	1.7	3957	18	SPURF4	S. pombe (972 h-) DNA f	1.11e+02	C	228	16	1.6	222	18	ATU82401	Arabidopsis thaliana p	4.48e+02
C	156	17	1.7	3957	18	YSPHYPR	Schizosaccharomyces po	1.11e+02	C	229	16	1.6	246	18	EARPOL	Equisetum arvense pol	4.48e+02
C	157	17	1.7	3959	18	SCYJR010W	S. cerevisiae chromsom	1.11e+02	C	230	16	1.6	252	18	S78910	[Mul element insertion	4.48e+02
C	158	17	1.7	3963	14	MMU40576	Mus musculus single-mi	1.11e+02	C	231	16	1.6	270	25	A17333	Nucleotide sequence 5	4.48e+02
C	159	17	1.7	5354	18	SCYLL021W	S. cerevisiae chromsom	1.11e+02	C	232	16	1.6	273	25	I00910	Sequence 2 from Patent	4.48e+02
C	160	17	1.7	6031	17	DMPOSTSEX	D. melanogaster mRNA fo	1.11e+02	C	233	16	1.6	273	25	E00074	DNA sequence of human-	4.48e+02

234	16	1.6	277	23	ARHSINS	Artificial gene for hu	4.48e+02																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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380	16	1.6	3947	19	MBU77466	Mycobacterium bovis BC	4.48e+02
381	16	1.6	3985	14	RNGPROC	R.norvegicus mRNA for	4.48e+02
382	16	1.6	4076	21	BVDP125E	Bovine viral diarrhea	4.48e+02
383	16	1.6	4082	18	ADCPHTCH	A. capillus-veneris L.	4.48e+02
384	16	1.6	4117	14	RNAU696	Rattus norvegicus mRNA	4.48e+02
385	16	1.6	4224	17	DM5HT2AR	D./melanogaster mRNA fo	4.48e+02
386	16	1.6	4235	19	ECU58768	Escherichia coli ela 1	4.48e+02
387	16	1.6	4260	17	D38159	Bombyx mori mRNA for x	4.48e+02
388	16	1.6	4304	14	MMKIN1	M.musculus mRNA for ki	4.48e+02
389	16	1.6	4305	19	STRETF	S.mutans fructosyltran	4.48e+02
390	16	1.6	4314	17	AF017084	Hirudo medicinalis rec	4.48e+02
391	16	1.6	4443	23	PRS303	Yeast integrative vect	4.48e+02
392	16	1.6	4456	23	PRS403	Yeast integrative vect	4.48e+02
393	16	1.6	4636	16	GGAAAD	Chicken alpha-A and al	4.48e+02
394	16	1.6	4841	17	PFSC03060	Plasmodium falciparum	4.48e+02
395	16	1.6	4844	19	ECU23775	Escherichia coli Galf	4.48e+02
396	16	1.6	4955	17	DMU37018	Drosophila melanogaste	4.48e+02
397	16	1.6	4967	23	PRS313	Yeast centromere vecto	4.48e+02
398	16	1.6	4970	23	PRS413	Yeast centromere vecto	4.48e+02
399	16	1.6	5038	18	SCYJL106W	S.cerevisiae chromosom	4.48e+02
400	16	1.6	5365	17	CEVZC374L	Caenorhabditis elegans	4.48e+02
401	16	1.6	5380	19	BMSDHCAB	B.macerans sdhc, sdha,	4.48e+02
402	16	1.6	5425	14	RATINSTI	Rat insulin-I (ins-1)	4.48e+02
403	16	1.6	5429	23	CVU89928	Cloning vector pHTSi-1	4.48e+02
404	16	1.6	5586	23	AF041808	Cloning vector ygalset	4.48e+02
405	16	1.6	5697	18	NCU50264	Neurospora crassa two-	4.48e+02
406	16	1.6	5703	14	MMSMGAS1	Mus musculus smooth mu	4.48e+02
407	16	1.6	5767	14	D83002	Mouse mRNA for tyrosin	4.48e+02
408	16	1.6	5797	23	PRS423	Yeast episomal vector	4.48e+02
409	16	1.6	5798	21	HSMICP4A	Marek's disease virus	4.48e+02
410	16	1.6	6143	18	FN062930	Filobasidiella neoform	4.48e+02
411	16	1.6	6373	21	AEVPDNA	Avian erythroblastosis	4.48e+02
412	16	1.6	6373	14	MMSNS	M.musculus mRNA for SN	4.48e+02
413	16	1.6	6388	19	MTU66108	Mycobacterium tubercul	4.48e+02
414	16	1.5	6400	15	SSCMYC	S.scrofa c-myc gene.	4.48e+02
415	16	1.6	6446	17	AF023484	Drosophila melanogaste	4.48e+02
416	16	1.6	6509	18	ATHPHTOCHB	Arabidopsis thaliana p	4.48e+02
417	16	1.6	6545	18	NCU53189	Neurospora crassa osmo	4.48e+02
418	16	1.6	6563	16	CHEKERBBF	Chicken c-erbB oncogen	4.48e+02
419	16	1.6	6597	21	MEAL1	Measles virus mRNA for	4.48e+02
420	16	1.6	6675	17	DMAC001881	Drosophila melanogaste	4.48e+02
421	16	1.6	6778	17	DMUADHG	Drosophila mulleri adh	4.48e+02
422	16	1.6	6786	23	CVU89927	Cloning vector pHTSi,	4.48e+02
423	16	1.6	6812	19	SPPARCETP	S.pneumoniae parC, par	4.48e+02
424	16	1.6	6824	25	A25909	Yeast integration vect	4.48e+02
425	16	1.6	7097	14	MMU82624	Mus musculus amyloid p	4.48e+02
426	16	1.6	7173	18	NTU59683	Nicotiana tabacum squa	4.48e+02
427	16	1.6	7241	21	HS1ATIF1	HSV1 (strain F) alpha-	4.48e+02
428	16	1.6	7305	19	KPU93843	Klebsiella pneumoniae	4.48e+02
429	16	1.6	7305	18	PTGIM62B	P.trichocarpa chitinas	4.48e+02
430	16	1.6	7689	17	DMTIMEL1	Drosophila melanogaste	4.48e+02
431	16	1.6	8673	19	AF003541	Mycoplasma pulmonis re	4.48e+02
432	16	1.6	8936	14	RNFAS	Rat mRNA for fatty aci	4.48e+02
433	16	1.6	9039	21	HTVMEL5	Human T-cell leukemia	4.48e+02
434	16	1.6	9136	14	RATFASA	Rattus norvegicus fatt	4.48e+02
435	16	1.6	9143	14	RNFASRNA	R.norvegicus FAS mRNA	4.48e+02
436	16	1.6	9246	19	U39723	Mycoplasma genitalium	4.48e+02
437	16	1.6	9675	19	BTPGI2XX	Bacillus thuringiensis	4.48e+02
438	16	1.6	10010	19	HTU32709	Haemophilus influenzae	4.48e+02
439	16	1.6	10080	19	MYCGLTX	Mycoplasma pulmonis g1	4.48e+02
440	16	1.6	10080	19	MYCGLTX	Mycoplasma pulmonis g1	4.48e+02
441	16	1.6	10161	19	AE000797	Methanobacterium therm	4.48e+02
442	16	1.6	10166	23	UCU89960	Cloning vector pEG202	4.48e+02
443	16	1.6	10181	19	ECAE000492	Escherichia coli K-12	4.48e+02
444	16	1.6	10380	19	AE000932	Methanobacterium therm	4.48e+02
445	16	1.6	10409	19	ECAE000316	Escherichia coli K-12	4.48e+02
446	16	1.6	10603	19	ECAE000249	Escherichia coli K-12	4.48e+02
447	16	1.6	10833	14	MMZP3G	Mus musculus mRNA for	4.48e+02
448	16	1.6	11370	18	PMCMG910	Pneumocystis carinii g	4.48e+02
449	16	1.6	11454	23	XXU01086	Cloning vector pYAC4 f	4.48e+02
450	16	1.6	11463	19	RHMNOLBTU	Rhizobium fredii modul	4.48e+02
451	16	1.6	11844	19	AE000107	Rhizobium sp. NGR234 p	4.48e+02
452	16	1.6	12571	19	AE000986	Archaeoglobus fulgidus	4.48e+02
453	16	1.6	13045	21	GHU17705	Gallid herpesvirus 1 i	4.48e+02
454	16	1.6	13143	19	U67563	Methanococcus jannasch	4.48e+02
455	16	1.6	13205	19	U67588	Methanococcus jannasch	4.48e+02
456	16	1.6	13232	17	DDID16466	Cellular slime mold M1	4.48e+02
457	16	1.6	13548	19	D90858	E.coli genomic DNA, Ko	4.48e+02
458	16	1.6	14011	17	CEJ26510	Caenorhabditis elegans	4.48e+02
459	16	1.6	15212	19	D90795	E.coli genomic DNA, Ko	4.48e+02
460	16	1.6	15595	19	GU39694	Mycoplasma genitalium	4.48e+02
461	16	1.6	15598	16	GGLRPA2MR	G.gallus mRNA for LRP/	4.48e+02
462	16	1.6	15676	19	D90857	E.coli genomic DNA, Ko	4.48e+02
463	16	1.6	15827	23	CVU13189	Cloning vector pYACneo	4.48e+02
464	16	1.6	16383	19	D90794	E.coli genomic DNA, Ko	4.48e+02
465	16	1.6	19024	17	RATFASYN	R.norvegicus FAS gene	4.48e+02
466	16	1.6	19615	17	CEJ05F1A	Caenorhabditis elegans	4.48e+02
467	16	1.6	20159	26	AC003666	Homo sapiens; HTGS pha	4.48e+02
468	16	1.6	21115	17	AB005911	Bombyx mori DNA for xa	4.48e+02
469	16	1.6	22245	17	CET27E9	Caenorhabditis elegans	4.48e+02
470	16	1.6	23713	14	RNFASDNA	R.norvegicus FAS gene	4.48e+02
471	16	1.6	23738	17	CEF08H9	Caenorhabditis elegans	4.48e+02
472	16	1.6	24711	17	CEJF03D2	Caenorhabditis elegans	4.48e+02
473	16	1.6	24903	17	CELAC7	Caenorhabditis elegans	4.48e+02
474	16	1.6	25951	16	AB004829	Fugu rubripes gene for	4.48e+02
475	16	1.6	26180	17	CEJ01B7	Caenorhabditis elegans	4.48e+02
476	16	1.6	27323	19	AE000789	Borrelia burgdorferi p	4.48e+02
477	16	1.6	27848	17	CEM01E5	Caenorhabditis elegans	4.48e+02
478	16	1.6	29807	14	MMU73107	Mus musculus adenosine	4.48e+02
479	16	1.6	29950	19	AF015775	Bacillus subtilis yoda	4.48e+02
480	16	1.6	30100	19	AF006665	Bacillus subtilis 168	4.48e+02
481	16	1.6	30969	17	CELT13B5	Caenorhabditis elegans	4.48e+02
482	16	1.6	32793	17	CEJL18F3	Caenorhabditis elegans	4.48e+02
483	16	1.6	32965	17	CEM01G7	Caenorhabditis elegans	4.48e+02
484	16	1.6	33010	17	CEJLZC196	Caenorhabditis elegans	4.48e+02
485	16	1.6	33539	17	CEJF54E7	Caenorhabditis elegans	4.48e+02
486	16	1.6	35126	17	CEJF1D11	Caenorhabditis elegans	4.48e+02
487	16	1.6	35126	17	CEJF1D11	Caenorhabditis elegans	4.48e+02
488	16	1.6	35976	17	CEJLF25B5	Caenorhabditis elegans	4.48e+02
489	16	1.6	36532	17	CEJF57B1	Caenorhabditis elegans	4.48e+02
490	16	1.6	36759	17	CEJ05F1	Caenorhabditis elegans	4.48e+02
491	16	1.6	36819	19	MTY20H10	Mycobacterium tubercul	4.48e+02
492	16	1.6	37154	17	CEJLR148	Caenorhabditis elegans	4.48e+02
493	16	1.6	37189	26	HSCB33B7	Human DNA sequence ***	4.48e+02
494	16	1.6	37549	18	SCXLTORFS	S.cerevisiae DNA from	4.48e+02
495	16	1.6	38383	17	CEJF35H8	Caenorhabditis elegans	4.48e+02
496	16	1.6	39215	17	CED1054	Caenorhabditis elegans	4.48e+02
497	16	1.6	39580	17	CEJF45H7	Caenorhabditis elegans	4.48e+02
498	16	1.6	40124	17	CEJF09E8	Caenorhabditis elegans	4.48e+02
499	16	1.6	40830	18	SPAC2C6	S.pombe chromosome I c	4.48e+02
500	16	1.6	40897	17	CEJL39D10	Caenorhabditis elegans	4.48e+02
501	16	1.6	41212	17	CEJF32B4	Caenorhabditis elegans	4.48e+02
502	16	1.6	41351	17	CEJLF42C5	Caenorhabditis elegans	4.48e+02
503	16	1.6	42042	17	CEJF34B4	Caenorhabditis elegans	4.48e+02
504	16	1.6	42793	18	SC9168	S.cerevisiae chromosom	4.48e+02
505	16	1.6	43576	14	CEC35D6	Caenorhabditis elegans	4.48e+02
506	16	1.6	43584	17	CEC08B6	Caenorhabditis elegans	4.48e+02
507	16	1.6	43576	14	AC003994	Mouse cosmid m53a271	4.48e+02
508	16	1.6	43895	18	SPAC4A8	Caenorhabditis elegans	4.48e+02
509	16	1.6	44000	26	HSAC000047	Homo sapiens clone c11	4.48e+02
510	16	1.6	45022	17	CEC34D1	Caenorhabditis elegans	4.48e+02
511	16	1.6	45022	17	SS56KBF	S.solfataricus 56 kbp	4.48e+02
512	16	1.6	56105	19	CEJF01D5	Caenorhabditis elegans	4.48e+02
513	16	1.6	56105	19	CEJF01D5	Caenorhabditis elegans	4.48e+02
514	16	1.6	58382	26	CET28A8	Bacillus subtilis geno	4.48e+02
515	16	1.6	65143	19	ATT10114	Arabidopsis thaliana D	4.48e+02
516	16	1.6	73037	18	AB007648	Arabidopsis thaliana g	4.48e+02
517	16	1.6	76329	18	AB007648	Arabidopsis thaliana g	4.48e+02
518	16	1.6	78064	26	HSAC000376	*** SEQUENCING IN PROG	4.48e+02
519	16	1.6	78344	18	TM017A05	Arabidopsis thaliana B	4.48e+02
520	16	1.6	78616	14	AC000398	Genomic sequence from	4.48e+02
521	16	1.6	79046	18	AB008267	Arabidopsis thaliana g	4.48e+02
522	16	1.6	80689	17	AC003053	Drosophila melanogaste	4.48e+02
523	16	1.6	80770	17	AB005240	Arabidopsis thaliana g	4.48e+02
524	16	1.6	82692	17	AC003924	Drosophila melanogaste	4.48e+02
525	16	1.6					

C	526	16	1.6	82697	18	ATT9A21	Arabidopsis thaliana D	4.48e+02	C	599	16	1.6	207730	19	BSTB0011	Bacillus subtilis comp	4.48e+02
C	527	16	1.6	82918	18	AB010071	Arabidopsis thaliana g	4.48e+02	C	600	16	1.6	212150	19	BSUB0020	Bacillus subtilis comp	4.48e+02
C	528	16	1.6	83450	18	AB009054	Arabidopsis thaliana g	4.48e+02	C	601	16	1.6	218062	26	HS388M5	Human DNA sequence ***	4.48e+02
C	529	16	1.6	85065	17	AC001660	Drosophila melanogaste	4.48e+02	C	602	16	1.6	222295	26	CEY7A9	Caenorhabditis elegans	4.48e+02
C	530	16	1.6	86566	8	HSU90583	Human 86Kb contig from	4.48e+02	C	603	16	1.6	222295	26	CEY7A9	Caenorhabditis elegans	4.48e+02
C	531	16	1.6	94382	26	AC003680	*** SEQUENCING IN PROG	4.48e+02	C	604	16	1.6	226018	26	HS90L6	Human DNA sequence ***	4.48e+02
C	532	16	1.6	95134	26	HS265J14	Human DNA sequence ***	4.48e+02	C	605	16	1.6	229546	26	HS268H5	Human DNA sequence ***	4.48e+02
C	533	16	1.6	97226	26	HS299D3	Human DNA sequence ***	4.48e+02	C	606	16	1.6	238582	26	AC003059	*** SEQUENCING IN PROG	4.48e+02
C	534	16	1.6	102815	26	HS366N23	Human DNA sequence ***	4.48e+02	C	607	16	1.6	242701	26	CEY51H1	Caenorhabditis elegans	4.48e+02
C	535	16	1.6	104861	18	ATU93215	Arabidopsis thaliana c	4.48e+02	C	608	16	1.6	249452	26	AC004085	Homo sapiens; HTGS pha	4.48e+02
C	536	16	1.6	106929	26	HS821D11	Human DNA sequence ***	4.48e+02	C	609	16	1.6	256664	26	CEY39G8	Caenorhabditis elegans	4.48e+02
C	537	16	1.6	107379	19	SEGCPIR	S.hygrosopicus gene c	4.48e+02	C	610	16	1.6	257948	26	HS212G6	Human DNA sequence ***	4.48e+02
C	538	16	1.6	108360	21	HS1ULR	Herpes simplex virus t	4.48e+02	C	611	16	1.6	263842	26	HS393P23	Human DNA sequence ***	4.48e+02
C	539	16	1.6	109560	18	F5114	Sequence of BAC F5114	4.48e+02	C	612	16	1.6	268735	26	AC003684	Homo sapiens; HTGS pha	4.48e+02
C	540	16	1.6	111062	26	HSAC001237	*** SEQUENCING IN PROG	4.48e+02	C	613	16	1.6	276261	26	HSAC000406	*** SEQUENCING IN PROG	4.48e+02
C	541	16	1.6	112444	26	AC003022	*** SEQUENCING IN PROG	4.48e+02	C	614	16	1.6	280217	26	CEY41E3	Caenorhabditis elegans	4.48e+02
C	542	16	1.6	112726	26	CEY21F11	Caenorhabditis elegans	4.48e+02	C	615	16	1.6	286079	26	CEY54G9	Caenorhabditis elegans	4.48e+02
C	543	16	1.6	114505	18	F20P5	Sequence of BAC F20P5	4.48e+02	C	616	16	1.6	291821	26	CEY48E1	Caenorhabditis elegans	4.48e+02
C	544	16	1.6	116156	18	ATAC002343	Arabidopsis thaliana B	4.48e+02	C	617	16	1.6	307751	26	CEY48B6	Caenorhabditis elegans	4.48e+02
C	545	16	1.6	118743	26	HS516C23	Human DNA sequence ***	4.48e+02	C	618	16	1.6	338534	19	ECOWW93	Escherichia coli K-12	4.48e+02
C	546	16	1.6	120000	26	HSAC000005	*** SEQUENCING IN PROG	4.48e+02	C	619	15	1.5	44	16	CHKOIH02	Chicken ovalinhibitor g	1.66e+03
C	547	16	1.6	122928	18	ATAC002387	Arabidopsis thaliana c	4.48e+02	C	620	15	1.5	161	16	AB001864	Kokanee salmon DNA for	1.66e+03
C	548	16	1.6	124225	18	IG002N01	Arabidopsis thaliana B	4.48e+02	C	621	15	1.5	171	16	QUFGFRH7	Quail DNA for fibrobla	1.66e+03
C	549	16	1.6	124225	18	IG002N01	Arabidopsis thaliana B	4.48e+02	C	622	15	1.5	188	15	OARGH2	Ovis aries growth horm	1.66e+03
C	550	16	1.6	124689	26	AC003060	*** SEQUENCING IN PROG	4.48e+02	C	623	15	1.5	217	15	OVIAGH4	Ovis aries growth horm	1.66e+03
C	551	16	1.6	126581	26	AC003957	*** SEQUENCING IN PROG	4.48e+02	C	624	15	1.5	270	18	TOBRANA	Nicotiana tabacum smal	1.66e+03
C	552	16	1.6	128116	26	HS191L6	Human DNA sequence ***	4.48e+02	C	625	15	1.5	273	17	FHU10316	Fasciola hepatica clon	1.66e+03
C	553	16	1.6	128340	26	AC002419	*** SEQUENCING IN PROG	4.48e+02	C	626	15	1.5	299	14	RNVN01	Rat gene fragmant for	1.66e+03
C	554	16	1.6	128598	19	D90912	Synechocystis sp. PCC6	4.48e+02	C	627	15	1.5	328	14	AF014497	Mus musculus sorbitol	1.66e+03
C	555	16	1.6	128607	26	HS313L4	Human DNA sequence ***	4.48e+02	C	628	15	1.5	331	14	MMALCDS	M. musculus MAL gene, e	1.66e+03
C	556	16	1.6	131597	26	AC004005	*** SEQUENCING IN PROG	4.48e+02	C	629	15	1.5	363	15	OVAAGH2	Ovis aries growth horm	1.66e+03
C	557	16	1.6	134706	26	HS230G1	Human DNA sequence ***	4.48e+02	C	630	15	1.5	384	21	HPGCIUS1P	Hepatitis C virus (iso	1.66e+03
C	558	16	1.6	143308	19	D90913	Synechocystis sp. PCC6	4.48e+02	C	631	15	1.5	405	13	E01795	mRNA sequence coding f	1.66e+03
C	559	16	1.6	146360	26	HS104C13	Human DNA sequence ***	4.48e+02	C	632	15	1.5	428	18	AFU19999	Avena fatua nondormanc	1.66e+03
C	560	16	1.6	147399	26	AC003667	Homo sapiens; HTGS pha	4.48e+02	C	633	15	1.5	481	14	RATMUSGLY	Rattus norvegicus glyc	1.66e+03
C	561	16	1.6	148103	26	HS1216H12	Human DNA sequence ***	4.48e+02	C	634	15	1.5	483	15	MTBTCPN10	B. taurus cpn 10 mRNA.	1.66e+03
C	562	16	1.6	148142	19	D90915	Synechocystis sp. PCC6	4.48e+02	C	635	15	1.5	523	25	IL4723	Sequence 2 from patent	1.66e+03
C	563	16	1.6	148583	26	CEY17D7	Caenorhabditis elegans	4.48e+02	C	636	15	1.5	549	18	VFLBKMR	V.faba mRNA for leghem	1.66e+03
C	564	16	1.6	148540	26	AC004103	Homo sapiens; HTGS pha	4.48e+02	C	637	15	1.5	598	16	XLBGLIR	Xenopus laevis mRNA fo	1.66e+03
C	565	16	1.6	149436	26	HS222E13	Human DNA sequence ***	4.48e+02	C	638	15	1.5	649	21	HS21CPI0	Herpes simplex virus t	1.66e+03
C	566	16	1.6	150894	19	D90904	Synechocystis sp. PCC6	4.48e+02	C	639	15	1.5	694	16	CHKATH	Gallus gallus avian th	1.66e+03
C	567	16	1.6	152261	21	HE11G	Herpes simplex virus (4.48e+02	C	640	15	1.5	706	14	MUSCSP1A	Mouse serine protease	1.66e+03
C	568	16	1.6	152708	26	HS964D12	Human DNA sequence ***	4.48e+02	C	641	15	1.5	722	18	SCCYCL	Yeast mRNA for cycloph	1.66e+03
C	569	16	1.6	153618	26	AC003106	Homo sapiens; HTGS pha	4.48e+02	C	642	15	1.5	725	14	MMPRKT	M. musculus mRNA for pr	1.66e+03
C	570	16	1.6	155398	26	AC003020	*** SEQUENCING IN PROG	4.48e+02	C	643	15	1.5	740	19	AF001201	Neisseria meningitidis	1.66e+03
C	571	16	1.6	155398	26	AC003020	*** SEQUENCING IN PROG	4.48e+02	C	644	15	1.5	755	15	OAGH2	Ovis aries growth horm	1.66e+03
C	572	16	1.6	159500	26	HS18601	Human DNA sequence ***	4.48e+02	C	645	15	1.5	796	14	MMMCSP2	Mouse mRNA for MCSP-2	1.66e+03
C	573	16	1.6	159877	26	HS217C2	Human DNA sequence ***	4.48e+02	C	646	15	1.5	826	17	OVU47812	Onchocerca volvulus cy	1.66e+03

672	15	1.5	1207	17	DMU51058	Drosophila willistoni	1.66e+03	C	745	15	1.5	2831	19	SSQACFREP	Staphylococcus sp. gen	1.66e+03
673	15	1.5	1213	17	DPU51080	Drosophila paulistorum	1.66e+03	C	746	15	1.5	2843	18	SCYKL125W	S.cerevisiae chromosom	1.66e+03
674	15	1.5	1220	17	DMU30470	Drosophila melanogaste	1.66e+03	C	747	15	1.5	2871	18	YSCRNAPOL	Saccharomyces cerevisi	1.66e+03
675	15	1.5	1222	15	BOVMR1B	Bovine BOLA-DRA mRNA f	1.66e+03	C	748	15	1.5	2885	16	DRPOU	D.rosio zp-50 POU gene	1.66e+03
676	15	1.5	1222	15	BTEENKE	Bovine messenger RNA f	1.66e+03	C	749	15	1.5	2931	17	DMR1570	Drosophila melanogaste	1.66e+03
677	15	1.5	1234	14	AF015311	Rattus norvegicus conn	1.66e+03	C	750	15	1.5	3002	17	S57174	arrestin homolog [Locu	1.66e+03
678	15	1.5	1238	18	BJY10847	Brassica juncea mRNA f	1.66e+03	C	751	15	1.5	3004	18	YSCTCFCl	S.cerevisiae transcrip	1.66e+03
679	15	1.5	1239	25	I55000	Sequence 22 from paten	1.66e+03	C	752	15	1.5	3012	25	I40808	Sequence 1 from patent	1.66e+03
680	15	1.5	1253	17	CELLIN39A	Caenorhabditis elegans	1.66e+03	C	753	15	1.5	3012	25	I68246	Sequence 1 from patent	1.66e+03
681	15	1.5	1278	16	GGRAB5CLP	G.gallus mRNA for rab5	1.66e+03	C	754	15	1.5	3015	19	CCU30321	Clostridium cellulolyt	1.66e+03
682	15	1.5	1285	16	SCU75453	Serinus canaria growth	1.66e+03	C	755	15	1.5	3027	18	SCYDL128W	S.cerevisiae chromosom	1.66e+03
683	15	1.5	1292	18	ATHPPHAC	Arabidopsis thaliana p	1.66e+03	C	756	15	1.5	3037	14	RNSCEAl	R.norvegicus mRNA I fo	1.66e+03
684	15	1.5	1309	16	CCDOPD1B	Cypripus carpio mRNA f	1.66e+03	C	757	15	1.5	3061	16	DRRNAHELI	R.norvegicus mRNA I fo	1.66e+03
685	15	1.5	1331	14	MMU01915	Mus musculus DNA topoi	1.66e+03	C	758	15	1.5	3071	14	RNRSCA3	R.norvegicus mRNA for	1.66e+03
686	15	1.5	1350	21	RVU22633	Rabies virus 8721AFS n	1.66e+03	C	759	15	1.5	3111	17	DRO22DC96Z	Drosophila melanogaste	1.66e+03
687	15	1.5	1380	19	BACALR	B.stearothermophilus a	1.66e+03	C	760	15	1.5	3126	14	RNSCEA2	R.norvegicus mRNA II f	1.66e+03
688	15	1.5	1388	17	D50584	Hemigrapsus sanguineus	1.66e+03	C	761	15	1.5	3134	25	I14728	Sequence 7 from patent	1.66e+03
689	15	1.5	1429	16	CHKBGC	Chicken B-G mRNA, 3' e	1.66e+03	C	762	15	1.5	3138	19	ECCODAB	E.coli codBA operon en	1.66e+03
690	15	1.5	1478	25	I36807	Sequence 27 from paten	1.66e+03	C	763	15	1.5	3199	15	DOGSNCE	Dog cardiac sarcolemma	1.66e+03
691	15	1.5	1484	18	SCYBR152W	S.cerevisiae chromosom	1.66e+03	C	764	15	1.5	3209	19	ECU23148	Escherichia coli gluta	1.66e+03
692	15	1.5	1512	14	MMU70656	Mus musculus sex deter	1.66e+03	C	765	15	1.5	3344	14	AF004666	Mus musculus sodium-ca	1.66e+03
693	15	1.5	1517	14	MLLY6F112	M.musculus Ly-6F.1 gen	1.66e+03	C	766	15	1.5	3390	25	I68269	Sequence 26 from paten	1.66e+03
694	15	1.5	1528	14	RATCHGA	Rattus norvegicus (cto	1.66e+03	C	767	15	1.5	3405	17	DMAC001719	Sequence 24 from paten	1.66e+03
695	15	1.5	1549	14	MMU70657	Mus musculus castaneus	1.66e+03	C	768	15	1.5	3416	25	I40830	Drosophila melanogaste	1.66e+03
696	15	1.5	1610	19	NGAZURIN	Neisseria gonorrhoeae	1.66e+03	C	769	15	1.5	3423	17	SGCYCBSPV	S.granularis mRNA for	1.66e+03
697	15	1.5	1622	19	MSESCACOAD	Megasphaera elsdeni s	1.66e+03	C	770	15	1.5	3432	17	DMPXL1HOM	Drosophila melanogaste	1.66e+03
698	15	1.5	1638	18	ATHAHP1B	A.thaliana mRNA for AH	1.66e+03	C	771	15	1.5	3443	17	DRO37DC12Z	Drosophila melanogaste	1.66e+03
699	15	1.5	1677	14	MUSJGR1AX	Mus musculus guanine n	1.66e+03	C	772	15	1.5	3456	17	DMLODE	D.melanogaster lodesta	1.66e+03
700	15	1.5	1682	19	ANAPETFI	Anabaena petfi gene fo	1.66e+03	C	773	15	1.5	3486	15	OATSHR	Ovis aries mRNA for th	1.66e+03
701	15	1.5	1711	14	RNCYP2B6	Rattus norvegicus cyto	1.66e+03	C	774	15	1.5	3494	18	PMCMSGF	Pneumocystis carinii (1.66e+03
702	15	1.5	1711	14	MUSJGR1A	Mus musculus guanine n	1.66e+03	C	775	15	1.5	3500	14	RNU93052	Rattus norvegicus calc	1.66e+03
703	15	1.5	1736	14	RATSR13	Rat SR13 myelin protei	1.66e+03	C	776	15	1.5	3504	17	DMKNR1	Drosophila Knr1 gene f	1.66e+03
704	15	1.5	1739	25	E077339	CDNA encoding beta 1,3	1.66e+03	C	777	15	1.5	3557	17	EHVSA	E.histolytica mRNA for	1.66e+03
705	15	1.5	1762	17	DROSIAB	Drosophila virilis SEV	1.66e+03	C	778	15	1.5	3574	14	MUSPRPMPB	Mouse PRP gene encodin	1.66e+03
706	15	1.5	1790	16	CHKBGA	Chicken B-G mRNA, comp	1.66e+03	C	779	15	1.5	3660	17	SP3A2	S.purpuratus mRNA for	1.66e+03
707	15	1.5	1807	14	MUSGAS3A	Mouse growth arrest sp	1.66e+03	C	780	15	1.5	3758	17	CELCKII	C.elegans casein kinas	1.66e+03
708	15	1.5	1807	17	CELCOL19A	C. elegans collagen (C	1.66e+03	C	781	15	1.5	3830	19	CLOCELB	Clostridium josui celB	1.66e+03
709	15	1.5	1816	25	I14726	Sequence 5 from patent	1.66e+03	C	782	15	1.5	3840	19	PDBCl	P. denitrificans bcl op	1.66e+03
710	15	1.5	1822	25	I14727	Sequence 6 from patent	1.66e+03	C	783	15	1.5	3840	19	PDEBC1	P. denitrificans bcl op	1.66e+03
711	15	1.5	1888	18	SCMNR1W30	Saccharomyces cerevisi	1.66e+03	C	784	15	1.5	3897	16	CHKH3A1	Chicken histone gene e	1.66e+03
712	15	1.5	1912	15	BOVATPSYN	Bovine mitochondrial a	1.66e+03	C	785	15	1.5	3899	15	SHPGHOV	Ovine growth hormone g	1.66e+03
713	15	1.5	1915	14	MMULIP2	M.musculus mRNA for UI	1.66e+03	C	786	15	1.5	4075	19	SOORFS	S.pneumoniae yorflA,B,	1.66e+03
714	15	1.5	1937	14	RATASPATB	Rat aspartate aminotra	1.66e+03	C	787	15	1.5	4075	14	MMU66473	Mus musculus preprogra	1.66e+03
715	15	1.5	1993	21	ADRORF1G	Rattus norvegicus susl py	1.66e+03	C	788	15	1.5	4118	17	YSCHATP	S.cerevisiae vacuolar	1.66e+03
716	15	1.5	1996	14	RRU15660	Cyprinus carpio mRNA f	1.66e+03	C	789	15	1.5	4166	21	DB6577	Human herpesvirus type	1.66e+03
717	15	1.5	2056	16	CCDOPD1A4	Xenopus laevis gamma-c	1.66e+03	C	791	15	1.5	4289	17	DMRLBC1	D.melanogaster genes R	1.66e+03
718	15	1.5	2057	16	XELCRYB	Rat mRNA for Ash-m, co	1.66e+03	C	792	15	1.5	4320	18	LETPRPFI	L. esculentum TPRP-Fl	1.66e+03
719	15	1.5	2099	14	RATASHM	S.cerevisiae chromosom	1.66e+03	C	793	15	1.5	4339	19	YSCPDRI	Yeast (S.cerevisiae) P	1.66e+03
720	15	1.5	2124	18	SCYDL129W	S.cerevisiae chromosom	1.66e+03	C	794	15	1.5	4378	18	STYCARABA	Salmonella typhimurium	1.66e+03
721	15	1.5	2169	18	SCYOR323C	Mus musculus protein k	1.66e+03	C	795	15	1.5	4591	14	MMTIMP3MI	M.musculus (Balb/C) TI	1.66e+03
722	15	1.5	2235	14	AF028009	Yeast transcription fa	1.66e+03	C	796	15	1.5	4676	21	CHU25806	Cercopithecine herpesv	1.66e+03
723	15	1.5	2242	18	YSCTF395C	Rat cystrathionine beta	1.66e+03	C	797	15	1.5	4937	18	ATCPY450D	A.thaliana gene cytoch	1.66e+03
724	15	1.5	2248	14	RATRCBSC	Mouse G-protein couple	1.66e+03	C	798	15	1.5	4968	15	AF034077	Equus caballus alpha-1	1.66e+03
725	15	1.5	2253	14	MUSGIR	Spodoptera frugiperda	1.66e+03	C	799	15	1.5	4980	15	BTROSGL1	Bos taurus rod outer s	1.66e+03
726	15	1.5	2255	17	SFU15038	P.anserina ASI gene, c	1.66e+03	C	800	15	1.5	5124	19	AF004822	Neisseria meningitidis	1.66e+03
727	15	1.5	2273	18	PAASIGNA	Mouse heat shock-relat	1.66e+03	C	801	15	1.5	5264	14	RNU61261	Rattus norvegicus lamt	1.66e+03
728	15	1.5	2298	14	MUSHSP70	Mouse mRNA for chromog	1.66e+03	C	802	15	1.5	5322	17	DMEHATPBS1	D.melanogaster H+-ATPa	1.66e+03
729	15	1.5	2340	14	MMGHRB	Sequence 11 from Paten	1.66e+03	C	803	15	1.5	5352	14	MMU26707	Mus musculus voltage-g	1.66e+03
730	15	1.5	2365	25	A38773	Mouse myocyte nuclear	1.66e+03	C	804	15	1.5	5423	19	ECNUSA2	E.coli nusA operon inc	1.66e+03
731	15	1.5	2370	14	MUSDNABIND	Bos taurus thyrotropin	1.66e+03	C	805	15	1.5	5467	25	I12880	Sequence 12 from paten	1.66e+03
732	15	1.5	2374	15	BTU15570	Mouse mRNA for tyrosin	1.66e+03	C	806	15	1.5	5686	19	CLOCELCGE	Clostridium cellulolyt	1.66e+03
733	15	1.5	2393	14	MUSTSPK	Mouse preproinsulin ge	1.66e+03	C	807	15	1.5	5721	17	DMU80223	Drosophila melanogaste	1.66e+03
734	15	1.5	2408	14	MNINSIIG	B.napus BnGRP10 gene e	1.66e+03	C	808	15	1.5	5783	17	AB007850	Athalia rosae mRNA for	1.66e+03
735	15	1.5	2412	18	BNGRP10G	H.sapiens TSH receptor	1.66e+03	C	809	15	1.5	5794	19	WZU14952	Weeksella zoohelcum Ac	1.66e+03
736	15	1.5	2415	25	A34990	Brassica rapa zinc-fin	1.66e+03	C	810	15	1.5	5798	14	RNU92079	Rattus norvegicus GlGF	1.66e+03
737	15	1.5	2477	18	BRU76555	O.doifleini hemocyanin	1.66e+03	C	811	15	1.5	5900	18	AF034614	Zymomonas mobilis carb	1.66e+03
738	15	1.5	2504	17	OCTODEA	C.cortunix FREK mRNA f	1.66e+03	C	812	15	1.5	6108	19	AMGI0B	A.majus globosa gene.	1.66e+03
739	15	1.5	2573	16	CCFRREK	Elephantulus rufescens	1.66e+03	C	813	15	1.5	6730	14	D86949	Mouse mRNA for plexin	1.66e+03
740	15	1.5	2580	15	BRU97339	S.cerevisiae chromosom	1.66e+03	C	814	15	1.5	7020	18	ATSBE21	Arabidopsis thaliana S	1.66e+03
741	15	1.5	2641	18	SCYBR123C	Emericella nidulans ca	1.66e+03	C	815	15	1.5	7065	19	STU18559	Salmonella typhimurium	1.66e+03
742	15	1.5	2674	18	ENU37803	Chicken retinal glutam	1.66e+03	C	816	15	1.5	7306	14	MUSPRPC2	Mouse proliline-rich pro	1.66e+03
743	15	1.5	2728	16	CHKGN	*** SEQUENCING IN PROG	1.66e+03	C	817	15	1.5	7557	19	EPFAD10RF	E.faecalis plasmid PAD	1.66e+03
744	15	1.5	2799	26	AC002808			C								

C	818	15	1.5	7560	17	TCHB	T.castaneum hunchback	1.66e+03
C	819	15	1.5	7578	19	PTU53507	Pseudomonas Jrl isopro	1.66e+03
C	820	15	1.5	7713	14	MUSRSLTMA	Mouse L1Md-A2 repetiti	1.66e+03
C	821	15	1.5	7829	19	RPPLAS	Buchnera aphidicola of	1.66e+03
C	822	15	1.5	8143	19	EAG97504	Briania amylovora HrpW	1.66e+03
C	823	15	1.5	8421	17	DVU39746	Drosophila virilis gla	1.66e+03
C	824	15	1.5	8473	17	DROFA1FA	Fruitfly fat facets mr	1.66e+03
C	825	15	1.5	8608	15	OCBCBIT1	O.cuniculus mRNA for b	1.66e+03
C	826	15	1.5	9138	16	DUKFA5A	Duck (A.platyrhynchos)	1.66e+03
C	827	15	1.5	9155	19	ABO00084	Rhizobium sp. NGR234 p	1.66e+03
C	828	15	1.5	9603	21	AF014811	Zucchini yellow mosai	1.66e+03
C	829	15	1.5	9603	14	CGU09104	Cricetulus griseus SIN	1.66e+03
C	830	15	1.5	9915	15	BTATPAAA	B.taurus atpAl gene fo	1.66e+03
C	831	15	1.5	10042	19	HPAE000574	Helicobacter pylori se	1.66e+03
C	832	15	1.5	10213	19	U39716	Mycoplasma genitalium	1.66e+03
C	833	15	1.5	10372	19	H1U32734	Haemophilus influenzae	1.66e+03
C	834	15	1.5	10512	19	ECABE000381	Escherichia coli K-12	1.66e+03
C	835	15	1.5	10536	19	U67488	Methanococcus jannasch	1.66e+03
C	836	15	1.5	10580	19	U67499	Methanococcus jannasch	1.66e+03
C	837	15	1.5	11817	14	MMU70015	Mus musculus lysosomal	1.66e+03
C	838	15	1.5	12260	21	AF041040	Pestivirus type 1 poly	1.66e+03
C	839	15	1.5	12720	25	I50980	Sequence 11 from paten	1.66e+03
C	840	15	1.5	12934	18	SCYKR054C	S.cerevisiae chromosom	1.66e+03
C	841	15	1.5	13453	19	ECABE000309	Escherichia coli K-12	1.66e+03
C	842	15	1.5	13605	19	BSORIGS	B.subtilis genes rpmH,	1.66e+03
C	843	15	1.5	14162	19	ECPO157	E.coli plasmid pO157 D	1.66e+03
C	844	15	1.5	14275	17	CEF57C2	Caenorhabditis elegans	1.66e+03
C	845	15	1.5	15222	21	HRU50363	Human respiratory sync	1.66e+03
C	846	15	1.5	15222	21	HRU50362	Human respiratory sync	1.66e+03
C	847	15	1.5	15222	21	RSHSEQ	Human respiratory sync	1.66e+03
C	848	15	1.5	15935	18	SCYLRI06C	S.cerevisiae chromosom	1.66e+03
C	849	15	1.5	16036	17	CEI26F2	Caenorhabditis elegans	1.66e+03
C	850	15	1.5	16956	18	S58126	LEU1-ATE1 loci: LEU1.	1.66e+03
C	851	15	1.5	17279	16	TFLGTFBPA	Snake (habu) gtfBP ge	1.66e+03
C	852	15	1.5	17576	17	CEY48E1A	Caenorhabditis elegans	1.66e+03
C	853	15	1.5	19371	17	CEK10G9	Caenorhabditis elegans	1.66e+03
C	854	15	1.5	20227	17	CEC01C7	Caenorhabditis elegans	1.66e+03
C	855	15	1.5	20500	21	IBAORFAB	Avian infectious bronc	1.66e+03
C	856	15	1.5	20668	18	SC9827	S.cerevisiae chromosom	1.66e+03
C	857	15	1.5	22071	17	CEK07G5	Caenorhabditis elegans	1.66e+03
C	858	15	1.5	22245	17	CEI27E9	Caenorhabditis elegans	1.66e+03
C	859	15	1.5	24910	17	CELC56G3	Caenorhabditis elegans	1.66e+03
C	860	15	1.5	27285	17	CELR105	Caenorhabditis elegans	1.66e+03
C	861	15	1.5	27502	18	ATAF001535	Arabidopsis thaliana c	1.66e+03
C	862	15	1.5	27576	17	CEP16B12	Caenorhabditis elegans	1.66e+03
C	863	15	1.5	27608	21	TBACGB	Avian infectious bronc	1.66e+03
C	864	15	1.5	27777	17	AC002447	Drosophila melanogaste	1.66e+03
C	865	15	1.5	28396	17	CELF10E7	Caenorhabditis elegans	1.66e+03
C	866	15	1.5	28922	17	CELC43G2	Caenorhabditis elegans	1.66e+03
C	867	15	1.5	29366	18	SC9571X	S.cerevisiae chromosom	1.66e+03
C	868	15	1.5	29820	17	CEF48F7	Caenorhabditis elegans	1.66e+03
C	869	15	1.5	30940	17	CELF41D9	Caenorhabditis elegans	1.66e+03
C	870	15	1.5	31418	17	CEC03C10	Caenorhabditis elegans	1.66e+03
C	871	15	1.5	32458	17	CER10E11	Caenorhabditis elegans	1.66e+03
C	872	15	1.5	32880	17	CEFA0F12	Caenorhabditis elegans	1.66e+03
C	873	15	1.5	33010	19	MTCY9F9	Mycobacterium tubercul	1.66e+03
C	874	15	1.5	34496	17	CELR11G1	Caenorhabditis elegans	1.66e+03
C	875	15	1.5	36309	17	CEFA5G2	Caenorhabditis elegans	1.66e+03
C	876	15	1.5	36535	17	CELK02E7	Caenorhabditis elegans	1.66e+03
C	877	15	1.5	36539	17	CEK08H2	Caenorhabditis elegans	1.66e+03
C	878	15	1.5	36977	17	CEI2K688	C. elegans cosmid ZK68	1.66e+03
C	879	15	1.5	37106	17	CEC04A11	Caenorhabditis elegans	1.66e+03
C	880	15	1.5	37404	18	SC8119	S.cerevisiae chromosom	1.66e+03
C	881	15	1.5	37730	18	YSCL8543	Saccharomyces cerevisi	1.66e+03
C	882	15	1.5	37787	17	CELT22B7	Caenorhabditis elegans	1.66e+03
C	883	15	1.5	38139	18	SPAC10F6	S.pombe chromosome I c	1.66e+03
C	884	15	1.5	38889	26	HSCB33B10	Human DNA sequence ***	1.66e+03
C	885	15	1.5	38967	17	CEIF25G6	Caenorhabditis elegans	1.66e+03
C	886	15	1.5	39292	18	SPAC11D3	S.pombe chromosome I c	1.66e+03
C	887	15	1.5	39353	17	CEF11A1	Caenorhabditis elegans	1.66e+03
C	888	15	1.5	39375	17	CELK11D12	Caenorhabditis elegans	1.66e+03
C	889	15	1.5	39581	17	CELXK1248	Caenorhabditis elegans	1.66e+03
C	890	15	1.5	40012	17	CELF07C3	Caenorhabditis elegans	1.66e+03
C	891	15	1.5	40340	18	YSCL8004	Saccharomyces cerevisi	1.66e+03
C	892	15	1.5	42759	18	AB004535	Schizosaccharomyces po	1.66e+03
C	893	15	1.5	43046	17	CELC09B8	Caenorhabditis elegans	1.66e+03
C	894	15	1.5	43441	17	CED2005	Caenorhabditis elegans	1.66e+03
C	895	15	1.5	43468	18	SC8358	S.cerevisiae chromosom	1.66e+03
C	896	15	1.5	43492	17	CELC14B9	C. elegans cosmid C14B	1.66e+03
C	897	15	1.5	43947	17	CELC04C3	Caenorhabditis elegans	1.66e+03
C	898	15	1.5	44264	17	CELC47D12	Caenorhabditis elegans	1.66e+03
C	899	15	1.5	44733	17	CELC50C3	C. elegans cosmid C50C	1.66e+03
C	900	15	1.5	45189	17	CELC34F11	Caenorhabditis elegans	1.66e+03
C	901	15	1.5	45510	17	CEC32A3	Caenorhabditis elegans	1.66e+03
C	902	15	1.5	48622	18	AB008286	Arabidopsis thaliana g	1.66e+03
C	903	15	1.5	50425	26	CED1025	Caenorhabditis elegans	1.66e+03
C	904	15	1.5	53899	26	CEH37N21	Caenorhabditis elegans	1.66e+03
C	905	15	1.5	55403	26	CEFO8G2	Mus musculus T cell re	1.66e+03
C	906	15	1.5	62031	14	AF021335	Saccharomyces cerevisi	1.66e+03
C	907	15	1.5	69023	18	SCD8035	Caenorhabditis elegans	1.66e+03
C	908	15	1.5	70640	26	CEH32K21	Caenorhabditis elegans	1.66e+03
C	909	15	1.5	73471	26	AC002509	Caenorhabditis elegans	1.66e+03
C	910	15	1.5	78064	26	HSAC000376	Caenorhabditis elegans	1.66e+03
C	911	15	1.5	81189	26	AC003034	Caenorhabditis elegans	1.66e+03
C	912	15	1.5	81493	18	AT81K8EN	A.thaliana 81kb genom	1.66e+03
C	913	15	1.5	82810	6	AT81K8EN	Human cosmid ILOXNC01	1.66e+03
C	914	15	1.5	83646	18	HSU67941	Arabidopsis thaliana g	1.66e+03
C	915	15	1.5	84510	18	AB005248	Arabidopsis thaliana g	1.66e+03
C	916	15	1.5	87831	26	HS125N5	Arabidopsis thaliana g	1.66e+03
C	917	15	1.5	88960	26	HS892F13	Human DNA sequence ***	1.66e+03
C	918	15	1.5	89846	14	AC002393	Human DNA sequence ***	1.66e+03
C	919	15	1.5	93037	18	ATF8F16	Mouse BAC24H12 Chromo	1.66e+03
C	920	15	1.5	93158	26	AC002334	Arabidopsis thaliana D	1.66e+03
C	921	15	1.5	95568	26	CEH05L14	Caenorhabditis elegans	1.66e+03
C	922	15	1.5	95645	26	AC003688	Caenorhabditis elegans	1.66e+03
C	923	15	1.5	98234	26	AC003102	Caenorhabditis elegans	1.66e+03
C	924	15	1.5	98527	18	AC004044	Arabidopsis thaliana B	1.66e+03
C	925	15	1.5	100145	26	AC003104	Arabidopsis thaliana B	1.66e+03
C	926	15	1.5	102972	26	AC000360	Caenorhabditis elegans	1.66e+03
C	927	15	1.5	105654	26	HS714B7	Human DNA sequence ***	1.66e+03
C	928	15	1.5	105654	18	ATAF001308	Arabidopsis thaliana c	1.66e+03
C	929	15	1.5	106572	26	HS206D15	Human DNA sequence ***	1.66e+03
C	930	15	1.5	1069125	26	U89959	Arabidopsis thaliana B	1.66e+03
C	931	15	1.5	109125	26	AC002328	Caenorhabditis elegans	1.66e+03
C	932	15	1.5	109194	26	HS934G17	Human DNA sequence ***	1.66e+03
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C	936	15	1.5	111401	19	EC0110K	Arabidopsis thaliana D	1.66e+03
C	937	15	1.5	113566	18	AC002330	E.coli K12 genome, 0-2	1.66e+03
C	938	15	1.5	116067	26	CEH37A05	Arabidopsis thaliana B	1.66e+03
C	939	15	1.5	118155	26	HS884M20	Caenorhabditis elegans	1.66e+03
C	940	15	1.5	119184	19	D90909	Human DNA sequence ***	1.66e+03
C	941	15	1.5	119704	18	OSCHLPLXX	Synechocystis sp. PCC6	1.66e+03
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C	943	15	1.5	121174	26	CEY69E1	Human DNA sequence ***	1.66e+03
C	944	15	1.5	121811	26	AC000096	Caenorhabditis elegans	1.66e+03
C	945	15	1.5	122459	26	HS510H16	Caenorhabditis elegans	1.66e+03
C	946	15	1.5	123080	26	HSAC000384	Caenorhabditis elegans	1.66e+03
C	947	15	1.5	123386	18	HS510H16	Human DNA sequence ***	1.66e+03
C	948	15	1.5	127098	26	HS971N18	Sequence of BAC F12F1	1.66e+03
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C	950	15	1.5	129913	26	HS63G5	Human DNA sequence ***	1.66e+03
C	951	15	1.5	131193	26	HS989H11	Human DNA sequence ***	1.66e+03
C	952	15	1.5	131318	26	HS510D11	Human DNA sequence ***	1.66e+03
C	953	15	1.5	131977	26	CEY42E10	Caenorhabditis elegans	1.66e+03
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C	955	15	1.5	133667	26	HS37J18	Human DNA sequence ***	1.66e+03
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C	958	15	1.5	140554	14	AC000399	Homo sapiens; HTGS pha	1.66e+03
C	959	15	1.5	144861	21	HHU43400	Genomic sequence from	1.66e+03
C	960	15	1.5	147399	26	AC003667	Human herpesvirus-7 (H	1.66e+03
C	961	15	1.5	148640	25	AC004103	Homo	

964	15	1.5	153080	21	AF037218	Human herpesvirus 7 st	1.66e+03
965	15	1.5	154619	19	D90917	Synechocystis sp. PCC6	1.66e+03
966	15	1.5	159527	26	HS13D10	Human DNA sequence ***	1.66e+03
967	15	1.5	160214	26	AC002327	*** SEQUENCING IN PROG	1.66e+03
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972	15	1.5	169692	26	HS57A13	Human DNA sequence ***	1.66e+03
973	15	1.5	170789	26	CEY76A2	Caenorhabditis elegans	1.66e+03
974	15	1.5	172106	26	CEY67D11	Caenorhabditis elegans	1.66e+03
975	15	1.5	172281	21	EBV	Epstein-Barr virus (EB	1.66e+03
976	15	1.5	172863	26	HS179N16	Human DNA sequence ***	1.66e+03
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978	15	1.5	179000	26	HSAC002059	*** SEQUENCING IN PROG	1.66e+03
979	15	1.5	180000	26	AC004063	*** SEQUENCING IN PROG	1.66e+03
980	15	1.5	184427	21	EHVU20824	Equine herpesvirus 2,	1.66e+03
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982	15	1.5	184855	26	HS90G24	Human DNA sequence ***	1.66e+03
983	15	1.5	186306	26	CEY6E2	Caenorhabditis elegans	1.66e+03
984	15	1.5	188337	26	CEY17B7	Caenorhabditis elegans	1.66e+03
985	15	1.5	188670	26	HSB55C20	Human DNA sequence ***	1.66e+03
986	15	1.5	189952	26	AC004106	Homo sapiens: HTGS pha	1.66e+03
987	15	1.5	199101	14	MMAE000665	Mus musculus TCR beta	1.66e+03
988	15	1.5	209100	19	BSUB0003	Bacillus subtilis comp	1.66e+03
989	15	1.5	213680	19	BSUB0012	Bacillus subtilis comp	1.66e+03
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992	15	1.5	226018	26	HS90L6	Human DNA sequence ***	1.66e+03
993	15	1.5	232597	26	AC002353	Homo sapiens: HTGS pha	1.66e+03
994	15	1.5	241331	26	HS94M16	Human DNA sequence ***	1.66e+03
995	15	1.5	256000	26	HSAC000353	Homo sapiens chromosome	1.66e+03
996	15	1.5	268735	26	AC003684	Homo sapiens: HTGS pha	1.66e+03
997	15	1.5	288886	26	AC002406	Mus musculus: HTGS pha	1.66e+03
998	15	1.5	330740	21	PBU42580	Paramecium bursaria Ch	1.66e+03
999	15	1.5	338534	19	ECOWW93	Escherichia coli K-12	1.66e+03
1000	15	1.5	349935	26	CEY39B6	Caenorhabditis elegans	1.66e+03

ALIGNMENTS

RESULT	1	A48343	1142 bp	DNA	PAT	07-MAR-1997
LOCUS		Sequence 1 from Patent WO9601898.				
DEFINITION		A48343				
ACCESSION		g2302133				
NID						
KEYWORDS						
SOURCE		unidentified.				
ORGANISM		unidentified.				
REFERENCE		1 (bases 1 to 1142)				
AUTHORS		Kieffer,B. and Simonin,F.				
TITLE		HUMAN KAPPA OPIOID RECEPTOR, NUCLEIC ACIDS AND USES THEREOF				
JOURNAL		Patent: WO 9601898-A 1 25-JAN-1996;				
COMMENT		UNIV PASTEUR (FR)				
FEATURES		Other publication FR 2722209 960112.				
source		Location/Qualifiers				
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		CHPVKALDFRPLKAKIINICILSSVGSIAIVIGTKVREDVDVTECSLOPDD				
		YSWDLFMKICVFIFAFVIVPLIITVCTILMIRLKSVRLLSGSREDRNLRRITRLV				
		LIVVAVFVVCWPIIHIFILVEALGSTSHSTAALSYFCIALGYTNSLNPIIYAFID				
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CDS

BASE COUNT

236 a 337 c 283 g 286 t

ORIGIN

Query Match 73.3%; Score 729; DB 25; Length 1142;
Best Local Similarity 98.8%; Pred. No. 0.00e+00;
Matches 849; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db	257	GATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAAGCTGGCTTTGGCAGATG	316
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Db	317	CTTTAGTTACTACAAACCATGCCCCCTTTCAGAGTACGGTCTACTTGATGAATTCCGTG	376
QY	160	CTTTAGTTACTACAAACCATGCCCCCTTTCAGAGTACGGTCTACTTGATGAATTCCGTG	219
Db	377	TTGGGAGTGTGCTGTGCAAGATAGTAAITTCATTGATTACTACACATGTTACACAGCA	436
QY	220	TTGGGAGTGTGCTGTGCAAGATAGTAAITTCATTGATTACTACACATGTTACACAGCA	279
Db	437	TCTTCACTTGACCATGATGAGCGGTGACCGCTACATTGCCGTGTCACCCCGTGAAGG	496
QY	280	TCTTCACTTGACCATGATGAGCGGTGACCGCTACATTGCCGTGTCACCCCGTGAAGG	339
Db	497	CTTTGACCTTCCGACACACCCCTTGAAGGCAAGATCATATATCTGCATCTGCTGTGT	556
QY	340	CTTTGACCTTCCGACACACCCCTTGAAGGCAAGATCATATATCTGCATCTGCTGTGT	399
Db	557	CGTCATCTGTGTCATCTCTGCAATAGTCTCTTGAGGACACCAAGTCAAGGAAAGCTCG	616
QY	400	CGTCATCTGTGTCATCTCTGCAATAGTCTCTTGAGGACACCAAGTCAAGGAAAGCTCG	459
Db	617	ATGTCATTGATGCTCTCTTGCAGTTCGCCAGATGATGACTACTCTCTGTTGGACCTCTCA	676
QY	460	ATGTCATTGATGCTCTCTTGCAGTTCGCCAGATGATGACTACTCTCTGTTGGACCTCTCA	519
Db	677	TGAAGATCTGCGCTCTTCATCTTTGCCCTTGATGATCCCTGTCCTCATCATATCTCTGCT	736
QY	520	TGAAGATCTGCGCTCTTCATCTTTGCCCTTGATGATCCCTGTCCTCATCATATCTCTGCT	579
Db	737	ACACCCGTGATGATCTGCTGCTCACAAGAGCGTCCGCTCTTCTTGCGTCCGAGAAAG	796
QY	580	ACACCCGTGATGATCTGCTGCTCACAAGAGCGTCCGCTCTTCTTGCGTCCGAGAAAG	639
Db	797	ATCGCAACCTGCGTAGGATCACACGAGCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCT	856
QY	640	ATNCAACCTGCGTAGGATCACACGAGCTGTCCTGCTGCTGCTGCTGCTGCTGCTGCT	699
Db	857	GCTGACTCCCATTTACATATTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	916
QY	700	GCTGACTCCCATTTACATATTTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	759
Db	917	CAGCTGCTCTCTCCAGTATTTACTTCTGCAATCGCCCTTAAGGCTATACCAACAGTACCTGA	976
QY	760	CAGCTGCTCTCTCCAGTATTTACTTCTGCAATCGCCCTTAAGGCTATACCAACAGTACCTGA	819
Db	977	ATCCCATTTCTCPACGCTTTCTTGATGAAACTTCAAGCGGTGTTCCGGGACTTCTGCT	1036
QY	820	ATCCCATTTCTCPACGCTTTCTTGATGAAACTTCAAGCGGTGTTCCGGGACTTCTGCT	879
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QY	880	TTCCACTGAAGATGAGGATGAGCGGCGNAGAGCACTAGCAGAGTCCGAAATACAGTTCAAG	939
Db	1097	ATCCTGCTTACCTGAGGGA 1115	
QY	940	ATCCTGCTTACCTGAGGGA 958	

RESULT 2 CPU04092 1733 bp mRNA ROD 24-MAY-1995
LOCUS Cavia porcellus Hartley kappa opioid receptor mRNA, complete cds.
DEFINITION U04092
ACCESSION g476106
NID
KEYWORDS

SOURCE guinea pig.
ORGANISM Cavia porcellus
REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
AUTHORS 1 (bases 1 to 1733)
TITLE Xie,G.X., Meng,F., Mansour,A., Thompson,R.C., Hoyersten,M.T., Goldstein,A., Watson,S.J. and Akil,H.
JOURNAL Primary structure and functional expression of a guinea pig kappa opiod (dynorphin) receptor
MEDLINE proc. Natl. Acad. Sci. U.S.A. 91 (9), 3779-3783 (1994)
REFERENCE 2 (bases 1 to 1733)
AUTHORS Xie,G.
JOURNAL Direct Submission
TITLE Submitted (07-DEC-1993) Guo-xi Xie, Mental Health Research Institute, The University of Michigan, 205 Zina Pitcher Place, Ann Arbor, MI 48109-0720, USA
FEATURES Location/Qualifiers
source 1..1733
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/strain="Hartley"
/db_xref="taxon:10141"
/clone="gpk1OR"
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/tissue_type="brain"
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3'UTR
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BASE COUNT 409 a 416 c 505 g 403 t
ORIGIN
Query Match 4.7%; Score 47; DB 14; Length 1733;
Best Local Similarity 100.0%; Pred. No. 4.79e-25;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 885 GATGATGACTACTCCTGGTGGGACCTCTTCATGAAGATCGCGTCTT 931
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QY 489 GATGATGACTACTCCTGGTGGGACCTCTTCATGAAGATCGCGTCTT 535
RESULT 3
LOCUS MMU16998 432 bp DNA ROD 07-DEC-1994
DEFINITION Mus musculus kappa opiod receptor (oprk1) gene, partial cds.
ACCESSION U16998
NID 9595936
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 432)
TITLE Grandy,D.K.
JOURNAL Mapping of the human kappa opiod receptor gene to chromosome 8q11.2-q12: no evidence for multiple kappa opiod receptor genes
REFERENCE 2 (bases 1 to 432)
AUTHORS Grandy,D.K.

TITLE Direct Submission
JOURNAL Submitted (07-NOV-1994) David K. Grandy, Vollum Institute, Oregon Health Sciences, University, 3181 S.W. Sam Jackson Park Road, Portland, OR 97201, USA
FEATURES Location/Qualifiers
source 1..432
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="R21mg1"
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BASE COUNT 114 a 92 c 85 g 141 t
ORIGIN

Query Match 3.3%; Score 33; DB 14; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.76e-11;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 336 ATAGTCTTGAGGACCAAGTCAAGGAGGT 368
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QY 423 ATAGTCTTGAGGACCAAGTCAAGGAGGT 455

RESULT 4
LOCUS MUSMORGP2 488 bp DNA ROD 12-APR-1996
DEFINITION Mouse MORGD gene for kappa-opioid receptor, exon 2.
ACCESSION D31664
NID 9643594
KEYWORDS G-protein associated; kappa opiod receptor; opiod drugs and peptides-binding; transmembrane protein.
SEGMENT 2 of 3
SOURCE Mus musculus
ORGANISM Mus musculus

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 488)
TITLE Nishi,M., Takeshima,H., Mori,M., Nakagawara,K. and Takeuchi,T.
JOURNAL Structure and chromosomal mapping of genes for the mouse +kappa-opioid receptor and an opiod receptor homolog (MOR-C) Biochemical and Biophysical Research Communication 205, 1353-1357 (1994)
REFERENCE 2 (bases 1 to 488)
AUTHORS Takeshima,H.
JOURNAL Direct Submission
TITLE Submitted (28-MAY-1994) to the DDBJ/EMBL/GenBank databases. Hiroshi Takeshima, Tokyo Institute of Psychiatry, Department of Neurochemistry; 2-1-8 Kamikitazawa, Setagaya-ku, Tokyo 156, Japan (Tel:03-3304-5701(ex.312), Fax:03-3329-8035)
COMMENT Submitted (28-May-1994) to DDBJ by: Hiroshi Takeshima
Department of Neurochemistry
Tokyo Institute of Psychiatry
2-1-8 Kamikitazawa, Setagaya-ku
Tokyo 156
Japan
Phone: 03-3304-5701 x312

FEATURES Fax: 03-3329-8035.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone_lib="phage lambda fixII"
89. .441
/note="second protein coding sequence (P2)"
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Best Local Similarity 100.0%; Pred. No. 1.76e-11;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 411 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 443
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QY 423 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 455
RESULT 5
LOCUS RNKOR2 658 bp DNA ROD 25-MAR-1995
DEFINITION Rattus norvegicus kappa opiod receptor gene, exon 3.
ACCESSION U17994
NID 9727257
KEYWORDS
SEGMENT
SOURCE 2 of 3
ORGANISM Norway rat.
Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 658)
AUTHORS Yakovlev,A.G., Krueger,K.E. and Faden,A.I.
TITLE Structure and expression of a rat kappa opiod receptor gene
JOURNAL J. Biol. Chem. 270 (12), 6421-6424 (1995)
MEDLINE 95204422
REFERENCE 2 (bases 1 to 658)
AUTHORS Yakovlev,A.G.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1994) Alexander G. Yakovlev, Georgetown
University School of Medicine, Neurology, 3900 Reservoir Rd.,
Washington, DC 20007, USA
FEATURES Location/Qualifiers
source 1. .658
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/sex="male"
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exon 226. .578
/number=3
/evidence=experimental
intron /evidence=experimental
/product="kappa opiod receptor"
579. .>658
/number=3
/evidence=experimental
BASE COUNT 201 a 128 c 122 g 207 t
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Query Match 3.3%; Score 33; DB 14; Length 658;
Best Local Similarity 100.0%; Pred. No. 1.76e-11;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 548 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 580
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QY 423 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 455
RESULT 6

LOCUS S77868S2 1109 bp DNA ROD 26-SEP-1995
DEFINITION kappa opiod receptor [mice, Genomic, 1109 nt, segment 2 of 3].
ACCESSION S77869
NID 9998530
KEYWORDS
SEGMENT
SOURCE 2 of 3
ORGANISM Mus sp.
Mus sp.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE 1 (bases 1 to 1109)
AUTHORS Liu,H.C., Lu,S., Augustin,L.B., Felsheim,R.F., Chen,H.C., Loh,H.H.
and Wei,L.N.
TITLE Cloning and promoter mapping of mouse kappa opiod receptor gene
JOURNAL Biochem. Biophys. Res. Commun. 209 (2), 639-647 (1995)
MEDLINE 95251663
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 166534] from the original journal article.
This sequence comes from Fig. 2.
FEATURES Location/Qualifiers
source 1. .1109
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ORIGIN
Query Match 3.3%; Score 33; DB 14; Length 1109;
Best Local Similarity 100.0%; Pred. No. 1.76e-11;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 693 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 725
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QY 423 ATAGTCCTTGAGGACCAAGTCAGGGAAGT 455
RESULT 7
LOCUS RATRORD 1273 bp mRNA ROD 21-DEC-1993
DEFINITION Rat mRNA for opiod receptor, complete cds.
ACCESSION D16534
NID 9409390
KEYWORDS G-protein coupled receptor; opiod receptor; transmembrane protein.
SOURCE Rattus norvegicus (strain Wistar) adult brain cDNA to mRNA, clone
PROR2.
ORGANISM Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 1273)
AUTHORS Nishi,M., Takeshima,H., Fukuda,K., Kato,S. and Mori,K.
TITLE cDNA cloning and pharmacological characterization of an opiod
JOURNAL receptor with high affinities for kappa-subtype-selective ligands
MEDLINE FEBS Lett. 330 (1), 77-80 (1993)
REFERENCE 93380575
AUTHORS Takeshima,H.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1993) to the DDBJ/EMBL/GenBank databases. Hiroshi
Takeshima, International Institute for Advanced Studies; c/o
Shimadzu Corporation N-80, 1 Nishinokyo-Kuware-cho, Kyoto 604,
Japan (Tel:075-823-1208, Fax:075-811-8186)
COMMENT Submitted (19-JUN-1993) to DDBJ by:
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International Institute
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c/o Shimadzu Corporation
N-80
1 Nishinokyo-Kuware-cho
Kyoto 604
Japan
Phone: 075-823-1208
Fax: 075-811-8186.
FEATURES Location/Qualifiers

source 1. .1273 /organism="Rattus norvegicus" /strain="Wistar" /db_xref="taxon:10116" /dev_stage="adult" /tissue_type="brain" gene /gene="ROR-D" 49. .1191 /gene="ROR-D" 49. .1191 /gene="ROR-D" /codon_start=1 /product="opioid receptor" /db_xref="pid:d1004487" /db_xref="pid:g415310" /translation="MESPIQIFRGEPPGPTCAPSACLLPNSSSWFPPNWAESDSNGSVGS EDOOLEPAHISPAIPVITAVYSVVFVGVGNSLVMFVIRYTKMKATNTIYFNLA LADALVTITMPFQSAVYIMNSWPFQDVLCIVISIDYNNMTSIFTLTMSVDRIAY CHPVKALDFRTPLKAKIINICIMWLASSVGSIAIVLGCTKVRQEDVDVIECSIQFPDDE YSWMDLFMKICVFVFAFVPLIIVCYTLMILRLKSVRLSGSREKDRNLRITKLV LVVAVAFIICWPIPHIFILVEALGSTSHSTAVLSSYFCIALGYTNSLNPVLYAFLD ENFKRCFRDFCFPIKMRMEROSTNRVRNTVQDPASMRDVGGMNKPV"

BASE COUNT 278 a 340 c 294 g 361 t

ORIGIN

Query Match 3.2%; Score 32; DB 14; Length 1273; Best Local Similarity 100.0%; Pred. No. 1.44e-10; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 337 TACATATTTTAACCTGGCTTTGGCAGATGCTTT 368
|||||
QY 132 TACATATTTTAACCTGGCTTTGGCAGATGCTTT 163

RESULT 8 LOCUS S81111 1288 bp mRNA ROD 02-AUG-1996 DEFINITION kappa-opioid receptor [alternatively spliced] [mice, C58/J, R1.1 thymoma cells, mRNA Partial, 1288 nt]. ACCESSION S81111 NID g1478285 KEYWORDS Mus sp. C58/J R1.1 thymoma cells. SOURCE Mus sp. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 1288) Belkowski,S.M., Zhu,J., Liu-Chen,L.Y., Eisenstein,T.K., Adler,M.W. and Rogers,T.J. Sequence of kappa-opioid receptor cDNA in the R1.1 thymoma cell line J. Neuroimmunol. 62 (1), 113-117 (1995) 96084989 JOURNAL GenBank staff at the National Library of Medicine created this MEDLINE entry [NCBI gibsbg 175931] from the original journal article. REMARK This sequence comes from Fig. 3. longer of two transcripts. COMMENT Location/Qualifiers 1. .1288 /organism="Mus sp." /db_xref="taxon:10095" 97. .1239 /gene="kappa-opioid receptor" 97. .1239 /gene="kappa-opioid receptor" /codon_start=1 /translation="MESPIQIFRGDPGPTCSPSACLLPNSSSWFPPNWAESDSNGSVGS EDOOLESAHISPAIPVITAVYSVVFVGVGNSLVMFVIRYTKMKATNTIYFNLA LADALVTITMPFQSAVYIMNSWPFQDVLCIVISIDYNNMTSIFTLTMSVDRIAY CHPVKALDFRTPLKAKIINICIMWLASSVGSIAIVLGCTKVRQEDVDVIECSIQFPDDE YSWMDLFMKICVFVFAFVPLIIVCYTLMILRLKSVRLSGSREKDRNLRITKLV LVVAVAFIICWPIPHIFILVEALGSTSHSTAVLSSYFCIALGYTNSLNPVLYAFLD ENFKRCFRDFCFPIKMRMEROSTNRVRNTVQDPASMRDVGGMNKPV"

BASE COUNT 283 a 336 c 305 g 364 t

ORIGIN

Query Match 3.2%; Score 32; DB 14; Length 1288; Best Local Similarity 100.0%; Pred. No. 1.44e-10; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 385 TACATATTTTAACCTGGCTTTGGCAGATGCTTT 416
|||||
QY 132 TACATATTTTAACCTGGCTTTGGCAGATGCTTT 163

RESULT 9 LOCUS RATKOR1A 1358 bp mRNA ROD 21-OCT-1993 DEFINITION Rat kappa opioid receptor mRNA, complete cds. ACCESSION L22001 NID g409236 KEYWORDS kappa opioid receptor; opioid receptor. SOURCE Rattus norvegicus Rattus norvegicus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Rattus. REFERENCE 1 (bases 1 to 1358) Chen,Y., Mestek,A., Liu,J. and Yu,L. Molecular cloning of a rat kappa opioid receptor reveals sequence similarities to the mu and delta opioid receptors Biochem. J. 295, 625-628 (1993) 94059008 MEDLINE location/Qualifiers 1. .1358 /organism="Rattus norvegicus" /db_xref="taxon:10116" /tissue_type="whole brain" 71. .1213 /codon_start=1 /evidence=experimental /product="kappa opioid receptor" /translation="MESPIQIFRGEPPGPTCAPSACLLPNSSSWFPPNWAESDSNGSVGS EDOOLEPAHISPAIPVITAVYSVVFVGVGNSLVMFVIRYTKMKATNTIYFNLA LADALVTITMPFQSAVYIMNSWPFQDVLCIVISIDYNNMTSIFTLTMSVDRIAY CHPVKALDFRTPLKAKIINICIMWLASSVGSIAIVLGCTKVRQEDVDVIECSIQFPDDE YSWMDLFMKICVFVFAFVPLIIVCYTLMILRLKSVRLSGSREKDRNLRITKLV LVVAVAFIICWPIPHIFILVEALGSTSHSTAVLSSYFCIALGYTNSLNPVLYAFLD ENFKRCFRDFCFPIKMRMEROSTNRVRNTVQDPASMRDVGGMNKPV"

BASE COUNT 304 a 353 c 320 g 381 t

ORIGIN

Query Match 3.2%; Score 32; DB 14; Length 1358; Best Local Similarity 100.0%; Pred. No. 1.44e-10; Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 359 TACATATTTTAACCTGGCTTTGGCAGATGCTTT 390
|||||
QY 132 TACATATTTTAACCTGGCTTTGGCAGATGCTTT 163

RESULT 10 LOCUS MUSKAPOPRE 1410 bp mRNA ROD 13-DEC-1993 DEFINITION Mouse kappa opioid receptor mRNA, complete cds. ACCESSION L11065 NID g348248 KEYWORDS kappa opioid receptor. SOURCE Mus musculus (library: Clontech #ML1036a) brain cDNA to mRNA. ORGANISM Mus musculus Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus. REFERENCE 1 (bases 1 to 1410) Yasuda,K., Raynor,K., Kong,H., Breder,C.D., Takeda,T., Reisine,T. and Bell,G.I. Cloning and functional comparison of kappa and delta opioid receptors from mouse brain

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 6736-6740 (1993)
MEDLINE 93342064
FEATURES
 Source
 Location/Qualifiers
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 /db_xref="taxon:10090"
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 /tissue_lib="Clontech #ML1036a"
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BASE COUNT 322 a 360 c 337 g 391 t
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 474 TACATATTAACTGGCTTTGGCAGATGCTTT 505
|||||
QY 132 TACATATTAACTGGCTTTGGCAGATGCTTT 163
RESULT 11
LOCUS RATKOR1B 2094 bp mRNA ROD 19-NOV-1993
DEFINITION Rattus norvegicus kappa opioid receptor (KOR-1) mRNA, complete cds.
ACCESSION L22536
NID 9425188
KEYWORDS G-protein coupled receptor; kappa opioid receptor; transmembrane protein.
SOURCE Rattus norvegicus (strain Sprague-Dawley) (library: lambda gt10)
adult brain (striatum) cDNA to mRNA.
ORGANISM Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 2094)
Li,S., Zhu,Y., Chen,C., Chen,Y.-W., de Riel,J.K., Ashby,B. and
Liu-Chen,L.-Y.
TITLE Molecular cloning and expression of a rat k opioid receptor
JOURNAL Biochem. J. 295, 629-633 (1993)
MEDLINE 94059009
FEATURES
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2094
polya_site

BASE COUNT 520 a 519 c 488 g 567 t
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 511 TACATATTAACTGGCTTTGGCAGATGCTTT 542
|||||
QY 132 TACATATTAACTGGCTTTGGCAGATGCTTT 163
RESULT 12
LOCUS E08874 2481 bp RNA PAT 26-NOV-1996
DEFINITION cDNA coding rat kappa-opioid receptor.
ACCESSION E08874
NID 92176978
KEYWORDS JP 1995070191-A/1.
SOURCE Rattus sp.
ORGANISM Rattus sp.
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 2481)
Kimimichi,S.
TITLE RECEPTOR PROTEIN, ITS PRODUCTION AND USE THEREOF
JOURNAL Patent: JP 1995070191-A 1 14-MAR-1995;
TAKEDA CHEM IND LTD
COMMENT OS Rattus sp. (rat)
PN JP 1995070191-A/1
PD 14-MAR-1995
PF 30-JUL-1993 JP 1993190261
PR 09-JUL-1993 JP 93P 170591
PI SATO KIMIMICHI
PC C07K14/47, C12N1/21, C12N15/09, C12P21/02//A61K38/00, A61K38/00,
PC (C12N1/21,
PC C12R1:19), (C12P21/02, C12R1:19), C07K99:00;
CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FH source 1..2481
FT FT /organism='Rattus sp.'
FT FT 111..1253
FT CDS /product='rat kappa-opioid receptor'.
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 399 TACATATTAACTGGCTTTGGCAGATGCTTT 430
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QY 132 TACATATTAACTGGCTTTGGCAGATGCTTT 163
RESULT 13
LOCUS RATKOR 2481 bp mRNA ROD 02-DEC-1993
DEFINITION Rattus norvegicus mRNA for kappa opioid receptor, complete cds.
ACCESSION D16829
NID 9404115
KEYWORDS kappa opioid receptor.
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Rattus.

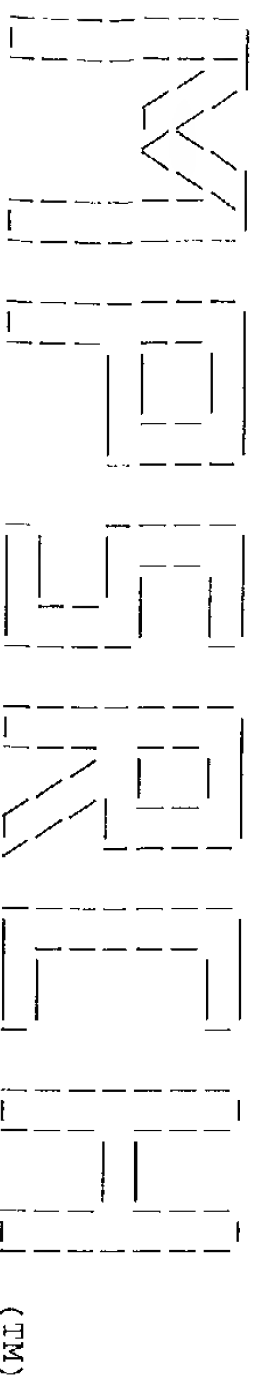
REFERENCE 1 (bases 1 to 2481)
AUTHORS Minami,M., Toya,T., Katao,Y., Maekawa,K., Nakamura,S., Onogi,T.,
Kaneko,S. and Satoh,M.
TITLE Cloning and expression of a cDNA for the rat kappa-opioid receptor
JOURNAL FEBS Lett. 329 (3), 291-295 (1993)
MEDLINE 93374033
REFERENCE 2 (bases 1 to 2481)
AUTHORS Minami,M.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases.
Masabumi Minami, Faculty of pharmaceutical Sciences, Kyoto
University, Department of Pharmacology; Kyoto, Kyoto 606-01, Japan
(E-mail:f51250@sakura.kudpc.kyoto-u.ac.jp, Tel:075-753-4546,
Fax:075-753-4586)
COMMENT Submitted (21-JUL-1993) to DDBJ by:
Masabumi Minami
Department of Pharmacology
Faculty of pharmaceutical Sciences
Kyoto University
Kyoto, Kyoto 606-01
Japan
Phone: 075-753-4546
Fax: 075-753-4586.
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ENFKRCFRDFCFPIKRMERQSTNRVRNTVQDPASMRDVGGMNKPV"
BASE COUNT 629 a 588 c 544 g 720 t
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Query Match 3.2%; Score 32; DB 14; Length 2481;
Best Local Similarity 100.0%; Pred. No. 1.44e-10;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 399 TACATATTTAACCTGGCTTGGCAGATGCTTT 430
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QY 132 TACATATTTAACCTGGCTTGGCAGATGCTTT 163
RESULT 14
LOCUS RNMOR3 4048 bp DNA ROD 25-MAR-1995
DEFINITION Rattus norvegicus kappa opioid receptor gene, exon 4 and complete
cds.
ACCESSION U17995
NID g727258
KEYWORDS 3 of 3
SEGMENT Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 4048)
AUTHORS Yakovlev,A.G., Krueger,K.E. and Faden,A.I.
TITLE Structure and expression of a rat kappa opioid receptor gene
JOURNAL J. Biol. Chem. 270 (12), 6421-6424 (1995)
MEDLINE 95204422
REFERENCE 2 (bases 1 to 4048)
AUTHORS Yakovlev,A.G.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1994) Alexander G. Yakovlev, Georgetown

University School of Medicine, Neurology, 3900 Reservoir Rd.,
Washington, DC 20007, USA
FEATURES
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89..3951)
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exons
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Db 469 GCCTTCTGTGATGAAGAACTCAACGGGTGTT 500
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QY 834 GCCTTCTGTGATGAAGAACTCAACGGGTGTT 865
RESULT 15
LOCUS RNM00442 4742 bp mRNA ROD 25-MAY-1994
DEFINITION Rattus norvegicus kappa opioid receptor mRNA, complete cds.
ACCESSION U00442
NID g403486
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Rattus.
REFERENCE 1 (bases 1 to 4742)
AUTHORS Meng,F., Xie,G.-X., Thompson,R.C., Mansour,A., Goldstein,A.,
Watson,S.J. and Akil,H.
TITLE Cloning and pharmacological characterization of a rat kappa opioid
receptor
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 9954-9958 (1993)
MEDLINE 94052210
REFERENCE 2 (bases 1 to 4742)
AUTHORS Meng,F.
TITLE Direct Submission
JOURNAL Submitted (05-AUG-1993) Fan Meng, Mental Health Research Institute,
University of Michigan, 205 Zina Pitcher Place, Ann Arbor, Michigan
48109, USA
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source location/Qualifiers
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/evidence=experimental
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polyA_signal 4719.4724
polyA_site 4742
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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 545 TACATATTTAACCTGGCTTTGGCAGATGCTTT 576
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QY 132 TACATATTTAACCTGGCTTTGGCAGATGCTTT 163



Release 3.0.4A John F. Collins, Biocomputing Research Unit.
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Msrch_n n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 21 01:24:58 1998; MasPar time 142.36 Seconds

Tabular output not generated. 810.633 Million cell updates/sec

Title: >US-08-292-694A-11
Description: (1-1000) from US08292694A.seq
Perfect Score: 994
N.A. Sequence: 1 AAGAGCAAAATCAGTAATC.....CCAGTATGACTAGTCGTGGA 1000
Comp: TICTTGGTTTATGATCATTTAG.....GGTCATCTACTGATCAGCACCT

Scoring table: TABLE jmetric
Gap 60

Nmatch STD : Dbase 0; Query 0

Searched: 159651 segs, 57698962 bases x 2

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database: n-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33

Statistics: Mean 7.723; Variance 3.020; scale 2.557

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	963	96.9	1000 13	Q75931	Human kappa opioid re	0.00e+00
2	729	73.3	1142 20	T12550	Human kappa opioid re	0.00e+00
3	245	24.6	2447 10	Q56702	Partial sequence of t	1.31e-231
4	32	3.2	1410 13	Q75926	Mouse kappa opioid re	1.52e-11
5	32	3.2	2481 15	Q86725	Mammalian kappa opioi	1.52e-11
6	29	2.9	1821 10	Q56700	Sequence of murine de	5.30e-09
7	29	2.9	2216 11	Q66656	Murine delta opioid r	5.30e-09
8	29	2.9	2272 13	Q75927	Mouse delta opioid re	5.30e-09
9	26	2.6	1618 14	Q89223	Transcription regulat	1.52e-06
10	26	2.6	1618 14	Q89222	Rat mu opioid recepto	1.52e-06
11	26	2.6	2070 12	Q79199	Rat mu-subtype opioi	1.52e-06
12	25	2.5	829 10	Q56703	Partial sequence of t	9.56e-06
13	25	2.5	1610 14	Q89226	Human mu opioid recep	9.56e-06
14	25	2.5	2160 15	Q93102	Human mu opiate recep	9.56e-06
15	21	2.1	21 20	T12553	Human kappa opioid re	1.09e-02

C	16	20	2.0	20	20	T12552	Human kappa opioid re	5.76e-02	
C	17	20	2.0	20	39	T12554	Human kappa opioid re	5.76e-02	
	18	20	2.0	20	1265	7	Q45654	Murine somatostatin r	5.76e-02
	19	20	2.0	20	1330	13	Q75928	Mouse opioid receptor	5.76e-02
	20	20	2.0	20	1567	14	Q89233	Rat opioid receptor c	5.76e-02
	21	20	2.0	20	1634	7	Q45653	Human somatostatin re	5.76e-02
	22	20	2.0	20	1981	10	Q56705	Partial sequence of t	5.76e-02
	23	20	2.0	20	2600	14	Q90096	Mouse kappa-3 opioid	5.76e-02
	24	20	2.0	20	2705	15	Q92972	Rat opiorph receptor	5.76e-02
	25	18	1.8	18	1227	9	Q54832	Sequence of clone WZ2	1.41e+00
	26	18	1.8	18	1227	23	T37306	Murine gonadotropin-r	1.41e+00
	27	18	1.8	18	1296	7	Q45657	Human somatostatin re	1.41e+00
	28	17	1.7	17	2237	15	Q89779	Co transporter protein	1.41e+00
	29	17	1.7	17	27	14	Q83683	Epsilon opioid recept	6.47e+00
C	30	17	1.7	17	489	5	Q34771	pcENP-B-1 cDNA.	6.47e+00
C	31	17	1.7	17	1538	31	T69549	Rat pheromone recepto	6.47e+00
C	32	17	1.7	17	2643	6	Q39212	CENP-B cDNA.	6.47e+00
C	33	17	1.7	17	11715	1	N81564	Genomic sequence enco	6.47e+00
C	34	17	1.7	17	11724	2	N70102	Complete genomic sequ	6.47e+00
C	35	17	1.7	17	11725	33	T79723	Human protein C gene.	6.47e+00
C	36	17	1.7	17	11725	22	T32796	Human protein C gene.	6.47e+00
C	37	16	1.6	16	20	30	T13871	Human K-ATP channel s	2.80e+01
	38	16	1.6	16	88	4	N10118	Gene encoding human i	2.80e+01
	39	16	1.6	16	90	4	N10117	Insulin B-chain duple	2.80e+01
	40	16	1.6	16	134	2	N61204	Sequence of avian ery	2.80e+01
	41	16	1.6	16	176	15	Q94407	Sardine derived osteo	2.80e+01
C	42	16	1.6	16	270	2	N81773	Sequence encoding hum	2.80e+01
C	43	16	1.6	16	354	3	N40255	Sequence encoding pro	2.80e+01
C	44	16	1.6	16	480	12	Q78151	Potato starch branchi	2.80e+01
	45	16	1.6	16	726	31	T77788	G-protein coupled rec	2.80e+01
C	46	16	1.6	16	822	12	Q74408	New flower bud induci	2.80e+01
C	47	16	1.6	16	959	21	T12944	Tsex.	2.80e+01
C	48	16	1.6	16	959	8	Q49499	Nucleotide sequence (2.80e+01
C	49	16	1.6	16	976	29	T63288	Partial human tryptop	2.80e+01
C	50	16	1.6	16	976	29	T63289	Human somatostatin re	2.80e+01
C	51	16	1.6	16	1130	23	T09250	Human somatostatin re	2.80e+01
C	52	16	1.6	16	1149	20	T09948	High-affinity melaton	2.80e+01
C	53	16	1.6	16	1173	29	T61866	Human ATP sensitive p	2.80e+01
C	54	16	1.6	16	1173	29	T61867	Mouse ATP sensitive p	2.80e+01
	55	16	1.6	16	1257	2	N70394	Sequence encoding hum	2.80e+01
C	56	16	1.6	16	1278	30	T67088	Human K-ATP channel s	2.80e+01
C	57	16	1.6	16	1332	30	T67087	Mouse K-ATP channel s	2.80e+01
	58	16	1.6	16	1351	7	Q45655	Human somatostatin re	2.80e+01
	59	16	1.6	16	1518	14	Q83682	Epsilon opioid recept	2.80e+01
	60	16	1.6	16	1796	7	Q45658	Murine somatostatin r	2.80e+01
	61	16	1.6	16	2028	15	Q89924	Protease Nexin-1 type	2.80e+01
	62	16	1.6	16	2029	3	Q20494	PN-I alpha analogue,	2.80e+01
	63	16	1.6	16	2029	3	Q20495	PN-I alpha analogue,	2.80e+01
	64	16	1.6	16	2029	3	Q20496	PN-I alpha analogue,	2.80e+01
	65	16	1.6	16	2029	1	N81281	Sequence of coding re	2.80e+01
	66	16	1.6	16	2031	1	N81282	Sequence of coding re	2.80e+01
	67	16	1.6	16	2031	15	Q89925	Protease Nexin-1 type	2.80e+01
	68	16	1.6	16	2032	3	Q22587	PN-I beta analogue,	2.80e+01
	69	16	1.6	16	2032	3	Q22585	PN-I beta analogue,	2.80e+01
	70	16	1.6	16	2032	3	Q22586	PN-I beta analogue,	2.80e+01
C	71	16	1.6	16	2169	32	T79804	Potato starch branchi	2.80e+01
C	72	16	1.6	16	2169	32	T79783	Potato starch branchi	2.80e+01
	73	16	1.6	16	2606	14	Q83527	P. falciparum E31a ge	2.80e+01
	74	16	1.6	16	2606	32	T72895	Plasmodium E31a gene.	2.80e+01
C	75	16	1.6	16	2649	8	Q51026	Human glutamate recep	2.80e+01
C	76	16	1.6	16	2955	17	T02798	Human glutamate recep	2.80e+01
C	77	16	1.6	16	2955	17	T02797	Human glutamate recep	2.80e+01
C	78	16	1.6	16	3128	17	T00774	Potato starch branchi	2.80e+01
	79	16	1.6	16	3369	28	T60335	TIM coding sequence.	2.80e+01
C	80	16	1.6	16	3407	18	Q91230	Human GluR2B receptor	2.80e+01
C	81	16	1.6	16	3407	9	Q54117	Human GluR2B receptor	2.80e+01
	82	16	1.6	16	3505	11	Q70829	Protein kinase (CKI	2.80e+01
	83	16	1.6	16	3505	16	Q92964	Human HRR25-like case	2.80e+01
	84	16	1.6	16	3505	15	Q99885	CKI-delta-3Hu isoform	2.80e+01
C	85	16	1.6	16	4170	28	T60334	TIM splice variant co	2.80e+01
C	86	16	1.6	16	4304	22	T32960	Mouse developmental k	2.80e+01
C	87	16	1.6	16	5198	28	T60333	TIM gene.	2.80e+01
C	88	16	1.6	16	6824	6	Q39050	K.lactis/S. cerevisae	2.80e+01

C	89	16	1.6	11478	32	T79805	Full length potato st	2.80e+01																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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235	1.5	1.5	3416	10	Q62282	CDNA coding human ova	1.13e+02	308	14	1.4	435	23	T37121	GM-CSF (N-linked site	4.24e+02
236	1.5	1.5	3504	1	Q05304	Clone lmd2 encoding i	1.13e+02	309	14	1.4	476	28	T47769	Xenothabdus luminesce	4.24e+02
237	1.5	1.5	3521	19	T18696	RAP-1 radiation prote	1.13e+02	310	14	1.4	476	29	T60501	5' lux fragment of pb	4.24e+02
238	1.5	1.5	3521	7	Q41226	Clone GP3 encoding ma	1.13e+02	311	14	1.4	495	15	Q86357	Human granulocyte mac	4.24e+02
239	1.5	1.5	3558	3	Q22596	Coding region of plas	1.13e+02	312	14	1.4	496	12	Q67878	Vaccinia E3l promoter	4.24e+02
240	1.5	1.5	3560	14	Q87444	Drosophila semaphorin	1.13e+02	313	14	1.4	499	1	N91631	Sequence of new sigma	4.24e+02
241	1.5	1.5	3586	10	Q56643	Human tyrosinase gene	1.13e+02	314	14	1.4	501	5	Q29154	Partial sequence of p	4.24e+02
242	1.5	1.5	3592	7	Q42411	Human CTR cDNA clone.	1.13e+02	315	14	1.4	514	2	Q12781	hGM-CSF/leu23A27Glu	4.24e+02
243	1.5	1.5	3710	2	Q12164	Sequence encoding Hum	1.13e+02	316	14	1.4	514	15	Q86358	Human granulocyte mac	4.24e+02
244	1.5	1.5	3856	1	Q03097	Enod2b genomic clone.	1.13e+02	317	14	1.4	563	2	Q17773	Sequence encoding can	4.24e+02
245	1.5	1.5	4417	2	Q12163	Sequence encoding can	1.13e+02	318	14	1.4	563	9	Q5055	Sequence of orphan re	4.24e+02
246	1.5	1.5	4488	8	Q51426	Human PACC cDNA clone	1.13e+02	319	14	1.4	573	11	Q63729	Pig somatotropin gene	4.24e+02
247	1.5	1.5	4670	4	Q25107	DHFR-AP2 fusion prote	1.13e+02	320	14	1.4	574	1	N91699	Part of the sequence	4.24e+02
248	1.5	1.5	6232	5	Q29269	Human calcium channel	1.13e+02	321	14	1.4	579	4	Q26671	Recombinant porcine s	4.24e+02
249	1.5	1.5	6578	19	T18767	RSV RNA-dependent RNA	1.13e+02	322	14	1.4	633	31	T60688	CDNA encoding soluble	4.24e+02
250	1.5	1.5	7175	6	Q37818	Sequence encoding the	1.13e+02	323	14	1.4	641	18	T19851	Human gene signature	4.24e+02
251	1.5	1.5	7175	15	Q84658	Human neuronal calcit	1.13e+02	324	14	1.4	654	31	T60686	CDNA encoding soluble	4.24e+02
252	1.5	1.5	7362	15	Q84657	Human neuronal calcit	1.13e+02	325	14	1.4	654	2	Q10269	Human BMP.	4.24e+02
253	1.5	1.5	7362	6	Q37817	Sequence encoding the	1.13e+02	326	14	1.4	661	2	N60246	Human granulocyte mac	4.24e+02
254	1.5	1.5	8201	20	T12170	pU64-5-CDK-BP cDNA cl	1.13e+02	327	14	1.4	665	2	N70571	Human gene encoding hum	4.24e+02
255	1.5	1.5	9515	14	Q55145	Pseudomonas aeruginos	1.13e+02	328	14	1.4	672	11	Q70140	Cadrac cDNA.	4.24e+02
256	1.5	1.5	10266	22	T33007	Mouse SRX-related gen	1.13e+02	329	14	1.4	684	29	T67447	H. pylori transporter	4.24e+02
257	1.5	1.5	10684	23	T33758	Control region isolat	1.13e+02	330	14	1.4	702	31	T60704	CDNA encoding soluble	4.24e+02
258	1.5	1.5	11298	33	T86756	Human high affinity I	1.13e+02	331	14	1.4	716	3	N40283	Sequence encoding swi	4.24e+02
259	1.5	1.5	11357	9	Q51024	Human FcERI beta chai	1.13e+02	332	14	1.4	723	29	T67921	H. pylori transporter	4.24e+02
260	1.5	1.5	12720	10	Q64211	L.lactis branched ami	1.13e+02	333	14	1.4	737	13	Q80344	DNA fragment functio	4.24e+02
261	1.5	1.5	13104	7	Q46852	Clone of recombinant	1.13e+02	334	14	1.4	738	3	N40082	Sequence encoding por	4.24e+02
262	1.5	1.5	14704	3	Q20685	PKS 741 insert contg.	1.13e+02	335	14	1.4	744	2	N92401	Sequence encoding lip	4.24e+02
263	1.5	1.5	15223	29	T63430	Respiratory syncytial	1.13e+02	336	14	1.4	744	2	N70674	Sequence encoding lip	4.24e+02
264	1.5	1.5	28804	23	T37329	Sphingnan biosynthetic	1.13e+02	337	14	1.4	755	1	N81117	Porcine somatotropin	4.24e+02
265	1.5	580073	27	T58840	Mycoplasma genitalium	1.13e+02	338	14	1.4	763	1	Q04018	Granulocyte macrophag	4.24e+02	
266	1.4	21	6	Q40363	Sequence of PCR prime	4.24e+02	339	14	1.4	773	2	N60457	Colony stimulating fa	4.24e+02	
267	1.4	21	14	Q83684	Epsilon opioid recept	4.24e+02	340	14	1.4	773	2	N80223	Sequence encoding hum	4.24e+02	
268	1.4	28	21	T32202	Yeast cAMP-dependent	4.24e+02	341	14	1.4	783	2	N93066	Clone encoding bovine	4.24e+02	
269	1.4	29	9	Q53869	Plasmodium yoelii spo	4.24e+02	342	14	1.4	787	14	Q84865	Human pcd-human-GM-CS	4.24e+02	
270	1.4	30	2	Q13759	D2 receptor probe.	4.24e+02	343	14	1.4	787	2	N60364	Human granulocyte mac	4.24e+02	
271	1.4	30	23	T18890	Calcium channel domai	4.24e+02	344	14	1.4	793	4	N20008	Hybrid human leukocyt	4.24e+02	
272	1.4	37	5	Q28822	Ribozyme.	4.24e+02	345	14	1.4	795	1	Q04263	Encodes Colon Cancer	4.24e+02	
273	1.4	38	9	Q55262	Stable hairpin ribozy	4.24e+02	346	14	1.4	798	3	Q34842	Encodes Vkapra region	4.24e+02	
274	1.4	40	29	T69522	Plasmid p1825f1l comp	4.24e+02	347	14	1.4	799	5	Q15228	arod gene.	4.24e+02	
275	1.4	42	5	Q33464	PACK Primer #6.	4.24e+02	348	14	1.4	813	4	Q24524	GM-CSF/IL-3 fusion pr	4.24e+02	
276	1.4	42	5	Q28821	Anti-tumour ribozyme	4.24e+02	349	14	1.4	813	4	Q27810	PIXY 321.	4.24e+02	
277	1.4	56	5	Q28823	Anti-tumour ribozyme	4.24e+02	350	14	1.4	825	4	Q27811	PIXY 344.	4.24e+02	
278	1.4	57	18	T05755	Polymerase Bst restri	4.24e+02	351	14	1.4	825	2	Q10950	IL-3/GM-CSF fusion pr	4.24e+02	
279	1.4	79	5	Q33795	Microsatellite sequen	4.24e+02	352	14	1.4	825	4	Q24525	IL-3/GM-CSF fusion pr	4.24e+02	
280	1.4	83	23	T34403	Oligonucleotide 220 f	4.24e+02	353	14	1.4	825	4	Q24525	Human IL-3/GM-CSF fus	4.24e+02	
281	1.4	90	7	Q47048	GM-CSF oligomer, sens	4.24e+02	354	14	1.4	825	3	Q20271	Human IL-3/GM-CSF fus	4.24e+02	
282	1.4	91	23	T34404	Oligonucleotide 221 f	4.24e+02	355	14	1.4	829	10	Q56703	Partial sequence of t	4.24e+02	
283	1.4	101	18	T19410	Human gene signature	4.24e+02	356	14	1.4	855	29	T68191	H. pylori secreted or	4.24e+02	
284	1.4	107	31	T60683	Beta chain of Class I	4.24e+02	357	14	1.4	856	30	T45356	Ecort fragment common	4.24e+02	
285	1.4	111	31	T47135	Beta chain of Class I	4.24e+02	358	14	1.4	863	4	N20093	Sequence of leukocyte	4.24e+02	
286	1.4	125	21	T22554	Human gene signature	4.24e+02	359	14	1.4	895	1	N91051	Sequence encoding exo	4.24e+02	
287	1.4	125	21	T22554	Human gene signature	4.24e+02	360	14	1.4	895	1	N91051	Sequence encoding exo	4.24e+02	
288	1.4	223	28	T33754	Human brain Expressed	4.24e+02	361	14	1.4	906	20	T18078	Potato calmodulin gen	4.24e+02	
289	1.4	225	28	T33755	Cellubrevin-1 partial	4.24e+02	362	14	1.4	911	2	N71002	Sequence encoding a h	4.24e+02	
290	1.4	230	28	T33752	Cellubrevin-1 partial	4.24e+02	363	14	1.4	921	2	Q11910	Toxoplasma gondii clo	4.24e+02	
291	1.4	279	2	Q13801	Brazil nut 12 kD suif	4.24e+02	364	14	1.4	923	31	T59276	DNA insert of clone F	4.24e+02	
292	1.4	295	22	T26677	Human gene signature	4.24e+02	365	14	1.4	923	29	T51436	Murine Mab SK48-E26 h	4.24e+02	
293	1.4	303	8	Q61356	Human brain Expressed	4.24e+02	366	14	1.4	934	21	T18374	Crtb gene.	4.24e+02	
294	1.4	307	19	T22658	Human gene signature	4.24e+02	367	14	1.4	956	22	T27051	STR7 (suppressor of t	4.24e+02	
295	1.4	310	20	T23300	Human gene signature	4.24e+02	368	14	1.4	1007	11	Q63999	Synthase factor B gen	4.24e+02	
296	1.4	312	8	Q59563	Human brain Expressed	4.24e+02	369	14	1.4	1042	2	Q12911	VNTR locus D1S129 f1	4.24e+02	
297	1.4	360	5	Q29149	WNI 58-9 antibody Hea	4.24e+02	370	14	1.4	1052	1	N90224	Malaria-specific DNA	4.24e+02	
298	1.4	362	8	Q60354	Human brain Expressed	4.24e+02	371	14	1.4	1053	29	T67539	H. pylori flagella-as	4.24e+02	
299	1.4	362	8	Q59041	Human brain Expressed	4.24e+02	372	14	1.4	1065	15	Q74149	Plasmid pSI4001 alpha	4.24e+02	
300	1.4	362	6	Q39629	Expressed Sequence Ta	4.24e+02	373	14	1.4	1065	29	T67990	H. pylori flagella-as	4.24e+02	
301	1.4	385	8	Q61432	Human brain Expressed	4.24e+02	374	14	1.4	1103	3	Q22493	Sequence encoding ovi	4.24e+02	
302	1.4	389	8	Q60166	Human brain Expressed	4.24e+02	375	14	1.4	1110	5	Q29155	Pituitary somatostati	4.24e+02	
303	1.4	402	10	Q64052	Sequence of the VH re	4.24e+02	376	14	1.4	1110	5	Q29155	Pituitary somatostati	4.24e+02	
304	1.4	415	1	N90274	Synthetic human granu	4.24e+02	377	14	1.4	1130	23	T09250	Human somatostatin re	4.24e+02	
305	1.4	415	1	N90383	Synthetic gene for hu	4.24e+02	378	14	1.4	1130	23	Q70736	NTFA-binding protein-	4.24e+02	
306	1.4	429	23	T37122	GM-CSF (N- and O-link	4.24e+02	379	14	1.4	1164	8	Q48976	Nucleotides 301-1464	4.24e+02	
307	1.4	432	4	Q24294	Ovine GM-CSF gene.	4.24e+02	380	14	1.4	1183	32	T79592	NTFA-binding protein	4.24e+02	

C	381	14	1.4	1183	24	T42222	Human TATA-binding pr	4.24e+02	C	454	14	1.4	1849	15	Q91284	T. longibrachiatum en	4.24e+02
C	382	14	1.4	1238	23	T39596	Triticum tauschii CRE	4.24e+02	C	455	14	1.4	1849	22	T32223	Trichoderma endogluca	4.24e+02
C	383	14	1.4	1241	4	Q27368	UGT1F Exon 1 from the	4.24e+02	C	456	14	1.4	1855	30	T66381	Human adrenal gland c	4.24e+02
C	384	14	1.4	1244	7	Q45656	Murine somatostatin r	4.24e+02	C	457	14	1.4	1864	8	Q46240	Herpes simplex virus	4.24e+02
C	385	2	1.4	1245	2	Q10268	Human BMP.	4.24e+02	C	458	14	1.4	1909	2	Q11919	Toxoplasma gondii clo	4.24e+02
C	386	14	1.4	1275	32	T74888	Xenopus neurogenic di	4.24e+02	C	459	14	1.4	1919	8	Q51094	JM haemagglutinin.	4.24e+02
C	387	14	1.4	1302	33	T67134	RAC protein kinase C-	4.24e+02	C	460	14	1.4	1928	22	T35140	Guinea pig L-asparagi	4.24e+02
C	388	14	1.4	1311	7	Q41469	E. coli thymidine pho	4.24e+02	C	461	14	1.4	1943	33	T48583	Human tub genomic seq	4.24e+02
C	389	14	1.4	1323	31	T60700	CDNA encoding soluble	4.24e+02	C	462	14	1.4	1969	29	T64531	Glutamate dehydrogena	4.24e+02
C	390	14	1.4	1341	15	Q90492	Rhodococcus rhodochro	4.24e+02	C	463	14	1.4	1981	10	Q56705	Partial sequence of t	4.24e+02
C	391	14	1.4	1344	31	T60705	CDNA encoding soluble	4.24e+02	C	464	14	1.4	1983	22	T32235	Nutmeg Class II type	4.24e+02
C	392	14	1.4	1351	7	Q45655	Human somatostatin re	4.24e+02	C	465	14	1.4	2008	15	Q94599	EIFE enterotoxin enco	4.24e+02
C	393	14	1.4	1360	22	T32234	Nutmeg Class II type	4.24e+02	C	466	14	1.4	2012	30	T68823	Cytosolic phospholipa	4.24e+02
C	394	14	1.4	1375	30	T67082	Hop latent virus coat	4.24e+02	C	467	14	1.4	2019	29	T47706	Human FRX2 gene.	4.24e+02
C	395	14	1.4	1398	20	T03700	Cotton UDP glucose sy	4.24e+02	C	468	14	1.4	2040	23	T36375	Human G-protein coupl	4.24e+02
C	396	14	1.4	1424	5	Q29273	Human calcium channel	4.24e+02	C	469	14	1.4	2044	17	T13167	Rat interleukin-1 typ	4.24e+02
C	397	14	1.4	1433	11	Q65397	Elm C10:O-acyl carrie	4.24e+02	C	470	14	1.4	2059	2	N60895	Sequence of plasmid p	4.24e+02
C	398	14	1.4	1433	22	T36108	Elm acyl-ACP thioeste	4.24e+02	C	471	14	1.4	2070	8	Q48515	Encodes rabbit HBI pr	4.24e+02
C	399	14	1.4	1433	14	Q92306	Elm class II thioeste	4.24e+02	C	472	14	1.4	2070	12	Q79199	Rat mu-subtype oploid	4.24e+02
C	400	14	1.4	1446	26	T45873	C5a-like seven transm	4.24e+02	C	473	14	1.4	2071	10	Q56945	A. niger pH 2.5 acid	4.24e+02
C	401	14	1.4	1474	22	T14710	Human CD20.4 antigen	4.24e+02	C	474	14	1.4	2071	10	Q58121	pH 2.5 acid phosphata	4.24e+02
C	402	14	1.4	1476	18	T08578	Zinc finger protein c	4.24e+02	C	475	14	1.4	2088	12	Q69003	Mouse amyloid precurs	4.24e+02
C	403	14	1.4	1476	1	N90613	CD20 cDNA.	4.24e+02	C	476	14	1.4	2088	4	Q27801	APP695.	4.24e+02
C	404	14	1.4	1476	22	T14713	Human CD20 antigen cd	4.24e+02	C	477	14	1.4	2095	2	Q13387	Mouse RXR-alpha codin	4.24e+02
C	405	14	1.4	1497	21	T06750	Resynthesised jojoba	4.24e+02	C	478	14	1.4	2096	29	T64543	NADP-specific glutama	4.24e+02
C	406	14	1.4	1506	29	T64547	NADP-specific glutama	4.24e+02	C	479	14	1.4	2108	33	T85326	Human TRAF inhibitor	4.24e+02
C	407	14	1.4	1507	28	T48511	Homology vector 443-8	4.24e+02	C	480	14	1.4	2110	7	Q41228	Human GP22 encoding m	4.24e+02
C	408	14	1.4	1507	12	Q68935	Fowlpox virus (FPV) g	4.24e+02	C	481	14	1.4	2112	30	T68826	Cytosolic phospholipa	4.24e+02
C	409	14	1.4	1517	2	Q13720	Phytoene dehydrogenas	4.24e+02	C	482	14	1.4	2117	22	T27050	SfR6 (suppressor of t	4.24e+02
C	410	14	1.4	1518	22	T37094	Phytoene dehydrogenas	4.24e+02	C	483	14	1.4	2130	14	Q89531	Human H-2RIIBP cDNA.	4.24e+02
C	411	14	1.4	1518	23	T40792	Phytoene dehydrogenas	4.24e+02	C	484	14	1.4	2137	29	T64542	NADP-specific glutama	4.24e+02
C	412	14	1.4	1522	23	T40793	Phytoene dehydrogenas	4.24e+02	C	485	14	1.4	2140	29	T64529	NADP-specific glutama	4.24e+02
C	413	14	1.4	1522	22	T37095	Phytoene dehydrogenas	4.24e+02	C	486	14	1.4	2160	15	Q93102	Human mu opiate recep	4.24e+02
C	414	14	1.4	1525	8	Q45958	hrXR-beta3.	4.24e+02	C	487	14	1.4	2170	17	T04098	Mouse prostaglandin-F	4.24e+02
C	415	14	1.4	1525	8	Q45958	hrXR-beta3.	4.24e+02	C	488	14	1.4	2179	29	T63181	FSH receptor gene wil	4.24e+02
C	416	14	1.4	1540	2	N80917	hrXR-beta3.	4.24e+02	C	489	14	1.4	2180	5	Q29377	FSHR DNA.	4.24e+02
C	417	14	1.4	1569	26	T28573	Sequence of the 3'-en	4.24e+02	C	490	14	1.4	2196	1	Q06815	Sequence encoding hea	4.24e+02
C	418	14	1.4	1573	3	Q22620	Bacterial antibiotic	4.24e+02	C	491	14	1.4	2230	2	N81778	Sequence of porcine g	4.24e+02
C	419	14	1.4	1588	31	T72721	Brassica synthase fac	4.24e+02	C	492	14	1.4	2232	15	Q96297	Human monocyle chemoa	4.24e+02
C	420	14	1.4	1610	14	Q89226	PAP-GM-CSF immunostim	4.24e+02	C	493	14	1.4	2256	1	N80604	Human APCP16814, amin	4.24e+02
C	421	14	1.4	1618	14	Q89223	Human mu oploid recep	4.24e+02	C	494	14	1.4	2256	3	Q20532	Sequence of clone lam	4.24e+02
C	422	14	1.4	1629	9	Q54496	Transcription regulat	4.24e+02	C	495	14	1.4	2256	7	Q42661	Lambda clone APCP1681	4.24e+02
C	423	14	1.4	1635	23	T37177	Alcaligenes bronchise	4.24e+02	C	496	14	1.4	2256	2	Q10014	Lambda clone APCP1681	4.24e+02
C	424	14	1.4	1642	8	Q45957	LKT-GnRH fusion of pc	4.24e+02	C	497	14	1.4	2265	4	Q27802	Clone lambda APCP1681	4.24e+02
C	425	14	1.4	1642	8	Q45957	hrXR-beta2.	4.24e+02	C	498	14	1.4	2278	15	Q94016	APP751.	4.24e+02
C	426	14	1.4	1642	22	T14599	hrXR-beta2.	4.24e+02	C	499	14	1.4	2278	15	Q94016	Rat 5HT transporter (4.24e+02
C	427	14	1.4	1648	4	Q25532	Squalene synthetase c	4.24e+02	C	500	14	1.4	2295	23	T31994	Nonsense-mediated mRN	4.24e+02
C	428	14	1.4	1674	17	T17846	Sequence of genomic c	4.24e+02	C	501	14	1.4	2297	23	T33949	Human Factor V cDNA P	4.24e+02
C	429	14	1.4	1679	13	Q80522	Canola palmitoyl-ACP-	4.24e+02	C	502	14	1.4	2297	23	T33956	Human Factor V heavy	4.24e+02
C	430	14	1.4	1680	15	Q74150	Human lymphocyte PF4A	4.24e+02	C	503	14	1.4	2313	12	Q74708	Human Factor V heavy	4.24e+02
C	431	14	1.4	1695	22	T36138	Plasmid pSI4001 alpha	4.24e+02	C	504	14	1.4	2333	11	Q66637	CDNA of APP 770 gene	4.24e+02
C	432	14	1.4	1713	23	T33900	Guinea pig L-asparagi	4.24e+02	C	505	14	1.4	2333	6	Q37948	Human Activin recepto	4.24e+02
C	433	14	1.4	1717	14	Q90052	Human G-protein coupl	4.24e+02	C	506	14	1.4	2373	21	T36700	Sequence of a DNA iso	4.24e+02
C	434	14	1.4	1718	14	Q90052	Mango class II thioes	4.24e+02	C	507	14	1.4	2385	12	T72725	Human PH30 beta chain	4.24e+02
C	435	14	1.4	1721	9	Q54257	Melanoma differentiat	4.24e+02	C	508	14	1.4	2385	31	Q70812	Her2-GM-CSF immunosti	4.24e+02
C	436	14	1.4	1722	15	Q94598	APP-REP 751 amyloid p	4.24e+02	C	509	14	1.4	2385	16	Q92947	Protein kinase (CK1a)	4.24e+02
C	437	14	1.4	1727	18	T16871	ShET2 enterotoxin loc	4.24e+02	C	510	14	1.4	2415	7	Q41056	Human HRR25-like case	4.24e+02
C	438	14	1.4	1738	18	T07280	Pepper Group 2 gene f	4.24e+02	C	511	14	1.4	2415	15	Q94017	Wilson disease gene e	4.24e+02
C	439	14	1.4	1738	22	T31616	Fragment of plasmid p	4.24e+02	C	512	14	1.4	2422	2	Q11711	Rat 5HT transporter c	4.24e+02
C	440	14	1.4	1755	8	Q49461	Plasmid pSCM525 fragm	4.24e+02	C	513	14	1.4	2442	20	T08125	Rat 5HT transporter (4.24e+02
C	441	14	1.4	1757	8	Q45956	Neurokinin-3 receptor	4.24e+02	C	514	14	1.4	2430	20	T08125	Shuttle vector PMUW15	4.24e+02
C	442	14	1.4	1757	8	Q45956	hrXR-beta1.	4.24e+02	C	515	14	1.4	2430	13	Q73844	Human syndecan-1 gene	4.24e+02
C	443	14	1.4	1762	5	Q29112	hrXR-beta1.	4.24e+02	C	516	14	1.4	2439	31	T63354	P. occultum DNA polym	4.24e+02
C	444	14	1.4	1766	15	Q97491	EIV HA (A2/Suffolk/89	4.24e+02	C	517	14	1.4	2439	1	Q04542	Bacillus subtilis epr	4.24e+02
C	445	14	1.4	1767	21	T26980	Plasmid pTECH2 + hng	4.24e+02	C	518	14	1.4	2451	1	Q04788	Extracellular proteas	4.24e+02
C	446	14	1.4	1767	21	T26980	Aspergillus oryzae ta	4.24e+02	C	519	14	1.4	2451	1	Q04788	Epr gene encoding ext	4.24e+02
C	447	14	1.4	1767	21	T26980	Aspergillus oryzae ta	4.24e+02	C	520	14	1.4	2476	21	T18377	Rat D2 dopamine recep	4.24e+02
C	448	14	1.4	1786	32	N71067	Human integrin-linked	4.24e+02	C	521	14	1.4	2492	12	T49480	Plasmid pmKH1.	4.24e+02
C	449	14	1.4	1797	1	Q04597	Sequence encoding equ	4.24e+02	C	522	14	1.4	2505	24	T45648	Thai catfish GHRH/PAC	4.24e+02
C	450	14	1.4	1800	2	Q14057	Equine hemagglutinin	4.24e+02	C	523	14	1.4	2505	24	T45648	Mouse haematopoietic-	4.24e+02
C	451	14	1.4	1816	24	T42315	Ela gene from human a	4.24e+02	C	524	14	1.4	2521	32	T85404	Putative human cadher	4.24e+02
C	452	14	1.4	1827	31	T63336	Olipalm ACP thioester	4.24e+02	C	525	14	1.4	2521	28	T47252	Human cadherin-12 cod	4.24e+02
C	453	14	1.4	1849	15	Q97716	Human host cell prote	4.24e+02	C	526	14	1.4	2539	3	Q15024	Bacillus subtilis ext	4.24e+02
							Endoglucanase-II geno	4.24e+02								Rat prolactin poly A	4.24e+02

C	527	14	1.4	2555	2	Q11009	Fibulin B.	4.24e+02	C	600	14	1.4	3550	5	Q31623	PIRX-2 containing trx	4.24e+02
C	528	14	1.4	2561	2	Q10400	D2 dopamine receptor	4.24e+02	C	601	14	1.4	3552	1	Q05875	prrx-2 plasmid sequen	4.24e+02
C	529	14	1.4	2574	14	Q76019	DNA encoding gp120 fr	4.24e+02	C	602	14	1.4	3557	2	N60801	Human pro-growth horm	4.24e+02
C	530	14	1.4	2577	6	Q36620	Expression plasmid po	4.24e+02	C	603	14	1.4	3565	14	Q84051	Sequence encoding mei	4.24e+02
C	531	14	1.4	2583	7	Q46606	Plasmid pLNT4ld codin	4.24e+02	C	604	14	1.4	3600	22	T13227	Thermostable enzyme (4.24e+02
C	532	14	1.4	2600	28	T43624	Chromatin regulator p	4.24e+02	C	605	14	1.4	3621	2	N60847	Human pre-prolactin g	4.24e+02
C	533	14	1.4	2623	32	T51715	cdNA for adenovirus E	4.24e+02	C	606	14	1.4	3623	7	Q41297	BMP-2 expression vect	4.24e+02
C	534	14	1.4	2641	5	Q30970	Non-cleavable, solubl	4.24e+02	C	607	14	1.4	3628	2	N60848	Plasmid sequence enco	4.24e+02
C	535	14	1.4	2692	9	Q51114	Sequence encoding met	4.24e+02	C	608	14	1.4	3632	9	Q56898	E.coli thioredoxin-hu	4.24e+02
C	536	14	1.4	2717	2	N60380	Plasmid pASpcq-SV(10)	4.24e+02	C	609	14	1.4	3632	14	Q90770	Thioredoxin/des-Pro-I	4.24e+02
C	537	14	1.4	2719	2	N60572	Genomic sequence enco	4.24e+02	C	610	14	1.4	3632	15	Q93133	Vector for thioredoxi	4.24e+02
C	538	14	1.4	2720	1	Q04081	Vector pASpcg-SV(10)	4.24e+02	C	611	14	1.4	3632	10	Q27476	pALtrxA/EK/IL1delta	4.24e+02
C	539	14	1.4	2755	5	Q30566	Vector pNN03	4.24e+02	C	612	14	1.4	3659	2	N60204	Thioredoxin-Interleuk	4.24e+02
C	540	14	1.4	2756	4	Q26646	Encodes 5HTT serotoni	4.24e+02	C	613	14	1.4	3664	11	Q62675	Interferon-pseudo-ome	4.24e+02
C	541	14	1.4	2761	1	Q04082	Vector pMT-Apo:GHS (H	4.24e+02	C	614	14	1.4	3664	11	Q62675	Plasmid pASK46 for ex	4.24e+02
C	542	14	1.4	2770	32	T78599	AS-30D tumour Type II	4.24e+02	C	615	14	1.4	3681	2	Q13578	Plasmid pKSEU5.	4.24e+02
C	543	14	1.4	2794	3	Q14238	LKT352 gene.	4.24e+02	C	616	14	1.4	3699	7	Q44179	Plasmid ppepe for clon	4.24e+02
C	544	14	1.4	2794	10	Q44760	Recombinant leukotoxi	4.24e+02	C	617	14	1.4	3699	27	T37237	Heavy chain minilocus	4.24e+02
C	545	14	1.4	2794	7	Q41317	Leukotoxin 352 gene i	4.24e+02	C	618	14	1.4	3712	15	Q23445	Vector pgpe.	4.24e+02
C	546	14	1.4	2817	7	T37179	P. haemolytica leukot	4.24e+02	C	619	14	1.4	3712	15	Q97490	Plasmid pPrrA1.	4.24e+02
C	547	14	1.4	2817	7	Q41322	GnRH-leukotoxin gene	4.24e+02	C	620	14	1.4	3735	3	Q14452	Rat prolactin gene in	4.24e+02
C	548	14	1.4	2820	11	Q66454	Xenopus thrombospondi	4.24e+02	C	621	14	1.4	3754	10	Q57880	Intermediate plasmid	4.24e+02
C	549	14	1.4	2822	1	N81664	Dengue virus type 3-d	4.24e+02	C	622	14	1.4	3754	13	Q84782	Protein-tyrosine-kina	4.24e+02
C	550	14	1.4	2838	7	Q41321	Somatostatin-leukotox	4.24e+02	C	623	14	1.4	3754	13	Q85420	Plasmid pTRCH1.	4.24e+02
C	551	14	1.4	2849	28	T48512	Homology vector 443-8	4.24e+02	C	624	14	1.4	3784	15	Q97492	Plasmid pTECH2.	4.24e+02
C	552	14	1.4	2849	12	Q70573	Homology vector 443-8	4.24e+02	C	625	14	1.4	3784	1	Q05326	Sequence encoding fis	4.24e+02
C	553	14	1.4	2849	12	Q68937	Fowlpox virus (FPV) g	4.24e+02	C	626	14	1.4	3803	1	Q03155	Sequence of the chlor	4.24e+02
C	554	14	1.4	2861	7	Q41323	Rotavirus VP4-leukoto	4.24e+02	C	627	14	1.4	3809	27	T61382	Parathyroid calcium r	4.24e+02
C	555	14	1.4	2867	13	Q84589	AMML chromosome inv(1	4.24e+02	C	628	14	1.4	3820	1	Q03517	Plasmid pFGH1 encodin	4.24e+02
C	556	14	1.4	2887	13	T68827	Hamster cytosolic pho	4.24e+02	C	629	14	1.4	3826	10	Q45288	Sequence of plasmid p	4.24e+02
C	557	14	1.4	2935	30	T44578	Calcium-independent c	4.24e+02	C	630	14	1.4	3833	2	N91060	Sequence of plasmid p	4.24e+02
C	558	14	1.4	2935	24	T05842	Calcium-independent c	4.24e+02	C	631	14	1.4	3850	1	N81634	Sequence of new plasm	4.24e+02
C	559	14	1.4	2935	19	T59199	Ca-independent phosph	4.24e+02	C	632	14	1.4	3851	33	T90019	Yellow tail/fin tuna	4.24e+02
C	560	14	1.4	2939	29	Q87350	Plasmid BGINV.	4.24e+02	C	633	14	1.4	3851	3	T79857	Yellowtail tuna DNA e	4.24e+02
C	561	14	1.4	2949	14	Q05086	Sequence encodes NAP-	4.24e+02	C	634	14	1.4	3878	6	Q40299	Sequence of plasmid p	4.24e+02
C	562	14	1.4	2949	1	N91050	Sequence encoding nov	4.24e+02	C	635	14	1.4	3879	7	Q46410	Leukotoxin genes hlyb	4.24e+02
C	563	14	1.4	2950	2	Q13675	SUP-B27 t(1;19) trans	4.24e+02	C	636	14	1.4	3887	8	Q51082	Plasmid pGCH4 which e	4.24e+02
C	564	14	1.4	3003	1	Q05745	Plasmid P_L-mu-smc(1e	4.24e+02	C	637	14	1.4	3919	13	Q80418	Human mgluR3 cDNA.	4.24e+02
C	565	14	1.4	3006	1	Q05085	Sequence encodes NAP	4.24e+02	C	638	14	1.4	3926	1	Q03736	Sequence of plasmid p	4.24e+02
C	566	14	1.4	3006	1	N91049	Sequence encoding nov	4.24e+02	C	639	14	1.4	3933	16	T03885	Human mucosal lymphoc	4.24e+02
C	567	14	1.4	3033	22	T30192	Peripheral nervous sy	4.24e+02	C	640	14	1.4	3944	5	Q29750	PCMX vector.	4.24e+02
C	568	14	1.4	3068	19	T16274	Pyrodictium occultum	4.24e+02	C	641	14	1.4	3957	18	T14077	Human dihydropyrimidi	4.24e+02
C	569	14	1.4	3104	2	N90296	DNA target sequence a	4.24e+02	C	642	14	1.4	3962	14	Q92520	Human mammary carcino	4.24e+02
C	570	14	1.4	3138	2	Q11712	Shuttle vector pMW16	4.24e+02	C	643	14	1.4	3969	8	Q49757	PTK gene HPTK5.	4.24e+02
C	571	14	1.4	3141	32	T47556	Human cytomegalovirus	4.24e+02	C	644	14	1.4	3976	4	Q25119	Expression vector pDS	4.24e+02
C	572	14	1.4	3194	10	Q58039	GM-CSF gene.	4.24e+02	C	645	14	1.4	3976	4	Q25119	Plasmid pGCH5 which e	4.24e+02
C	573	14	1.4	3213	25	T42119	M-lats gene encoding	4.24e+02	C	646	14	1.4	3977	8	Q51081	Plasmid pGCH5 which e	4.24e+02
C	574	14	1.4	3215	8	Q48933	mOSF-2.	4.24e+02	C	647	14	1.4	3977	12	Q87704	Plasmid pDS56/RBSII,S	4.24e+02
C	575	14	1.4	3229	9	Q54213	Bovine IFNgamma/LKT c	4.24e+02	C	648	14	1.4	3977	12	Q87707	Plasmid pDS56/RBSII,S	4.24e+02
C	576	14	1.4	3249	14	Q82748	pRb2 retinoblastoma t	4.24e+02	C	649	14	1.4	3977	12	Q73431	Plasmid pDS56/RBSII,S	4.24e+02
C	577	14	1.4	3266	18	T11192	Plasmid pASK75 compri	4.24e+02	C	650	14	1.4	3977	12	Q87683	Plasmid pDS56/RBSII,S	4.24e+02
C	578	14	1.4	3275	3	N97129	Partial sequence of m	4.24e+02	C	651	14	1.4	3977	12	Q87706	Plasmid pDS56/RBSII,S	4.24e+02
C	579	14	1.4	3311	3	Q22771	Bovine IL-2 - LKT chi	4.24e+02	C	652	14	1.4	3977	12	Q87690	Plasmid pDS56/RBSII,S	4.24e+02
C	580	14	1.4	3311	33	T70377	Cytohesin 1.	4.24e+02	C	653	14	1.4	3977	12	Q87700	Plasmid pDS56/RBSII,S	4.24e+02
C	581	14	1.4	3337	22	T34620	P. vivax Esp-1 blood	4.24e+02	C	654	14	1.4	3977	12	Q87702	Plasmid pDS56/RBSII,S	4.24e+02
C	582	14	1.4	3343	1	Q04655	Plasmid p10169 encodi	4.24e+02	C	655	14	1.4	3977	12	Q87705	Plasmid pDS56/RBSII,S	4.24e+02
C	583	14	1.4	3353	9	Q54258	Amyloid precursor pro	4.24e+02	C	656	14	1.4	3977	12	Q87709	Plasmid pDS56/RBSII,S	4.24e+02
C	584	14	1.4	3353	1	Q04496	Sequence of gene enco	4.24e+02	C	657	14	1.4	3977	12	Q87703	Plasmid pDS56/RBSII,S	4.24e+02
C	585	14	1.4	3353	2	Q14097	Amyloid precursor pro	4.24e+02	C	658	14	1.4	3977	12	Q87694	Plasmid pDS56/RBSII,S	4.24e+02
C	586	14	1.4	3384	33	T86165	Nucleotide sequence o	4.24e+02	C	659	14	1.4	3977	12	Q87712	Plasmid pDS56/RBSII,S	4.24e+02
C	587	14	1.4	3403	15	Q92573	Human placenta derive	4.24e+02	C	660	14	1.4	3977	12	Q87711	Plasmid pDS56/RBSII,S	4.24e+02
C	588	14	1.4	3415	5	Q34608	Expression plasmid pd	4.24e+02	C	661	14	1.4	3977	12	Q87685	Plasmid pDS56/RBSII,S	4.24e+02
C	589	14	1.4	3415	2	Q12784	pDS56/RBSII-1 sequenc	4.24e+02	C	662	14	1.4	3977	12	Q87688	Plasmid pDS56/RBSII,S	4.24e+02
C	590	14	1.4	3416	2	Q12783	pDS56/RBSII sequence.	4.24e+02	C	663	14	1.4	3977	12	Q87699	Plasmid pDS56/RBSII,S	4.24e+02
C	591	14	1.4	3416	5	Q34607	Expression plasmid pd	4.24e+02	C	664	14	1.4	3977	12	Q87689	Plasmid pDS56/RBSII,S	4.24e+02
C	592	14	1.4	3423	17	T00771	GST-SEP Fusion gene f	4.24e+02	C	665	14	1.4	3977	12	Q87686	Plasmid pDS56/RBSII,S	4.24e+02
C	593	14	1.4	3423	17	T00771	GST-SEP Fusion gene f	4.24e+02	C	666	14	1.4	3977	12	Q87692	Plasmid pDS56/RBSII,S	4.24e+02
C	594	14	1.4	3440	2	Q13728	pDS56/RBSII, 6xHis ve	4.24e+02	C	667	14	1.4	3977	12	Q87703	Plasmid pDS56/RBSII,S	4.24e+02
C	595	14	1.4	3440	1	Q06303	Sequence of plasmid p	4.24e+02	C	668	14	1.4	3984	17	T07310	Vector plasmid pPOPE-	4.24e+02
C	596	14	1.4	3457	8	Q48468	Nitrate reductase Nia	4.24e+02	C	669	14	1.4	3984	25	T42118	H-lats gene encoding	4.24e+02
C	597	14	1.4	3474	5	Q29146	pMTNF-MPH plasmid for	4.24e+02	C	670	14	1.4	3993	20	T28277	Plasmid pMV306 sequen	4.24e+02
C	598	14	1.4	3496	28	T48237	Neuronal nicotinic ac	4.24e+02	C	671	14	1.4	4003	1	Q06305	Sequence of plasmid p	4.24e+02
C	599	14	1.4	3546	22	T40235	GPIa precursor cDNA f	4.24e+02	C	672	14	1.4	4004	1	Q06306	PIRX-2 containing trx	4.24e+02

673	14	1.4	4009	12	Q70219	Plasmid pIG2 for TNF	4.24e+02
674	14	1.4	4020	2	N71016	Sequence of LAM/HTLV	4.24e+02
675	14	1.4	4045	12	Q70942	Plasmid pND211 contai	4.24e+02
676	14	1.4	4046	7	Q42525	Cardiac adenylyl cycl	4.24e+02
677	14	1.4	4054	2	Q11888	Collagenase gene.	4.24e+02
678	14	1.4	4059	17	T08475	Eukaryotic expression	4.24e+02
679	14	1.4	4059	24	T41899	Vector PAPEx-1.	4.24e+02
680	14	1.4	4059	17	T12239	Eucaryotic (CMV) expr	4.24e+02
681	14	1.4	4067	10	O63192	Human adeno-associate	4.24e+02
682	14	1.4	4068	1	N90730	Sequence of plasmid p	4.24e+02
683	14	1.4	4080	23	T31993	Nonsense-mediated mRN	4.24e+02
684	14	1.4	4114	14	Q90777	Thioredoxin/IL-11 gen	4.24e+02
685	14	1.4	4120	29	T64421	Plasmid pMV206.	4.24e+02
686	14	1.4	4120	3	Q21502	Vector pMV206 for clo	4.24e+02
687	14	1.4	4151	8	O51524	Rabbit sodium ion/hyd	4.24e+02
688	14	1.4	4163	5	Q32349	Template clone Fab Nq	4.24e+02
689	14	1.4	4164	15	T04575	Plasmid PAT-1 sequenc	4.24e+02
690	14	1.4	4171	18	Q74082	Oncostatin M receptor	4.24e+02
691	14	1.4	4176	3	N90709	Sequence of plasmid p	4.24e+02
692	14	1.4	4181	5	Q29345	MCC gene of chromosom	4.24e+02
693	14	1.4	4189	2	Q05397	Secretion Vector pSEC	4.24e+02
694	14	1.4	4203	2	Q14000	Leukotoxin genes.	4.24e+02
695	14	1.4	4204	2	Q10279	Sequence of plasmid p	4.24e+02
696	14	1.4	4207	1	N92031	Sequence of recombina	4.24e+02
697	14	1.4	4277	6	Q40280	Sequence of clone pS2	4.24e+02
698	14	1.4	4290	22	T18394	Receptor type tyrosin	4.24e+02
699	14	1.4	4290	26	T51235	Receptor-type tyrosin	4.24e+02
700	14	1.4	4290	24	T42593	Coding sequence for r	4.24e+02
701	14	1.4	4294	14	Q92325	Plasmid pBGC646.	4.24e+02
702	14	1.4	4296	20	T28272	Plasmid pMH28 sequenc	4.24e+02
703	14	1.4	4320	32	T73388	DNA encoding HSP72 an	4.24e+02
704	14	1.4	4341	10	Q62391	Vector pVAC1.	4.24e+02
705	14	1.4	4368	17	T03133	Human dihydropyrimidi	4.24e+02
706	14	1.4	4369	17	T03143	Human dihydropyrimidi	4.24e+02
707	14	1.4	4403	8	O48899	Eradutoxina-TRIP fusi	4.24e+02
708	14	1.4	4421	28	T58319	DNA sequence of hepat	4.24e+02
709	14	1.4	4432	12	Q74206	Expression vector V1J	4.24e+02
710	14	1.4	4432	16	T01113	Encodes ampicillin re	4.24e+02
711	14	1.4	4443	2	N70627	Sequence of peplomer	4.24e+02
712	14	1.4	4450	1	N81025	Plasmid pTPI04-4.	4.24e+02
713	14	1.4	4454	30	T66462	Plasmid pTPI04-8 conta	4.24e+02
714	14	1.4	4466	1	N90286	Sequence of pHCV-34 e	4.24e+02
715	14	1.4	4477	3	Q22962	HCV CKS-Core fusion g	4.24e+02
716	14	1.4	4481	6	Q38265	HCV CKS-Core fusion g	4.24e+02
717	14	1.4	4481	3	Q21677	HCV CKS-Core expressi	4.24e+02
718	14	1.4	4481	6	Q38250	HCV CKS-Core expressi	4.24e+02
719	14	1.4	4482	11	Q62662	PJO200 expression vec	4.24e+02
720	14	1.4	4515	8	Q46823	PLISC-SE vector.	4.24e+02
721	14	1.4	4539	14	Q87347	Plasmid pINVI.	4.24e+02
722	14	1.4	4565	1	Q04077	Human 32K alveolar su	4.24e+02
723	14	1.4	4577	33	T72813	Mouse SPT6 cDNA.	4.24e+02
724	14	1.4	4599	22	T27052	RRP3 telomerase-assoc	4.24e+02
725	14	1.4	4608	2	N81407	Sequence of new recom	4.24e+02
726	14	1.4	4608	1	N90288	Plasmid pTP70-1	4.24e+02
727	14	1.4	4621	31	T69889	Human cyclin D1-human	4.24e+02
728	14	1.4	4645	1	N92023	Recombinant plasmid p	4.24e+02
729	14	1.4	4648	2	Q12770	Alpha-glucosidase-Arg	4.24e+02
730	14	1.4	4651	2	Q12756	Alpha-glucosidase/Arg	4.24e+02
731	14	1.4	4651	1	N92044	Sequence of recombina	4.24e+02
732	14	1.4	4655	4	Q25108	DHFR-APP fusion prote	4.24e+02
733	14	1.4	4660	1	N90266	Plasmid pTPGIF2.	4.24e+02
734	14	1.4	4668	1	Q04519	Recombinant plasmid p	4.24e+02
735	14	1.4	4673	4	Q25100	DHFR-APP fusion prote	4.24e+02
736	14	1.4	4690	5	Q29910	RBI, PDI coexpression	4.24e+02
737	14	1.4	4691	16	Q92546	pComb3 expression vec	4.24e+02
738	14	1.4	4715	1	Q05083	Plasmid pSG1-12 of E.	4.24e+02
739	14	1.4	4715	1	N90284	Plasmid pGRF2-15 cont	4.24e+02
740	14	1.4	4716	1	Q05376	Portion of plasmid pG	4.24e+02
741	14	1.4	4732	1	Q03700	Recombinant plasmid p	4.24e+02
742	14	1.4	4760	1	Q05204	Portion of plasmid pG	4.24e+02
743	14	1.4	4762	1	N81675	Plasmid pBSFOLEK1 con	4.24e+02
744	14	1.4	4774	1	N81424	Plasmid pBLAK1 stably	4.24e+02
745	14	1.4	4788	13	Q85367	MIP-1-alpha.	4.24e+02

C	819	14	1.4	5690 15	Q86902	Rat receptor type-pro	4.24e+02	C	892	14	1.4	7298 7	Q47192	Plasmid pHCV-162 codi	4.24e+02
C	820	14	1.4	5703 22	T34110	Anti-IL-5 humanised a	4.24e+02	C	893	14	1.4	7336 1	N91856	Plasmid pBNA-1.	4.24e+02
C	821	14	1.4	5727 3	Q14935	pBx46 sequence.	4.24e+02	C	894	14	1.4	7330 30	T69982	Canarypox virus DNA c	4.24e+02
C	822	14	1.4	5750 7	Q43814	pRLD3D4 construct.	4.24e+02	C	895	14	1.4	7351 32	T47529	Canarypox virus DNA c	4.24e+02
C	823	14	1.4	5779 1	Q05367	Recombinant plasmid p	4.24e+02	C	896	14	1.4	7360 18	T15930	DHFR/inttron (WTrassD)	4.24e+02
C	824	14	1.4	5836 33	T84444	Human prostate-specif	4.24e+02	C	897	14	1.4	7399 5	Q33479	HDPACK1.	4.24e+02
C	825	14	1.4	5836 15	O96296	Human prostate-specif	4.24e+02	C	898	14	1.4	7456 2	Q10686	Plasmid pBNA-1.	4.24e+02
C	826	14	1.4	5864 33	T72812	Human SPT6 cDNA.	4.24e+02	C	899	14	1.4	7474 31	T171320	Plasmid pBNA-1.	4.24e+02
C	827	14	1.4	5865 33	T90692	Plasmid FBdelPRDSAF c	4.24e+02	C	900	14	1.4	7533 2	N70491	Entire sequence of hi	4.24e+02
C	828	14	1.4	5931 7	Q43701	Sequence of the human	4.24e+02	C	901	14	1.4	7533 1	N81970	Plasmid pEMpl-tPA.	4.24e+02
C	829	14	1.4	6010 28	T59676	Plasmid pRIT14129 cod	4.24e+02	C	902	14	1.4	7566 7	Q42160	Plasmid pPS0212 contg	4.24e+02
C	830	14	1.4	6020 1	Q06648	Plasmid FBdelPASAF co	4.24e+02	C	903	14	1.4	7607 8	Q49754	PTK gene lptK-2.	4.24e+02
C	831	14	1.4	6028 33	T90689	Plasmid FBdelPASAF co	4.24e+02	C	904	14	1.4	7607 16	T03097	Protein tyrosine-kin	4.24e+02
C	832	14	1.4	6044 20	T28280	Plasmid pMV361-lux se	4.24e+02	C	905	14	1.4	7625 31	T71323	Hybrid activation vec	4.24e+02
C	833	14	1.4	6061 33	T90690	Plasmid FBdelPMOSAF c	4.24e+02	C	906	14	1.4	7653 17	T00770	Sirolimus effector pr	4.24e+02
C	834	14	1.4	6062 3	Q20732	Plasmid pBdelPMOSAF c	4.24e+02	C	907	14	1.4	7653 17	T00770	Sirolimus effector pr	4.24e+02
C	835	14	1.4	6096 2	N70871	Plasmid pTP68-1.	4.24e+02	C	908	14	1.4	7791 15	Q84660	Human neuronal calciu	4.24e+02
C	836	14	1.4	6115 29	T63235	Eukaryotic expression	4.24e+02	C	909	14	1.4	7808 15	T33872	Human neuronal calciu	4.24e+02
C	837	14	1.4	6165 16	Q92547	Expression vector, pP	4.24e+02	C	910	14	1.4	7824 23	T33872	Human RAP1 cDNA.	4.24e+02
C	838	14	1.4	6170 18	Q98929	Vector p19LUC sense s	4.24e+02	C	911	14	1.4	7824 15	Q74052	Human interleukin-1-b	4.24e+02
C	839	14	1.4	6171 20	T28279	Plasmid pMV261-lux se	4.24e+02	C	912	14	1.4	7824 23	Q74052	Human interleukin-1-b	4.24e+02
C	840	14	1.4	6176 27	T49226	Plasmid pGR0403R for	4.24e+02	C	913	14	1.4	7859 7	T33872	Human RAP1 cDNA.	4.24e+02
C	841	14	1.4	6207 7	Q43813	pRLD2D3D4 construct.	4.24e+02	C	914	14	1.4	7859 7	T33872	Human RAP1 cDNA.	4.24e+02
C	842	14	1.4	6229 20	T29220	Beta-lactamase vector	4.24e+02	C	915	14	1.4	7897 20	T27555	Shuttle vector pSW6.	4.24e+02
C	843	14	1.4	6231 30	T66737	CMV-BL for extracell	4.24e+02	C	916	14	1.4	8045 17	Q25185	Shuttle vector pSW6.	4.24e+02
C	844	14	1.4	6231 30	T70309	Plasmid pCMV-BL encod	4.24e+02	C	917	14	1.4	8083 14	Q90133	Shuttle vector pSW6	4.24e+02
C	845	14	1.4	6244 13	Q76269	phCMV*-1-controlled p	4.24e+02	C	918	14	1.4	8135 14	Q90134	Subtilisin N62D/G16D	4.24e+02
C	846	14	1.4	6254 18	Q98916	TGF-beta responsive e	4.24e+02	C	919	14	1.4	8136 29	T63236	Plasmid pBHVkex-1::g	4.24e+02
C	847	14	1.4	6254 18	Q98918	TGF-beta responsive e	4.24e+02	C	920	14	1.4	8149 14	Q90135	Plasmid pBHVkex-1::g	4.24e+02
C	848	14	1.4	6265 18	Q98917	TGF-beta responsive e	4.24e+02	C	921	14	1.4	8157 24	T35165	Plasmid pBHVkex-3::B	4.24e+02
C	849	14	1.4	6274 7	Q43812	pRLD2D3.ApAl const	4.24e+02	C	922	14	1.4	8316 13	Q74450	Plasmid pHL-D2 used	4.24e+02
C	850	14	1.4	6285 22	T34109	Anti-IL-5 humanised a	4.24e+02	C	923	14	1.4	8388 13	Q62611	myod retroviral expre	4.24e+02
C	851	14	1.4	6312 20	T03696	Plasmid pBETA92, enco	4.24e+02	C	924	14	1.4	8400 9	T12907	Novel expression plas	4.24e+02
C	852	14	1.4	6327 22	T90691	Plasmid FBdelPGASAF c	4.24e+02	C	925	14	1.4	8501 22	T59271	Plasmid pAV.CMYLacZ.	4.24e+02
C	853	14	1.4	6327 22	T32301	Dermatomyositis speci	4.24e+02	C	926	14	1.4	8509 30	T59271	Vector pAPEX-3P.	4.24e+02
C	854	14	1.4	6350 23	T35198	Plasmid pUC19-SFG.	4.24e+02	C	927	14	1.4	8540 24	Q65628	Sequence of pHEB030.	4.24e+02
C	855	14	1.4	6365 7	Q41173	Plasmid LXSNI-R1-IL2 c	4.24e+02	C	928	14	1.4	8540 24	Q65628	Plasmid pHL-D2 (MFA1	4.24e+02
C	856	14	1.4	6367 17	T12661	Vector COSFclink.	4.24e+02	C	929	14	1.4	8584 24	T35166	Sequence encoding hum	4.24e+02
C	857	14	1.4	6376 4	Q27951	pVE149.	4.24e+02	C	930	14	1.4	8590 24	N60404	Plasmid pD2pick(MFA1p	4.24e+02
C	858	14	1.4	6387 22	T30354	Chimeric cytochrome P	4.24e+02	C	931	14	1.4	8591 33	T84562	Plasmid pCUL621 encod	4.24e+02
C	859	14	1.4	6387 6	Q36498	Chimeric cytochrome P	4.24e+02	C	932	14	1.4	8710 17	Q89550	Plasmid pCUL621 encod	4.24e+02
C	860	14	1.4	6407 29	T64413	Plasmid pMV101.	4.24e+02	C	933	14	1.4	8710 17	Q89550	pSC11 FlpV E1.	4.24e+02
C	861	14	1.4	6414 3	Q20733	PAD-CMV1 expression v	4.24e+02	C	934	14	1.4	8797 27	T32227	DNA cassette for amph	4.24e+02
C	862	14	1.4	6414 1	Q06283	PAD-CMV1 contg. a Tum	4.24e+02	C	935	14	1.4	8808 22	T32227	Plasmid pBHL46.	4.24e+02
C	863	14	1.4	6452 22	T30193	Peripheral nervous sy	4.24e+02	C	936	14	1.4	8810 2	N60061	Sequence encoding von	4.24e+02
C	864	14	1.4	6464 18	Q98933	Vector HBVLuc.	4.24e+02	C	937	14	1.4	8920 17	T07652	Carbamoyl-phosphate-s	4.24e+02
C	865	14	1.4	6555 30	T70315	Plasmid pCMV-BLIGM en	4.24e+02	C	938	14	1.4	9046 15	T07652	pSC11 FlpV N.	4.24e+02
C	866	14	1.4	6557 18	Q43361	Anti-IGF VH expressio	4.24e+02	C	939	14	1.4	9046 15	T07652	Transcription factor	4.24e+02
C	867	14	1.4	6630 7	T79882	Sequence of clrcular	4.24e+02	C	940	14	1.4	9108 16	T03104	Plasmid pRK5.tkl1-1.1	4.24e+02
C	868	14	1.4	6658 33	Q79545	Tomato immunity 2 gen	4.24e+02	C	941	14	1.4	9144 23	T18951	Plasmid pBE346.	4.24e+02
C	869	14	1.4	6714 13	Q48465	PMB254b plasmid expre	4.24e+02	C	942	14	1.4	9193 2	N60365	Sequence of LAV virus	4.24e+02
C	870	14	1.4	6722 8	Q48465	Plasmid pg+host6 cont	4.24e+02	C	943	14	1.4	9208 11	Q65629	Vector contg. TCAE 8	4.24e+02
C	871	14	1.4	6722 8	Q48465	Plasmid pg+host6 cont	4.24e+02	C	944	14	1.4	9208 11	Q65629	Merosin cDNA.	4.24e+02
C	872	14	1.4	6749 32	T47561	Cytomegalovirus pp65	4.24e+02	C	945	14	1.4	9208 11	Q65629	pXJCT-hGM-CSF express	4.24e+02
C	873	14	1.4	6749 32	T47564	Cytomegalovirus pp65	4.24e+02	C	946	14	1.4	9208 11	Q65629	Sequence of cDNA clon	4.24e+02
C	874	14	1.4	6824 6	Q39050	K.lactis/S. cerevisiae	4.24e+02	C	947	14	1.4	9208 11	Q65629	P. falciparum transmi	4.24e+02
C	875	14	1.4	6827 8	Q49753	pTK gene SAL-S1.	4.24e+02	C	948	14	1.4	9208 11	Q65629	Plasmid pBHL13 used f	4.24e+02
C	876	14	1.4	6827 16	T03101	Protein tyrosine-kin	4.24e+02	C	949	14	1.4	9208 11	Q65629	Sequence of entire HI	4.24e+02
C	877	14	1.4	6889 18	T15931	DHFR/inttron (WTrassD)	4.24e+02	C	950	14	1.4	9208 11	Q65629	Retro virus vector p5	4.24e+02
C	878	14	1.4	6925 23	T33942	Human Factor V cDNA.	4.24e+02	C	951	14	1.4	9208 11	Q65629	ROD HIV-2 isolate com	4.24e+02
C	879	14	1.4	6925 23	T33942	Human Factor V cDNA.	4.24e+02	C	952	14	1.4	9208 11	Q65629	Sequence of clone HIV	4.24e+02
C	880	14	1.4	6926 17	T12652	IL-4.Y124D/IgG1 fusio	4.24e+02	C	953	14	1.4	9208 11	Q65629	HIV-1 NL4-3 genomic D	4.24e+02
C	881	14	1.4	6942 17	Q86480	Merosin partial cDNA,	4.24e+02	C	954	14	1.4	9208 11	Q65629	Inositol-3-phosphate	4.24e+02
C	882	14	1.4	6953 19	T17115	Rhodopsin gene.	4.24e+02	C	955	14	1.4	9208 11	Q65629	Shuttle vector pAdDel	4.24e+02
C	883	14	1.4	6961 33	T84508	Rabbit LDL receptor a	4.24e+02	C	956	14	1.4	9208 11	Q65629	Plasmid pBE92.	4.24e+02
C	884	14	1.4	6977 8	Q48213	Hind III - Not I thro	4.24e+02	C	957	14	1.4	9208 11	Q65629	Transposon delivery v	4.24e+02
C	885	14	1.4	7059 9	Q55004	Humanised anti-CD18 A	4.24e+02	C	958	14	1.4	9208 11	Q65629		
C	886	14	1.4	7091 32	T47530	H6 promoted cytomegal	4.24e+02	C	959	14	1.4	9208 11	Q65629		
C	887	14	1.4	7174 2	N91062	Sequence of plasmid p	4.24e+02	C	960	14	1.4	9208 11	Q65629		
C	888	14	1.4	7223 28	T62602	Luciferase expression	4.24e+02	C	961	14	1.4	9208 11	Q65629		
C	889	14	1.4	7228 8	C50201	Vector p37ML-10D.	4.24e+02	C	962	14	1.4	9208 11	Q65629		
C	890	14	1.4	7291 24	T41476	Haemophilus adhesio	4.24e+02	C	963	14	1.4	9208 11	Q65629		
C	891	14	1.4	7291 12	Q67860	AlVAC subgenomic frag	4.24e+02	C	964	14	1.4	9208 11	Q65629		

C 965	14	1.4	10241 18	T10690	Expression vector pB1	4.24e+02
C 966	14	1.4	10288 31	T71322	Plasmid pCB51 encodin	4.24e+02
C 967	14	1.4	10366 12	Q67401	Huntingtin DNA\T15 g	4.24e+02
C 968	14	1.4	10367 33	T80057	Sequence of plasmid p	4.24e+02
C 969	14	1.4	10367 10	Q58701	pLRB332.	4.24e+02
C 970	14	1.4	10443 31	T71319	Plasmid pTB72 encodin	4.24e+02
C 971	14	1.4	10558 18	Q98914	TGF-beta responsive e	4.24e+02
C 972	14	1.4	10569 18	Q98913	TGF-beta responsive e	4.24e+02
C 973	14	1.4	10704 7	Q43846	Plasmid pAH4625.	4.24e+02
C 974	14	1.4	10723 31	T49303	CDNA sequence encodin	4.24e+02
C 975	14	1.4	10723 31	T49304	CDNA encoding polypro	4.24e+02
C 976	14	1.4	10844 7	Q43848	Plasmid pAH4808.	4.24e+02
C 977	14	1.4	10930 20	Q81225	Plasmid pM16.	4.24e+02
C 978	14	1.4	10950 20	Q81225	Retro virus vector p5	4.24e+02
C 979	14	1.4	10970 12	Q73735	DNA cassette for amphi	4.24e+02
C 980	14	1.4	11093 27	T50855	Plasmid pAH4602.	4.24e+02
C 981	14	1.4	11529 7	Q43844	Construct pHEBO-DR-RE	4.24e+02
C 982	14	1.4	11616 12	Q67390	Nucleotide sequence o	4.24e+02
C 983	14	1.4	12283 2	Q10353	Lymphocyte specific i	4.24e+02
C 984	14	1.4	12537 24	T41705	Sequence of human mus	4.24e+02
C 985	14	1.4	12923 3	N90338	Rat acyl peptide hydr	4.24e+02
C 986	14	1.4	13206 1	Q05243	Plasmid pCB50 encodin	4.24e+02
C 987	14	1.4	13414 31	T71321	Myotonic dystrophy ge	4.24e+02
C 988	14	1.4	13747 7	Q47342	Plasmid pAH4611.	4.24e+02
C 989	14	1.4	13999 7	Q43845	Plasmid pVSVFL(+) inc	4.24e+02
C 990	14	1.4	14311 24	T38744	PKS 741 insert contg.	4.24e+02
C 991	14	1.4	14704 3	Q20685	HPLA2-8 gene.	4.24e+02
C 992	14	1.4	15328 13	Q81139	Alphavirus-based euka	4.24e+02
C 993	14	1.4	16656 21	T30787	HCW Toledo strain no	4.24e+02
C 994	14	1.4	18318 24	T41418	Shuttle vector pAdel	4.24e+02
C 995	14	1.4	19307 20	T27558	Shuttle vector pAdel	4.24e+02
C 996	14	1.4	19307 20	T27558	Gene for biosynthetic	4.24e+02
C 997	14	1.4	37895 24	T34137	T. niueum Cyclosporin	4.24e+02
C 998	14	1.4	46899 9	Q54386	Human polycystic kidn	4.24e+02
C 999	14	1.4	53577 28	T18551	Total base sequence o	4.24e+02
C 1000	14	1.4	134525 1	Q04525		

ALIGNMENTS

RESULT	1	
ID	Q75931	standard; DNA; 1000 BP.
AC	Q75931;	
DT	18-AUG-1995	(first entry)
DE	Human kappa opioid receptor partial cDNA fragment.	
KW	Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;	
KW	transmembrane domain; somatostatin; receptor; human; expression vector;	
KW	truncate; chimeric; assay; probe; ss.	
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	CDS	102..989
FT	/*tag= a	
FT	/product= partial human kappa opioid receptor	
PN	W09428132-A.	
PD	08-DEC-1994.	
PE	20-MAY-1994; U05747.	
PR	20-MAY-1993; US-066296.	
PR	30-JUL-1993; US-100694.	
PR	05-NOV-1993; US-147592.	
PA	(ARCH-) ARCH DEV CORP.	
PI	Bell GI, Reisine T, Yasuda K;	
DR	WPI; 95-022804/03.	
DR	P-PSDB; R67672.	
PT	Polynucleotides and peptides derived from opioid receptor	
PT	polypeptides - for use in therapeutic compositions and in	
PT	screening assays for useful drug substances.	
PS	Claim 10; Page 236-239; 300pp; English.	
CC	The partial nucleotide sequence of the novel human kappa opioid receptor	
CC	gene. The gene was isolated from a human brain hippocampus cDNA library	
CC	using a probe from the mouse kappa opioid receptor gene (Q75926). The	
CC	gene is missing the N-terminal sequence. The C-terminal sequence is	
CC	very similar to the mouse kappa opioid receptor sequence. Of the	
CC	C-terminal 293 amino acids, 281 residues are identical and 6 residues	

CC	have conservative substitutions. The gene encoding the human opioid
CC	receptor can be placed in a suitable expression vector for production of
CC	the protein in a cell. The opioid receptors thus produced are useful for
CC	the development of novel assays designed to select or improve substances,
CC	capable of interacting with the opioid receptor proteins, for use in
CC	diagnosis, drug design and therapeutic applications.
SQ	Sequence 1000 BP; 238 A; 253 C; 225 G; 278 T;
Query Match	
Best Local Similarity 99.9%; Score 963; DB 13; Length 1000;	
Matches 999; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Db	1 aagaagcaaatcagtaatccaaaggtatcacaaacattcaccttattggtttgac 60
QY	1 AAGAAGCAAAATCAGTAATCCAAAGGCTATCAAAACACATTCACTTATGGGGTTTGAC 60
Db	61 ttgaaatgagggaaatgctatgttctttcttttagatatacaaaagatgaagacag 120
QY	61 TTGAAATGAGGGAAATGCTATTGTTCTTTCTTTAGATACACAAAGATGAAGACAG 120
Db	121 caaccaacatttacatatattaacctgtcttgacagatgcttagttactacaacatgac 180
QY	121 CAACCAACATTTACATATTTTAACCTGGCTTGGCAGATGCTTAGTTACTACACCAATGC 180
Db	181 cctttcagagtagcgtctactcttgatgaatccctgtccttttggggatgtgctgcaaga 240
QY	181 CCTTCAGAGTAGCGGTCTACTTGATGAATTCCTGGCCCTTTTGGGATGTGCTGTGCAAGA 240
Db	241 tagtaattccatttactactacaacatgttcaaccagcatcttcaaccttgacaatgata 300
QY	241 TAGTAATTTCCATTGATTACTACACACATGTTACACAGCATCTTCACCTTGACCAATGATGA 300
Db	301 gcgtgacgcgtacattgcgltgtgccacccgcgtgaagccttttgacttcgcacacccct 360
QY	301 GCGTGACCGCTACATTGCCGTGTGCCACCCCGTGAAGCCTTTGGAATTCCGGACACCCCT 360
Db	361 tgaagccaagatcatcaatatctgcattctgtgtgtcgtatctgttgatctctg 420
QY	361 TGAAGCCAAGATCATCAATATCTGCATCTGGCTGCTGCTGCATCTGTGGCACTCTG 420
Db	421 caatagtccttgagggacccaaagtcaggggaaggtgtcgtatgtcattgagtcgtctgc 480
QY	421 CAATAGTCCTTGAGGCACCAAGTCAAGGGAAGTGTGATGTGATGCTGCTTGC 480
Db	481 agttccagatgatgaactactcctgtgtggaacctcttcattgaagatctgcgtcttcatt 540
QY	481 AGTTCAGATGATGACTACTCTGCTGTGGACCTCTTCATGAAGATCTGCGTCTTCATCT 540
Db	541 ttgccttcgtcatccctgtcctcatcatcatcgtctgtctacacccctgatctcgtcgtc 600
QY	541 TTGCCTTCGTGATCCCTGTCTCATCATCATGCTGTGTACACCCCTGATGATCCTGCGTGC 600
Db	601 tcaagangtccggtcctttctgtgtcctccgagagaagaatnucacacctgctgtaggata 660
QY	601 TCAAGANNGTCCGGCTCTTCTGTGGCTCCCGAGAGAAAGATNNCAACCTGGCTAGGATCA 660
Db	661 ccagactggtcctgtgtgtgtgtgagcagtccttcgtcgtcgtgactcccatcaacatat 720
QY	661 CCAAGACTGTCCTGTGTGTGTGGGAGCACCCTCCACACACAGCTGCTCTCTCCAGCTATT 720
Db	721 tcaatcctgtgtgaggtctctggggagacacctcccaagacacagctgtctctcagctatt 780
QY	721 TCAATCCTGTGTGAGGCTCTGGGAGACACCTCCACACACAGCTGCTCTCTCCAGCTATT 780
Db	781 actctgcatacgcttgagctataccaacagtagcctgaatcccatctcctaagcctttc 840
QY	781 ACTTCTGCATGCGCTTAGGCTATACCAACAGTAGCCTGAATCCCATTTCTTACGCTTTC 840
Db	841 ttgatgaaactcaagcggtgttccggaactctgtcttccactgaagatgagatgag 900
QY	841 TTGATGAAAACTCAAGCGGTGTTCCGGGACTTGTCTTCCACTGAAGATGAGATGG 900
Db	901 agcgcnagagcactagcagagtcggaataacagttcagatctcgttaccctgagggaga 960


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QY 901 AGCGCNAGAGACTAGCAGAGTCCGAATACAGTTCAGGATCCTGCTTAACTGAGGAGA 960
Db 961 tcgatggatgatgaataaaccagtatgactagtcgtgga 1000
QY 961 TCGATGGGATGATGATAAACCAGTATGACTAGTCGTGGA 1000

RESULT 2
ID T12550 standard; cDNA; 1142 BP.
AC T12550;
DT 03-SEP-1996 (first entry)
DE Human kappa opioid receptor cDNA.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
OS neurology; diagnosis; ds.
FH Homo sapiens.
FH key Location/Qualifiers
FT CDS 1..1142
FT /*tag= a
FT /product= kappa_opioid_receptor
FT /note= "incomplete termination codon"
PN WO9601898-A1.
PD 25-JAN-1996.
PF 07-JUL-1995; F00912.
PR 11-JUL-1994; ER-008531.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B, Simonin F;
DR WPI; 96-097628/10.
DR P-PSDB; R68722.
PT New nucleic acid encoding the human Kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators
PS Claim 3; Page 13-15; 30pp; French.
CC This sequence codes for the human kappa opioid receptor and was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 1142 BP; 236 A; 337 C; 283 G; 286 T;

Query Match 73.3%; Score 729; DB 20; Length 1142;
Best Local Similarity 98.8%; Pred. No. 0.00e+00;
Matches 849; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 257 gatacaaaagatgaagacagcaaccaattacatatattacacctggcttggcagatg 316
QY 100 GATACACAAAGATGAAGACAGCAACCAACATTTACATATTTAACTGGCTTGGCAGATG 159
Db 317 cttagtactacaacacatggcccttcagagtlacggtctactatgaattccctggcctt 376
QY 160 CTTTAGTACTACAAACCATGCCCTTCAGAGTACGGTCTACTGATGAATTCCTGCCCTT 219
Db 377 ttgggagtgtgctgtgcaagatagaattccattgtattactacaacatgttcaaccagca 436
QY 220 TTGGGGATGTGCTGTGCAAGATAGTAAATTTCATGTGATTACTACACAATGTTCAACCA 279
Db 437 tcttcacctgacacatgatgatgagcgtgagccgctacatattgcccgtgtgcccacccgtgaag 496
QY 280 TCTTCACTTGACCAATGATGAGCGCGTGAACCCGCTACATTGCCGTGTGCCACCCCGTGAAGG 339
Db 497 ctttggaactccgacacacccttgaaagcacaagatcatcaatatctgtcatctgtgctgt 556
QY 340 CTTTGGACTTCGACACACCCTTGAAAGGCAAGATCATCATATCTGCACTCGGCTGTGT 399
Db 557 cgtcatcgtttggcatctctgcaatagtccttggagagcaccacaagtcaaggagacgtgtg 616
QY 400 CGTCACTGTGTGGCATCTCTGCAATAGTCTCTTGAGGACACCAAGTCAAGGAAGTGTG 459
Db 617 atgtcatgtagtgctccttgcagttcccaagatgatgactactcctgtgtggacctcttca 676
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QY 460 ATGTCATGAGTGTGCTGCTTGACAGTTCACAGATGATGACTACTCTCTGTTGGAGACCTCTTCA 519
Db 677 tgaagatcgcgtctctcatccttgccttgatgataccctgtctccatcatcatcgtctgtct 736
QY 520 TGAAGATCTGCGTCTTCACTCTTGCTTCGTGATCCCTGCTTCCATCATCATCGTCTGCT 579
Db 737 acaccctgatgatccttgctgtctcaagagcgtccgctccttcttgctcccgagagaag 796
QY 580 ACACCCTGATGATCCTTGCGTCTCAAGANNNGTCCGGCTCCTTCTTGCTCCCGAGAGAAAG 639
Db 797 atgcgaacctgcgttaggatcaccaagactggtcctggtgtgtgtgagcagtcctcgtcgtct 856
QY 640 ATNNCAACTGCTGATGGAICACCAAGCTGCTCCTGTTGGTGGCAGTCTTCTGCTGCT 699
Db 857 gctggaactcccatcacatatatcactcctggtgagagcctctgaggagaccctccacagca 916
QY 700 GCTGGACTCCCATTCACATATTTCACTCTGTTGGAGGCTCTGGGAGACACCTCCACAGCA 759
Db 917 cagctgctctctccagctattactctgcatgcgccttagtcctatataccaacagtagcctga 976
QY 760 CAGCTGCTCTCTCCAGCTATTTACTTCTGCATCGCCTTAGGCTATACCAACAGTAGCCTGA 819
Db 977 atcccatctctacgccttctcttgatgataaacttcaagcgtgtttccggaactctgtct 1036
QY 820 ATCCCATTTCTCTACGCGCTTCTTGTGAAGAACTTCAGACGGGTGTTCCGGGACTTCTGCT 879
Db 1037 ttccactgaaagatgagagatgagcgcgcagagcactagcagagtcogaatatcagttcagg 1096
QY 880 TTCCACTGAAGATGAGNATGGAGCGCNAGACACTAGCAGAGTCCGAATATACAGTTCAAG 939
Db 1097 atcctgcttaccctgagga 1115
QY 940 ATCTGCTTACCTGAGGA 958

RESULT 3
ID Q56702 standard; DNA; 2447 BP.
AC Q56702;
DT 15-SEP-1994 (first entry)
DE Partial sequence of the human kappa opioid receptor
DE genomic clone H14 (KORa).
KW Opioid receptor; morphine; opiate; ss.
OS Homo sapiens.
PN WO9404552-A.
PD 03-MAR-1994.
PF 13-AUG-1993; U07665.
PR 13-AUG-1992; US-929200.
PA (REGC ) UNIV CALIFORNIA.
PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
DR WPI; 94-083099/10.
PT DNA encoding opioid receptors and antibodies against this
PT receptor - used to express and locate these receptors, and screen
PT cpts. for opioid (ant)agonist activity
PS Example; Fig 8b; 74pp; English.
CC To isolate opiate receptor genomic clones, 300,000 human genomic
CC clones and a similar number of mouse genomic clones were probed
CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 Pst/XbaI
CC fragment. One mouse clone and three human genomic clones were
CC isolated. The 3 human clones had very different EcoRI patterns
CC which indicated that three different genes were represented by the
CC human genomic clones which were designated H3, H14 and H20. H14 maps
CC to chromosome 8. It encodes the human kappa opioid receptor.
SQ Sequence 2447 BP; 683 A; 512 C; 498 G; 747 T;

Query Match 24.6%; Score 245; DB 10; Length 2447;
Best Local Similarity 100.0%; Pred. No. 1.31e-231;
Matches 245; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ccttgcccttttgggagtgtgtgtgcaagatagtaatttcattgattactacacatgt 60
QY 211 CCTGGCCTTTTGGGAGATGTGTGTGCAAGATAGTAATTTCATTGATTACTACAAACATGT 270
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CC Seven putative membrane-spanning regions were identified. The DOR-1
CC clone produces a delta receptor with a predicted mol. wt. of 40,558
CC kaltons prior to post-translational modifications.
SQ Sequence 1821 BP; 339 A; 559 C; 541 G; 382 T;

Query Match 2.9%; Score 29; DB 10; Length 1821;
Best Local Similarity 100.0%; Pred. No. 5.30e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 446 accatgatgagcgtgaccgctacattgc 474
|||||
QY 291 ACCATGATGAGCGGTGACCGCTACATTGC 319

RESULT 7
ID Q66656 standard; cDNA; 2216 BP.
AC Q66656;
DT 19-JAN-1995 (first entry)
DE Murine delta opioid receptor coding sequence.
KW delta opioid; enkephalin; receptor; mouse; murine; analgesic; pain;
KW drug addiction; neurological disorder; psychiatric; disorder;
KW cardiovascular disorder; ds.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 59..1174
FT /*tag= a
FT /product= opioid_receptor
PN FR2697850-A.
PD 13-MAY-1994.
PF 10-NOV-1992; 013526.
PR 10-NOV-1992; FR-013526.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B;
DR WPI; 94-178255/22.
DR P-PSDB; R66503.
PT New nucleic acid encoding opioid receptor - and related
PT polypeptide, antisense nucleic acid, probes, recombinant cells
PT and ligands, useful in diagnosis and treatment of e.g.
PT neurological disorders
PS Claim 3; Page 16-18; 29pp; French.
CC A cDNA bank constructed from hybridoma NG108-15, was used to
CC transfect COS-1 cells. The cells were tested for ability to bind
CC tritium-labelled Tyr-D-Thr-Gly-Phe-Leu-Thr, in the presence or
CC absence of the opioid antagonist naloxone. Clone K56 was isolated
CC from a positive colony and found to contain a 2216bp insert. This
CC cDNA encodes a delta opioid (enkephalin) receptor with apparent
CC dissociation constant 1.4nM and Bmax 3.9-6.4 pmole/mg protein.
SQ Sequence 2216 BP; 460 A; 647 C; 649 G; 460 T;

Query Match 2.9%; Score 29; DB 11; Length 2216;
Best Local Similarity 100.0%; Pred. No. 5.30e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 476 accatgatgagcgtgaccgctacattgc 504
|||||
QY 291 ACCATGATGAGCGGTGACCGCTACATTGC 319

RESULT 8
ID Q75927 standard; DNA; 2272 BP.
AC Q75927;
DT 17-AUG-1995 (first entry)
DE Mouse delta opioid receptor MOR1 cDNA.
KW Mouse; kappa; delta; mu; opioid receptor; brain; primer; PCR; amplify;
KW transmembrane domain; somatostatin; receptor; human; expression vector;
KW truncate; chimeric; assay; probe; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 12..1130
FT /*tag= a
FT /product= mouse delta opioid receptor
PN W09428132-A.
PD 08-DEC-1994.

PF 20-MAY-1994; U05747.
PR 20-MAY-1993; US-066296.
PR 30-JUL-1993; US-100694.
PR 05-NOV-1993; US-147592.
PA (ARCH-) ARCH DEV CORP.
PI Bell GI, Reisine T, Yasuda K;
DR WPI; 95-022804/03.
DR P-PSDB; R67670.
PT Polynucleotides and peptides derived from opioid receptor
PT polypeptides - for use in therapeutic compositions and in
PT screening assays for useful drug substances.
PS Claim 6; Page 215-221; 300pp; English.
CC The nucleotide sequence of the novel mouse delta opioid receptor gene
CC MOR1. The gene was isolated from a mouse brain cDNA library using a
CC fragment (amplified from the cDNA library with primers Q75929-30) as a
CC probe. The primers are based on the conserved sequences present in the
CC second and third transmembrane domains of somatostatin (SRIF) receptor
CC subtypes SS1R1, SS1R2 and SS1R3. The 1.3 kb EcoRI-SacI fragment from the
CC CMV promoter-based expression vector pCMV-6c. The resultant construct
CC pCMV-msl-2 was transfected into COS-1 cells for protein production. The
CC gene encoding the opioid receptor can be used to produce complete,
CC truncated or chimeric opioid receptor proteins. The opioid receptors
CC thus produced are useful for the development of novel assays designed to
CC select or improve substances, capable of interacting with the opioid
CC receptor proteins, for use in diagnosis, drug design and therapeutic
CC applications.
SQ Sequence 2272 BP; 485 A; 665 C; 650 G; 472 T;

Query Match 2.9%; Score 29; DB 13; Length 2272;
Best Local Similarity 100.0%; Pred. No. 5.30e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 429 accatgatgagcgtgaccgctacattgc 457
|||||
QY 291 ACCATGATGAGCGGTGACCGCTACATTGC 319

RESULT 9
ID Q89223 standard; cDNA; 1618 BP.
AC Q89223;
DT 20-OCT-1995 (first entry)
DE Transcription regulatory protein cDNA.
KW Mu opioid receptor; MOR-1; gene therapy; diagnostic;
KW transcription regulatory protein; ss.
OS Rattus sp.
FH Key Location/Qualifiers
FT CDS 339..1235
FT /*tag= a
FT W09507983-A.
PN 23-MAR-1995.
PD 13-SEP-1994; U10358.
PR 13-SEP-1993; US-120601.
PA (INDV) UNIV INDIANA FOUNDD.
PI Xu L;
DR WPI; 95-131351/17.
DR P-PSDB; R71965.

PT New nucleic acid encoding new human mu opioid receptor - and
PT related vectors, transformed cells, antibodies etc., useful in
PT diagnosis, treatment and drug screening.
PS Disclosure; Page 199-203; 266pp; English.
CC A 365 bp fragment of the mouse delta opioid receptor was used to
CC screen a rat brain cDNA library under low stringency conditions.
CC One positive clone included the sequence given in Q89222, encoding a
CC mu opioid receptor, MOR-1 (R71964). Sequence analysis revealed an
CC alternative reading frame (Q89223) encoding a zinc
CC finger-containing transcription regulatory protein (R71965).
SQ Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;

Query Match 2.6%; Score 26; DB 14; Length 1618;
Best Local Similarity 100.0%; Pred. No. 1.52e-06;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db	652	gattactacaacatgttcaccagcat	677
QY	255	GATTACTACAACATGTTCCACCAGCAT	280

RESULT	ID	10	Q89222	standard; cDNA; 1618 BP.
AC	Q89222;			
DT	20-OCT-1995		(first entry)	
DE	Rat mu opioid receptor cDNA.			
KW	Mu opioid receptor; MOR-1; gene therapy; diagnostic; ss.			
OS	Rattus sp.			
EH	Key	Location/Qualifiers		
FT	CDS	214..1410		
FT	/*tag= a			
PN	W09507983-A.			
PD	23-MAR-1995.			
PF	13-SEP-1994; U10358.			
PR	13-SEP-1993; U5-120601.			
PA	(INDV) UNIV INDIANA FOUND.			
PI	Yu L;			
DR	WPI; 95-131351/17.			
DR	P-PSDB; R71964.			
PT	New nucleic acid encoding new human mu opioid receptor - and related vectors, transformed cells, antibodies etc., useful in diagnosis, treatment and drug screening.			
PT	disclosure; Page 190-194; 266pp; English.			
PS	A 365 bp fragment of the mouse delta opioid receptor was used to screen a rat brain cDNA library under low stringency conditions.			
CC	One positive clone included the sequence given in Q89222, encoding a mu opioid receptor, MOR-1 (R71964). MOR-1 was stably expressed in transfected CHO cells.			
CC	Sequence 1618 BP; 390 A; 486 C; 370 G; 372 T;			

```

RESULT      11
ID          Q79199 standard; cDNA; 2070 BP.
AC          Q79199;
DT          19-APR-1995 (first entry)
DE          Rat mu-subtype opioid receptor cDNA.
KW          Mu-subtype opioid receptor; MSOR; drug addiction; ds.
OS          Rattus rattus.
FH          key                      Location/Qualifiers
FT          CDS                      83..1154
FT          /*tag= a
FT          /product= Mu-subtype_opioid_receptor
PN          BP-612845-A.
PD          31-AUG-1994.
PF          09-FEB-1994; 101968.
PR          26-FEB-1993; US-026140.
PA          (AMCY ) AMERICAN CYANAMID CO.
PI          Corbett MJ, Eppler CM, Shieh H, Zysk JR;
DR          WPI; 94-265963/33.
DR          P-PADB; R65188.
PT          Pure mu-type opioid receptor protein - and nucleic acid coding
PT          for it
PS          Claim 1; Fig 11; 39pp; English.
CC          R65188 is the rat mu-subtype opioid receptor protein purified
CC          from rat brain membranes, with biotinyl-b-endorphin (R56666)
CC          as its ligand. It is encoded by the nucleotide sequence Q79199
CC          which was synthesised using Q71022 and Q71023 as PCR primers.
CC          R65188 is useful for identifying other receptor subtypes, for
CC          screening new opioid ligands, and for studying mechanisms of
CC          opioid action, e.g. drug addiction.
CC          Sequence 2070 BP; 526 A; 564 C; 423 G; 557 T;

```

Query Match	2.6%;	Score 26;	DB 12;	Length 2070;
Best Local Similarity	100.0%;	Pred. No. 1.52e-06;		
Matches	26;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Db	404	gattactacacatgttcaccagcat	429	
QY	255	GATTACTACAACATGTTCCACGCAAT	280	

RESULT 12
 ID Q56703 standard; DNA; 829 BP.
 AC Q56703;
 DT 15-SEP-1994 (first entry)
 DE Partial sequence of the human mu opioid receptor
 DE genomic clone H20 (MORA).
 KW Opioid receptor; morphine; opiate; ss.
 OS Homo sapiens.
 PN W09404552-A.
 PD 03-MAR-1994.
 PF 13-AUG-1993; U07665.
 PR 13-AUG-1992; US-929200.
 PA (REGC) UNIV CALIFORNIA.
 PI Edwards RH, Evans CJ, Kaufman D, Keith DE;
 DR WPI; 94-083099/10.
 PT DNA encoding opioid receptors and antibodies against this
 PT receptor - used to express and locate these receptors, and screen
 PT cpds. for opioid (ant)agonist activity
 PS Example; Fig 8c; 74pp; English.
 CC To isolate opiate receptor genomic clones, 300,000 human genomic
 CC clones and a similar number of mouse genomic clones were probed
 CC with the 1.1 kb mouse delta opioid receptor clone DOR-1 pst/XbaI
 CC fragment. One mouse clone and three human genomic clones were
 CC isolated. The 3 human clones had very different EcoRI patterns
 CC which indicated that three different genes were represented by the
 CC human genomic clones which were designated H3, H14 and H20. H20 maps
 CC to chromosome 6. It encodes the human mu receptor. In addition, H20
 CC appears to contain a CACACA marker (Q56704) which provides a means
 CC to track the inheritance of this gene.
 SQ Sequence 829 BP; 182 A; 205 C; 134 G; 214 T;

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RESULT      13
ID          Q89226 standard; cDNA; 1610 BP.
AC          Q89226;
DT          20-OCT-1995 (first entry)
DE          Human mu opioid receptor cDNA.
KW          Mu opioid receptor; MOR; gene therapy; diagnostic; ss.
OS          Homo sapiens.
FT          Key
FT          CDS
              Location/Qualifiers
              239..1441
/*tag=      a
PN          W09507983-A.
PD          23-MAR-1995.
PF          13-SEP-1994; U10358.
PR          13-SEP-1993; US-120601.
PA          (INDV ) UNIV INDIANA FOUND.
PI          YU L;
DR          WP1; 95-131351/17.
P-PSDB; R71966.
PT          New nucleic acid encoding new human mu opioid receptor - and
PT          related vectors, transformed cells, antibodies etc., useful in
PT          diagnosis, treatment and drug screening.
PS          Claim 5; Page 208-210; 266pp; English.
CC          A cDNA library constructed from human caudate nucleus mRNA was

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CC screened with rat mu opioid receptor cDNA under conditions of
CC low stringency. One positive clone included the sequence given in
CC Q89226, encoding a mu opioid receptor MOR (R71964). The cDNA
CC is used for prodn. of recombinant MOR, in gene therapy, etc.
SQ Sequence 1610 BP; 384 A; 467 C; 359 G; 400 T;

Query Match 2.5%; Score 25; DB 14; Length 1610;
Best Local Similarity 100.0%; Pred. No. 9.56e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1113 tcgtctgtgactccattcacat 1137
|||
QY 694 TCGTCTGTGACTCCCATTCACAT 718

RESULT 14
ID Q93102 standard; cDNA; 2160 BP.
AC Q93102;
DE 11-DEC-1995 (first entry)
DE Human mu opiate receptor cDNA.
KW Mu opiate receptor; hMOR; opiate agonist; opiate antagonist;
KW drug abuse; analgesic; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 213..1415
FT /*tag= a
PN WO9520667-A1.
PD 03-AUG-1995.
PF 30-JAN-1995; U01144.
PR 28-JAN-1994; US-188275.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (USSH) US SEC DEPT HEALTH.
PI Johnson PS, Persico AM, Uhl G, Wang J;
DR WPI; 95-275452/36.
DR P-PSDB; R76780.

PT New DNA encoding human mu opiate receptor - used esp. for screening
PT cpds. for activity as opiate agonists or antagonists
PS Claim 4; Page 24-25; 49pp; English.
CC hMOR cDNA was obtd. from a human cerebral cortical cDNA library
CC screened with fragments of a rat mu opiate receptor. Cloned hMOR
CC DNA can be used as probes to examine the structure and function of
CC hMOR genes or to screen individuals for susceptibility to drug
CC abuse. Expression in e.g. COS cells allows production of
CC recombinant hMOR.
SQ Sequence 2160 BP; 563 A; 566 C; 455 G; 576 T;

Query Match 2.5%; Score 25; DB 15; Length 2160;
Best Local Similarity 100.0%; Pred. No. 9.56e-06;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1087 tcgtctgtgactccattcacat 1111
|||
QY 694 TCGTCTGTGACTCCCATTCACAT 718

RESULT 15
ID T12553 standard; cDNA; 21 BP.
AC T12553;
DT 04-SEP-1996 (first entry)
DE Human kappa opioid receptor partial 3'-cDNA PCR primer RM6.
KW Human; kappa opioid receptor; psychiatric disorder; cardiovascular;
KW neurology; diagnosis; polymerase chain reaction; ss.
OS Synthetic.
PN WO9601898-A1.
PD 25-JAN-1996.
PF 07-JUL-1995; F00912.
PR 11-JUL-1994; FR-008531.
PA (UYST-) UNIV PASTEUR STRASBOURG LOUIS.
PI Kieffer B, Simonin F;
DR WPI; 96-097628/10.
PT New nucleic acid encoding the human Kappa opioid receptor - useful
PT in diagnosis and therapy, and for isolating receptor ligands and
PT modulators

PS Example 2; Page 9; 30pp; French.

CC The sequence coding for the human kappa opioid receptor was
CC obtained from two overlapping cDNA fragments isolated from a
CC human placental cDNA library. The fragments were amplified from
CC the library using PCR primers based on the sequence of human
CC genomic clones which hybridised with a murine delta receptor cDNA
CC probe. Specifically, primers RP69 and RH84 (T12551 and T12552)
CC amplified a 508 bp fragment comprising the 5'-region of the coding
CC sequence; primers RM6 and RP70 (T12553 and T12554) amplified a
CC 760 bp fragment comprising the 3'-region of the coding sequence.
CC The fragments were ligated via an EcoRI site at position 365.
CC Nucleotide probes derived from the kappa opioid receptor
CC coding sequence are useful for diagnosis of neurological, cardio-
CC vascular and psychiatric disorders associated with opioid
CC receptors.
SQ Sequence 21 BP; 4 A; 4 C; 5 G; 8 T;

Query Match 2.1%; Score 21; DB 20; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.09e-02;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 gtctactgtatgaattccttg 21
|||
QY 195 GTCTACTTGATGAATTCCTTG 215

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Apr 21 01:09:36 1998; MasPar time 715.34 Seconds

Tabular output not generated. 1177.303 Million cell updates/sec

Title: >US-08-292-694A-11

Description: (1-1000) from US08292694A.seq

Perfect Score: 994

N.A. Sequence: 1 AAGAAGCAAAATCAGTAAATC.....CCAGTATGACTAGTCTGTGA 1000

Comp: TTCTTCGTTTATTAGTCAATTAG.....GGTCATTACTGATCAGCACCT

Scoring table: TABLE jmetric

Gap 50

Nmatch STD : Dbase 0; Query 0

Searched: 1126798 seqs, 421087984 bases x 2

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database:

emb1-est

1:em_est1 2:em_est2 3:em_est3 4:em_est4 5:em_est5

6:em_est6 7:em_est8 8:em_gss

Database:

genbank-est

9:gb_est1 10:gb_est2 11:gb_est3 12:gb_est4 13:gb_est5

14:gb_est6 15:gb_est7 16:gb_est8 17:gb_est9 18:gb_est10

19:gb_est11 20:gb_ests 21:gb_gss 22:gb_est12 23:gb_est13

Statistics: Mean 9.203; Variance 1.229; scale 7.491

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	137	13.8	153	10	R31984	yh62c10.r1 Homo sapien	0.00e+00
2	112	11.3	183	10	R81583	yj04b04.r1 Homo sapien	2.36e-256
3	19	1.9	206	18	AA317847	EST19840 Retina II Hom	6.71e-06
4	19	1.9	360	21	B50520	CIT-HSP-459E23.TV CIT-	6.71e-06
5	19	1.9	360	22	CELK096D7F	C.elegans cDNA clone y	6.71e-06
6	19	1.9	415	9	M75869	CEL06A11 Caenorhabditi	6.71e-06
7	19	1.9	521	23	AA447244	zw93c04.r1 Soares tota	6.71e-06
8	18	1.8	187	13	HSAADHHz	H. sapiens putatively	3.21e-04
9	18	1.8	224	12	H74768	313 Brassica napus CDN	3.21e-04
10	18	1.8	261	18	AA331167	EST35211 Embryo, 8 wee	3.21e-04
11	18	1.8	261	11	H38470	yp69b06.r1 Homo sapien	3.21e-04
12	18	1.8	316	18	AA296456	EST11038 Umbilical vei	3.21e-04
13	18	1.8	337	19	AA361360	EST170628 T-cell lympho	3.21e-04
14	18	1.8	364	21	FR0019360	F.rubripes GSS sequenc	3.21e-04
15	18	1.8	367	9	T01065	WEST01786 Caenorhabdit	3.21e-04

C	16	18	1.8	433	10	R81332	yj04b04.s1 Homo sapien	3.21e-04
C	17	18	1.8	440	15	w76111	zd65c03.r1 Soares feta	3.21e-04
C	18	18	1.8	447	9	T94320	ye37h04.s1 Homo sapien	3.21e-04
C	19	18	1.8	447	20	G29478	human STS SHGC-33760.	3.21e-04
C	20	18	1.8	466	10	R15256	yf89d03.r1 Homo sapien	3.21e-04
C	21	18	1.8	630	13	w22330	65H12 Human retina cDN	3.21e-04
C	22	17	1.7	127	20	HUMC5577	Human chromosome 5 LAN	1.25e-02
C	23	17	1.7	168	15	AA093468	EST25114 Cerebellum II	1.25e-02
C	24	17	1.7	198	18	AA322475	KK4722.seq.F Fetal hea	1.25e-02
C	25	17	1.7	238	10	R39553	yc95e11.s1 Homo sapien	1.25e-02
C	26	17	1.7	242	12	N21596	Human STS UT466, 5' pr	1.25e-02
C	27	17	1.7	259	20	HUMT7466A	EST37206 Homo sapiens	1.25e-02
C	28	17	1.7	274	11	T31698	NIB1978 Normalized inf	1.25e-02
C	29	17	1.7	290	14	T16896	C.elegans cDNA clone y	1.25e-02
C	30	17	1.7	300	22	C11273	yj60d04.r1 Homo sapien	1.25e-02
C	31	17	1.7	300	10	R50578	zw39f05.s1 Soares tota	1.25e-02
C	32	17	1.7	311	22	AA405560	yf73a09.s1 Homo sapien	1.25e-02
C	33	17	1.7	327	10	R40686	human STS WT-8958.	1.25e-02
C	34	17	1.7	331	20	G07052	zo58f04.r1 Stratagene	1.25e-02
C	35	17	1.7	344	16	AA158837	mm84f08.r1 Stratagene	1.25e-02
C	36	17	1.7	352	17	AA073530	mm84f08.r1 Stratagene	1.25e-02
C	37	17	1.7	352	17	AA073530	mm84f08.r1 Stratagene	1.25e-02
C	38	17	1.7	352	9	T55579	yb39d09.s1 Homo sapien	1.25e-02
C	39	17	1.7	354	14	R85458	yq26h04.s1 Soares feta	1.25e-02
C	40	17	1.7	357	14	R75136	MDBI081 Mouse brain, S	1.25e-02
C	41	17	1.7	357	9	T83796	yd65e10.r1 Homo sapien	1.25e-02
C	42	17	1.7	358	13	N85608	yj79e06.r1 Homo sapien	1.25e-02
C	43	17	1.7	359	10	R55445	EST26915 Cerebellum II	1.25e-02
C	44	17	1.7	361	18	AA324050	ye05f09.r1 Homo sapien	1.25e-02
C	45	17	1.7	363	9	T93658	Mouse embryonal carcin	1.25e-02
C	46	17	1.7	373	23	MUS73F04	mouse embryonal carcin	1.25e-02
C	47	17	1.7	381	11	R86041	YPI2h05.r1 Homo sapien	1.25e-02
C	48	17	1.7	398	16	N43613	SW3ICAl179SK Bruglia ma	1.25e-02
C	49	17	1.7	399	9	T86078	yd76e10.r1 Homo sapien	1.25e-02
C	50	17	1.7	400	20	G14676	human STS SHGC-11837.	1.25e-02
C	51	17	1.7	405	11	T31706	EST37356 Homo sapiens	1.25e-02
C	52	17	1.7	417	15	AA147259	zo38f05.r1 Stratagene	1.25e-02
C	53	17	1.7	429	12	N21161	yx47d06.s1 Homo sapien	1.25e-02
C	54	17	1.7	430	11	R94666	yx42e10.r1 Homo sapien	1.25e-02
C	55	17	1.7	439	13	N74629	za55c07.s1 Homo sapien	1.25e-02
C	56	17	1.7	440	22	AA431600	zw70c08.r1 Soares test	1.25e-02
C	57	17	1.7	451	10	R24706	yq43a01.r1 Homo sapien	1.25e-02
C	58	17	1.7	451	15	w56291	zdl5d03.s1 Soares feta	1.25e-02
C	59	17	1.7	454	15	AA156452	z151f07.s1 Soares preg	1.25e-02
C	60	17	1.7	455	21	B60908	T19D2TF TAMU Arabidops	1.25e-02
C	61	17	1.7	463	15	AA118221	MBACFCE6F07T3 Bruglia ma	1.25e-02
C	62	17	1.7	463	16	N59403	yv51d05.s1 Soares feta	1.25e-02
C	63	17	1.7	476	9	T62904	yc70g06.s1 Homo sapien	1.25e-02
C	64	12	1.7	478	12	H62758	yr46d06.r1 Homo sapien	1.25e-02
C	65	17	1.7	489	23	AA500746	vf96e12.r1 Soares mous	1.25e-02
C	66	17	1.7	502	13	w37077	zb20g09.r1 Soares feta	1.25e-02
C	67	17	1.7	513	16	w85753	zh55c03.r1 Soares feta	1.25e-02
C	68	17	1.7	536	14	AA029713	ze95f03.s1 Soares feta	1.25e-02
C	69	17	1.7	553	17	AA144197	mr75d01.r1 Stratagene	1.25e-02
C	70	17	1.7	559	17	AA239704	my15c07.r1 Barstead mo	1.25e-02
C	71	17	1.7	582	19	w87636	zh67b10.s1 Soares feta	1.25e-02
C	72	17	1.7	584	19	w87635	zh67b10.r1 Soares feta	1.25e-02
C	73	21	1.7	588	21	FR0022200	F.rubripes GSS sequenc	1.25e-02
C	74	17	1.7	597	21	FR0026106	F.rubripes GSS sequenc	1.25e-02
C	75	17	1.7	598	21	FR0022185	F.rubripes GSS sequenc	1.25e-02
C	76	17	1.7	608	21	AA166889	zq40f06.r1 Stratagene	1.25e-02
C	77	17	1.7	610	17	FR0022211	F.rubripes GSS sequenc	1.25e-02
C	78	17	1.7	619	17	AA184382	mt53h07.r1 Stratagene	1.25e-02
C	79	17	1.7	654	13	w27800	37h3 Human retina cDNA	1.25e-02
C	80	17	1.7	938	16	AA203200	zx57a04.r1 Soares feta	1.25e-02
C	81	17	1.7	987	13	w28981	54f1 Human retina cDNA	1.25e-02
C	82	17	1.7	987	13	w34891	mc62g05.r1 Soares mous	1.25e-02
C	83	16	1.6	96	14	w89735	mf66h07.r1 Soares mous	3.92e-01
C	84	16	1.6	105	13	N77425	yz31f06.r1 Homo sapien	3.92e-01
C	85	16	1.6	115	12	N21160	yx47d05.s1 Homo sapien	3.92e-01
C	86	16	1.6	147	22	CELK006DZR	C.elegans cDNA clone y	3.92e-01
C	87	16	1.6	152	15	N97330	0019m7 gmbPfHb3.1, G.	3.92e-01
C	88	16	1.6	183	23	MUSA6E08	Mouse embryonal carcin	3.92e-01

89	16	1.6	191 21	B60346	CIT-HSP-2007G24.TFB CT	3.92e-01	162	16	1.6	355 15	CHEST1742	C.hircus mRNA for EST1	3.92e-01
90	16	1.6	192 21	B34996	HS-1026-A1-F09-MR.abi	3.92e-01	163	16	1.6	356 11	H41632	yo09h09.r1 Homo sapien	3.92e-01
91	16	1.6	205 14	R75166	MDB1107R Mouse brain,	3.92e-01	164	16	1.6	357 15	AA063697	T3321 MYAT4 bloodstrea	3.92e-01
92	16	1.6	208 20	G18171	human STS SHGC-4711 cl	3.92e-01	165	16	1.6	359 22	C06590	similar to insulin 1.	3.92e-01
93	16	1.6	216 22	C02941	Human Heart cDNA, clon	3.92e-01	166	16	1.6	360 22	C13438	C.elegans cDNA clone y	3.92e-01
94	16	1.6	224 10	R62395	yj53e11.s1 Homo sapien	3.92e-01	167	16	1.6	360 22	CELRK062H7F	C.elegans cDNA clone y	3.92e-01
95	16	1.6	225 16	AA055301	zf17g03.r1 Soares feta	3.92e-01	168	16	1.6	360 22	CELRK069A6F	C.elegans cDNA clone y	3.92e-01
96	16	1.6	225 22	C02820	Human Heart cDNA, clon	3.92e-01	169	16	1.6	360 22	CELRK088A6F	C.elegans cDNA clone y	3.92e-01
97	16	1.6	226 19	AA369827	EST81350 Prostate glan	3.92e-01	170	16	1.6	362 16	AA170972	ms45f06.r1 Life Tech m	3.92e-01
98	16	1.6	233 19	AA378862	EST91608 Synovial sarc	3.92e-01	171	16	1.6	364 9	T49458	ya75f05.r1 Homo sapien	3.92e-01
99	16	1.6	234 14	W06754	SMEEST0390 Schistosoma	3.92e-01	172	16	1.6	366 19	AA375808	EST88141 Hsc172 cells	3.92e-01
100	16	1.6	237 20	G05485	human STS WI-9956.	3.92e-01	173	16	1.6	369 14	W98150	mg13f01.r1 Soares mous	3.92e-01
101	16	1.6	238 22	C16936	Human placenta cDNA 5'	3.92e-01	174	16	1.6	370 12	HUMEST3F9	Homo sapiens thymus MR	3.92e-01
102	16	1.6	242 21	B44234	HS-1059-A1-C04-MF.abi	3.92e-01	175	16	1.6	370 9	T82209	yd95g09.r1 Homo sapien	3.92e-01
103	16	1.6	243 20	G02858	Rattus norvegicus geno	3.92e-01	176	16	1.6	371 15	N97686	1015C3 czappPDD2.1, De	3.92e-01
104	16	1.6	246 21	RN082592	EST86965 HSC172 cells	3.92e-01	177	15	1.6	372 9	T80290	yd03h05.r1 Homo sapien	3.92e-01
105	16	1.6	247 19	AA374773	similar to none.	3.92e-01	178	16	1.6	373 12	H58782	yr36c07.s1 Homo sapien	3.92e-01
106	16	1.6	250 22	C05799	Astatoreochromis allua	3.92e-01	179	16	1.6	374 9	T09212	EST07105 Homo sapiens	3.92e-01
107	16	1.6	252 20	R34687	yh87c07.s1 Homo sapien	3.92e-01	180	16	1.6	374 15	AA156009	zo48a08.s1 Stratagene	3.92e-01
108	16	1.6	265 10	CE15C7	C. elegans cDNA clone	3.92e-01	181	16	1.6	378 11	H09467	Y197g05.r1 Homo sapien	3.92e-01
109	16	1.6	269 22	CE15C7	EST80608 Placenta II H	3.92e-01	182	16	1.6	381 12	H98553	yx11a02.s1 Homo sapien	3.92e-01
110	16	1.6	270 19	AA369228	H.sapiens (D2S2372) DN	3.92e-01	183	16	1.6	382 10	R63334	yi07e12.r1 Homo sapien	3.92e-01
111	16	1.6	270 19	HSa061YF9	EST04161 Homo sapiens	3.92e-01	184	16	1.6	383 23	AA133701	z192a05.r1 Stratagene	3.92e-01
112	16	1.6	276 9	T06272	EST04161 Homo sapiens	3.92e-01	185	16	1.6	383 13	ATP51121	A. thaliana transcribe	3.92e-01
113	16	1.6	278 12	H85454	YV87b08.s1 Homo sapien	3.92e-01	186	16	1.6	383 21	B73858	T25122TF TAMY Arabidop	3.92e-01
114	16	1.6	280 14	W18754	mc02a07.r1 Soares mous	3.92e-01	187	16	1.6	386 17	AA127125	zr21g11.r1 Stratagene	3.92e-01
115	16	1.6	280 17	AA247973	k1160.seq.F Human feta	3.92e-01	188	16	1.6	386 15	AA123396	zn68h10.s1 Stratagene	3.92e-01
116	16	1.6	283 23	AA460020	zx49h11.s1 Soares test	3.92e-01	189	16	1.6	386 23	R1CS14569A	Rice cDNA, partial seq	3.92e-01
117	16	1.5	283 13	N80275	yu67e12.s1 Homo sapien	3.92e-01	190	16	1.6	388 11	H38475	yp69c06.r1 Homo sapien	3.92e-01
118	16	1.6	288 12	H64514	PK27g04.r1 Caenorhabdi	3.92e-01	191	16	1.6	389 9	T83468	yd46g03.r1 Homo sapien	3.92e-01
119	16	1.6	290 10	R04706	EST27g04.r1 Caenorhabdi	3.92e-01	192	16	1.6	391 10	R65823	yi127d01.s1 Homo sapien	3.92e-01
120	16	1.6	292 18	AA325123	EST28075 Cerebellum II	3.92e-01	193	16	1.6	391 15	W91217	mf172d10.r1 Soares mous	3.92e-01
121	16	1.6	294 22	C06971	similar to insulin 1.	3.92e-01	194	16	1.6	392 14	W65949	me08a07.r1 Soares mous	3.92e-01
122	16	1.6	294 9	T79088	yd69d01.r1 Homo sapien	3.92e-01	195	16	1.6	393 16	AA161077	zo58f07.s1 Stratagene	3.92e-01
123	16	1.6	294 20	G07280	human STS WI-9426.	3.92e-01	196	16	1.6	395 18	AA270719	va67d01.r1 Soares mous	3.92e-01
124	16	1.6	294 14	HSC0WC062	H. sapiens partial CDN	3.92e-01	197	16	1.6	396 22	C06974	similar to insulin 1.	3.92e-01
125	16	1.6	296 10	R72114	Yf87b02.r1 Homo sapien	3.92e-01	198	16	1.6	397 22	C06805	EST86290 HSC172 cells	3.92e-01
126	16	1.6	298 18	AA317371	EST19352 Retina II Hom	3.92e-01	199	16	1.6	397 19	AA374186	zw91b10.s1 Soares tota	3.92e-01
127	16	1.6	300 22	C07250	C.elegans cDNA clone y	3.92e-01	200	16	1.6	398 23	AA447097	zwn91b10.s1 Soares tota	3.92e-01
128	16	1.6	305 18	AA313062	EST183859 Pancreas tum	3.92e-01	201	16	1.6	399 10	R53690	zg84h07.r1 Homo sapien	3.92e-01
129	16	1.6	307 23	AA455834	zx96f11.r1 Soares ovar	3.92e-01	202	16	1.6	401 15	W24831	zc65g05.r1 Soares feta	3.92e-01
130	16	1.6	307 17	AA073611	mm84a09.r1 Stratagene	3.92e-01	203	16	1.6	402 16	N64091	YV60a04.r1 Soares feta	3.92e-01
131	16	1.6	308 17	AA248148	csq0618.seq.F Human fe	3.92e-01	204	16	1.6	403 22	CELRK005G2F	C.elegans cDNA clone y	3.92e-01
132	16	1.6	309 13	HSC1HF011	H. sapiens partial CDN	3.92e-01	205	16	1.6	404 14	T27030	NIBT161A09r Infant bra	3.92e-01
133	16	1.6	311 9	T05855	EST03744 Homo sapiens	3.92e-01	206	16	1.6	404 11	H46264	yo15e02.s1 Homo sapien	3.92e-01
134	16	1.6	311 9	T07687	EST05577 Homo sapiens	3.92e-01	207	16	1.6	405 18	AA325631	EST28649 Cerebellum II	3.92e-01
135	16	1.6	311 13	ATT51673	A. thaliana transcribe	3.92e-01	208	16	1.6	405 10	R55659	Yg88b09.r1 Homo sapien	3.92e-01
136	16	1.6	315 18	AA333726	EST37843 Embryo, 9 wee	3.92e-01	209	16	1.6	405 15	BNAF0090E	Brassica rapa (clone F	3.92e-01
137	16	1.6	321 14	W34984	mc34a03.r1 Soares mous	3.92e-01	210	16	1.6	405 11	H49525	yo24e01.s1 Homo sapien	3.92e-01
138	16	1.6	322 23	R41926	Yg04d09.s1 Homo sapien	3.92e-01	211	16	1.6	405 18	AA335531	EST33941 Epilidymus Ho	3.92e-01
139	16	1.6	324 18	AA308937	EST179938 Retina I Hom	3.92e-01	212	16	1.6	405 11	T24256	crs1346 Ricinus commun	3.92e-01
140	16	1.6	324 18	MUS88F06	Mouse embryonal carcin	3.92e-01	213	16	1.6	405 17	AA183954	no96c07.r1 Stratagene	3.92e-01
141	16	1.6	325 23	B70905	CIT-HSP-2063E16.TFR CIT	3.92e-01	214	16	1.6	409 21	FR0003406	F. rubripes G5S sequenc	3.92e-01
142	16	1.6	326 21	AA158048	zo57f09.r1 Stratagene	3.92e-01	215	16	1.6	409 17	AA214731	PMY0121 K61a Lambda Za	3.92e-01
143	16	1.6	327 16	HSC2WC011	H. sapiens partial CDN	3.92e-01	216	16	1.6	412 22	C06600	similar to insulin 1.	3.92e-01
144	16	1.6	329 13	T91903	ye02a05.r1 Homo sapien	3.92e-01	217	16	1.6	413 11	H18119	yn47g07.s1 Homo sapien	3.92e-01
145	16	1.6	333 9	AA459169	zx88e09.r1 Soares ovar	3.92e-01	218	16	1.6	414 16	AA191778	rs06a04.r1 Sommer Pris	3.92e-01
146	16	1.6	336 23	H84942	YV88b07.s1 Homo sapien	3.92e-01	219	16	1.6	415 22	C06513	similar to insulin 1.	3.92e-01
147	16	1.6	337 12	C06608	similar to insulin 1.	3.92e-01	220	16	1.6	416 10	R79893	yi85d01.r1 Homo sapien	3.92e-01
148	16	1.6	337 22	CELK129E4R	C.elegans cDNA clone y	3.92e-01	221	16	1.6	416 21	B35568	HS-1029-A2-C11-MR.abi	3.92e-01
149	16	1.6	338 21	B57940	CIT-HSP-2011A22.TF CIT	3.92e-01	222	16	1.6	418 22	C06840	similar to insulin 1.	3.92e-01
150	16	1.6	340 22	AA442600	zv57h02.r1 Soares test	3.92e-01	223	16	1.6	420 14	W97618	vb69d10.r1 Barstead mo	3.92e-01
151	16	1.6	341 9	T81386	similar to insulin 1.	3.92e-01	224	16	1.6	420 14	C07149	mg01g07.r1 Soares mous	3.92e-01
152	16	1.6	341 18	AA337075	EST42014 Endometrial t	3.92e-01	225	16	1.6	421 14	W98374	mg13g08.r1 Soares mous	3.92e-01
153	16	1.6	342 19	HSPD06937	H.sapiens EST sequence	3.92e-01	226	16	1.6	422 10	R82066	Yj06g01.s1 Homo sapien	3.92e-01
154	16	1.6	344 19	AA125750	Z123C08.r1 Soares preg	3.92e-01	227	16	1.6	423 15	AA031897	zk17g06.r1 Soares preg	3.92e-01
155	16	1.6	346 21	B76141	RPC111-13L24.TP RPC111	3.92e-01	228	16	1.6	423 15	H96129	YV18b06.r1 Soares feta	3.92e-01
156	16	1.6	350 11	H30456	Y124f05.s1 Homo sapien	3.92e-01	229	16	1.6	425 22	C06514	similar to insulin 1.	3.92e-01
157	16	1.6	351 23	R18111	Rice cDNA, partial seq	3.92e-01	230	16	1.6	426 22	AA053065	z171c05.r1 Stratagene	3.92e-01
158	16	1.6	352 10	T63811	YC21f08.r1 Homo sapien	3.92e-01	231	16	1.6	428 22	C06536	similar to insulin 1.	3.92e-01
159	16	1.6	354 9	T63811		3.92e-01	232	16	1.6	428 22	C03237	Human Heart cDNA, clon	3.92e-01
160	16	1.6					233	16	1.6			EST183839 Pancreas tum	3.92e-01
161	16	1.6					234	16	1.6				

C	235	16	1.6	429	22	C06642	similar to insulin 1.	3.92e-01		C	308	16	1.6	470	14	W59193	md79d03.r1	Soares mous	3.92e-01	
C	236	16	1.6	431	12	H85699	ys68e04.r1	3.92e-01		C	309	16	1.6	470	17	AA138697	mq40b10.r1	Barstead MP	3.92e-01	
C	237	16	1.6	432	19	AA151154	z140a12.s1	3.92e-01		C	310	16	1.6	471	12	H66735	yr83f11.r1	Homo sapien	3.92e-01	
C	238	16	1.6	433	14	W80332	me90e12.r1	3.92e-01		C	311	16	1.6	471	10	R28157	yh65b11.r1	Homo sapien	3.92e-01	
C	239	16	1.6	433	16	AA212412	mu78a10.r1	3.92e-01		C	312	16	1.6	472	22	AA410475	zt30g02.r1	Soares ovar	3.92e-01	
C	240	16	1.6	434	9	T61622	yb86g11.s1	3.92e-01		C	313	16	1.6	473	17	AA153039	mq53f05.r1	Soares 2NbM	3.92e-01	
C	241	16	1.6	434	22	C06831	similar to insulin 1.	3.92e-01		C	314	16	1.6	474	16	AA213580	zg93b05.r1	Stratagene	3.92e-01	
C	242	16	1.6	435	9	T72706	yd19c09.r1	3.92e-01		C	315	16	1.6	474	23	AA510608	vg37a05.r1	Soares mous	3.92e-01	
C	243	16	1.6	435	15	W94191	zdt7d07.r1	3.92e-01		C	316	16	1.6	474	14	W41996	mb14g09.r1	Soares mous	3.92e-01	
C	244	16	1.6	435	20	G00423	fruit fly STS Dm021 c	3.92e-01		C	317	16	1.6	475	10	R81264	yf01a02.r1	Homo sapien	3.92e-01	
C	245	16	1.6	435	14	W42146	mb14g02.r1	3.92e-01		C	318	16	1.6	475	14	W29439	mb99a10.r1	Soares mous	3.92e-01	
C	246	16	1.6	436	12	N24406	yx14h08.r1	3.92e-01		C	319	16	1.6	479	14	W71414	me40d01.r1	Soares mous	3.92e-01	
C	247	16	1.6	436	21	FR0013110	F.rubripes GSS sequenc	3.92e-01		C	320	16	1.6	479	17	AA231224	mw37e03.r1	Soares mous	3.92e-01	
C	248	16	1.6	436	21	FR0004011	F.rubripes GSS sequenc	3.92e-01		C	321	16	1.6	480	20	G34598	human STS SHGC-51939.	yp42b07.r1	Homo sapien	3.92e-01
C	249	16	1.6	437	11	H50250	yo28g05.s1	3.92e-01		C	322	16	1.6	480	11	H30322	mg98h04.r1	Soares mous	3.92e-01	
C	250	16	1.6	437	14	W53233	md19e08.r1	3.92e-01		C	323	16	1.6	480	14	AA008786	ml16b03.r1	Soares mous	3.92e-01	
C	251	16	1.6	437	15	W73089	zd54c09.r1	3.92e-01		C	324	16	1.6	481	14	AA028719	ml16b03.r1	Soares mous	3.92e-01	
C	252	16	1.6	437	12	N35398	yy23f06.s1	3.92e-01		C	325	16	1.6	481	15	AA063788	mj88a10.r1	Soares mous	3.92e-01	
C	253	16	1.6	439	9	T83089	yd40f05.r1	3.92e-01		C	326	16	1.6	483	14	W70639	me34c11.r1	Soares mous	3.92e-01	
C	254	16	1.6	440	18	AA350536	EST57858 Infant brain	3.92e-01		C	327	16	1.6	484	14	W34494	na98g09.r1	Soares mous	3.92e-01	
C	255	16	1.6	440	10	R55955	yg89d09.s1	3.92e-01		C	328	16	1.6	486	14	W78469	me79a01.r1	Soares mous	3.92e-01	
C	256	16	1.6	440	14	W36672	mb89b02.r1	3.92e-01		C	329	16	1.6	486	22	C06154	similar to none.	mw26c09.r1	Soares mous	3.92e-01
C	257	16	1.6	441	11	H18211	yn47g12.s1	3.92e-01		C	330	16	1.6	487	17	AA242327	zw76h09.r1	Soares test	3.92e-01	
C	258	16	1.6	442	14	AA050021	mj39b10.r1	3.92e-01		C	331	16	1.6	488	22	AA431537	yw06a11.s1	Soares mela	3.92e-01	
C	259	16	1.6	443	16	AA067682	mm26h10.r1	3.92e-01		C	332	16	1.6	488	15	H96502	ys88e10.s1	Homo sapien	3.92e-01	
C	260	16	1.6	443	15	AA135386	zo28a07.s1	3.92e-01		C	333	16	1.6	489	10	R55683	HS-1029-A1-E02-MR.abi	similar to insulin 1.	3.92e-01	
C	261	16	1.6	443	13	N66818	za09b12.s1	3.92e-01		C	334	16	1.6	491	21	B35459	C07167	mv61b08.r1	Soares mous	3.92e-01
C	262	16	1.6	444	14	W58917	md50a09.r1	3.92e-01		C	335	16	1.6	491	17	AA218221	mf73b10.r1	Soares mous	3.92e-01	
C	263	16	1.6	444	19	AA136777	zk99d05.r1	3.92e-01		C	336	16	1.6	491	15	W89617	va71f05.r1	Soares mous	3.92e-01	
C	264	16	1.6	444	12	N41001	xy80g04.s1	3.92e-01		C	337	16	1.6	492	18	AA2761368	yf61a08.s1	Homo sapien	3.92e-01	
C	265	16	1.6	444	14	W61555	md80a10.r1	3.92e-01		C	338	16	1.6	492	10	R37636	yt63h09.r1	Soares 2NbM	3.92e-01	
C	266	16	1.6	444	17	AA107202	mm90e09.r1	3.92e-01		C	339	16	1.6	493	17	AA189661	yd59c03.s1	Homo sapien	3.92e-01	
C	267	16	1.6	445	15	W73194	zd54c09.s1	3.92e-01		C	340	16	1.6	493	9	T91051	mf63b07.r1	Soares mous	3.92e-01	
C	268	16	1.6	446	23	AA462647	vf90h06.r1	3.92e-01		C	341	16	1.6	493	17	AA154487	ms24h07.r1	Stratagene	3.92e-01	
C	269	16	1.6	447	10	R45064	yg38c04.s1	3.92e-01		C	342	16	1.6	494	17	AA166132	CIT-HSP-215111.TVB CIT	mg40a10.r1	Soares mous	3.92e-01
C	270	16	1.6	447	17	AA261490	mz87a01.r1	3.92e-01		C	343	16	1.6	494	16	AA17858	md02g03.r1	Soares mous	3.92e-01	
C	271	16	1.6	448	13	N78731	zb05a11.s1	3.92e-01		C	344	16	1.6	495	15	W89252	mh44d11.r1	Soares mous	3.92e-01	
C	272	16	1.6	448	15	W16214	mb63f04.r1	3.92e-01		C	345	16	1.6	496	21	B47607	vg77g07.r1	Barstead MP	3.92e-01	
C	273	16	1.6	449	15	W31611	zb91d12.r1	3.92e-01		C	346	16	1.6	496	16	AA002949	ml194e02.r1	Stratagene	3.92e-01	
C	274	16	1.6	449	23	AA542347	yr99a02.r1	3.92e-01		C	347	16	1.6	497	16	AA106437	mi12f11.r1	Soares mous	3.92e-01	
C	275	16	1.6	449	12	H72129	vh81g10.r1	3.92e-01		C	348	16	1.6	497	14	W54315	vi87g09.r1	Stratagene	3.92e-01	
C	276	16	1.6	449	23	AA517756	vb10h04.r1	3.92e-01		C	349	16	1.6	498	16	AA017858	mg10c09.r1	Barstead MP	3.92e-01	
C	277	16	1.6	449	18	AA542236	VK28b05.r1	3.92e-01		C	350	16	1.6	498	23	AA473478	mi12f11.r1	Soares mous	3.92e-01	
C	278	16	1.6	450	23	AA542236	mg66g06.r1	3.92e-01		C	351	16	1.6	498	16	AA017858	mi12f11.r1	Soares mous	3.92e-01	
C	279	16	1.6	450	14	AA007961	yp69e06.r1	3.92e-01		C	352	16	1.6	498	16	AA028699	vi87g09.r1	Stratagene	3.92e-01	
C	280	16	1.6	451	11	H38486	yp93e07.r1	3.92e-01		C	353	16	1.6	501	23	AA499000	mq10c09.r1	Barstead MP	3.92e-01	
C	281	16	1.6	451	10	R56374	zp74e05.s1	3.92e-01		C	354	16	1.6	502	17	AA120314	mg26f01.r1	Soares mous	3.92e-01	
C	282	16	1.6	452	16	AA186879	similar to insulin 1.	3.92e-01		C	355	16	1.6	502	21	FR0024232	F.rubripes GSS sequenc	3.92e-01		
C	283	16	1.6	452	22	C06788	EST179643 Retina II Ho	3.92e-01		C	356	16	1.6	502	14	AA039651	ze37b06.r1	Soares feta	3.92e-01	
C	284	16	1.6	453	18	AA308826	mg68f04.r1	3.92e-01		C	357	16	1.6	503	14	AA017896	zx37g07.s1	Soares tota	3.92e-01	
C	285	16	1.6	453	14	AA008047	zk68c10.r1	3.92e-01		C	358	16	1.6	503	14	AA017896	mi20f10.r1	Soares mous	3.92e-01	
C	286	16	1.6	454	19	AA045756	MTA.A01.088.A MTA adul	3.92e-01		C	359	16	1.6	504	17	AA028337	mr84b07.r1	Stratagene	3.92e-01	
C	287	16	1.6	454	14	AA032302	zw28f09.r1	3.92e-01		C	360	16	1.6	504	14	AA153053	mi31c11.r1	Soares mous	3.92e-01	
C	288	16	1.6	455	23	AA456816	yd30b03.s1	3.92e-01		C	361	16	1.6	504	14	AA033146	mi39f02.r1	Soares mous	3.92e-01	
C	289	16	1.6	456	9	T81772	vj35e06.r1	3.92e-01		C	362	16	1.6	504	14	AA033146	vc38b01.r1	Barstead MP	3.92e-01	
C	290	16	1.6	457	23	AA537909	me79g10.r1	3.92e-01		C	363	16	1.6	505	18	AA273335	yx74c05.r1	Soares ovar	3.92e-01	
C	291	16	1.6	457	14	W25114	me79g10.r1	3.92e-01		C	364	16	1.6	506	12	N39767	mx87d12.r1	Soares mous	3.92e-01	
C	292	16	1.6	457	14	W78259	md53f04.r1	3.92e-01		C	365	16	1.6	507	17	AA456177	zx37g07.r1	Soares tota	3.92e-01	
C	293	16	1.6	457	14	W58945	yn67c12.s1	3.92e-01		C	366	16	1.6	508	23	AA424598	mx87d12.r1	Soares mous	3.92e-01	
C	294	16	1.6	457	11	H24554	yf23c02.r1	3.92e-01		C	367	16	1.6	508	21	AA449921	zx37g07.r1	Soares tota	3.92e-01	
C	295	16	1.6	459	10	R09585	mm70c03.r1	3.92e-01		C	368	16	1.6	508	23	FR0022519	F.rubripes GSS sequenc	3.92e-01		
C	296	16	1.6	459	17	AA071753	yl84g09.s1	3.92e-01		C	369	16	1.6	509	14	AA475312	vh20f06.r1	Soares mous	3.92e-01	
C	297	16	1.6	460	11	H06968	mw46b07.r1	3.92e-01		C	370	16	1.6	509	14	W97879	mj35g04.r1	Soares mous	3.92e-01	
C	298	16	1.6	463	16	AA198155	mg75f02.r1	3.92e-01		C	371	16	1.6	510	14	AA049533	mg47a10.r1	Soares mous	3.92e-01	
C	299	16	1.6	463	14	AA008206	mg43c04.r1	3.92e-01		C	372	16	1.6	512	23	MUSGS00532	Mouse 3'-directed CDN	mm44b12.r1	Stratagene	3.92e-01
C	300	16	1.6	465	14	AA002391	CpEST.283 unizAPCPIOWA	3.92e-01		C	373	16	1.6	513	23	MUSGS00532	mm44b12.r1	Stratagene	3.92e-01	
C	301	16	1.6	466	19	AA397504	zq15e05.s1	3.92e-01		C	374	16	1.6	514	16	AA067929	z184b07.r1	Stratagene	3.92e-01	
C	302	16	1.6	466	17	AA218901	mf30d03.r1	3.92e-01		C	375	16	1.6	518	15	AA086107	zw35e12.s1	Soares ovar	3.92e-01	
C	303	16	1.6	466	15	W83396	yp92e05.r1	3.92e-01		C	3									

C	381	16	1.6	522 17	AA239498	my21b12.r1 Barstead mo	3.92e-01	C	454	15	1.5	107 18	AA301831	EST14873 Aorta endothe	9.51e+00
C	382	16	1.6	523 22	C18799	Human placenta cDNA 5'	3.92e-01	C	455	15	1.5	117 14	HSAAAAA1M	H. sapiens putatively	9.51e+00
C	383	16	1.6	524 23	AA530040	vj15c10.r1 Barstead mo	3.92e-01	C	456	15	1.5	139 11	H43697	yo80c03.s1 Homo sapien	9.51e+00
C	384	16	1.6	533 19	AA397494	CpEST.299 unizAPC10WA	3.92e-01	C	457	15	1.5	151 10	R06040	ye89e08.r1 Homo sapien	9.51e+00
C	385	16	1.6	538 16	N57857	yv60b04.s1 Soares feta	3.92e-01	C	458	15	1.5	157 14	W70486	me21b06.r1 Soares mous	9.51e+00
C	386	16	1.6	545 9	T78443	yd68b07.s1 Homo sapien	3.92e-01	C	459	15	1.5	163 14	N89052	K7549F Fetal heart, Ia	9.51e+00
C	387	16	1.6	548 10	R39446	yc95c07.s1 Homo sapien	3.92e-01	C	460	15	1.5	165 15	W20689	mc21g05.r1 Soares mous	9.51e+00
C	388	16	1.6	549 22	AA434056	zw24d01.r1 Soares ovar	3.92e-01	C	461	15	1.5	166 16	AA021420	ze66f08.r1 Soares reti	9.51e+00
C	389	16	1.6	549 21	B71032	CIT-HSP-2063L11.TF CIT	3.92e-01	C	462	15	1.5	169 22	AA193361	zr39g02.r1 Soares NhM	9.51e+00
C	390	16	1.6	550 16	AA089086	mm51d12.r1 Stratagene	3.92e-01	C	463	15	1.5	175 19	AA368456	EST179737 Placenta I Ho	9.51e+00
C	391	16	1.6	551 16	AA193799	rs03f12.r1 Sommer Pris	3.92e-01	C	464	15	1.5	201 20	G21490	human STS WI-16697.	9.51e+00
C	392	16	1.6	553 23	AA530381	vj48d04.r1 Stratagene	3.92e-01	C	465	15	1.5	201 18	AA338945	EST43994 Fetal brain I	9.51e+00
C	393	16	1.6	554 22	AA436968	zv72g05.r1 Soares tota	3.92e-01	C	466	15	1.5	204 18	AA331175	EST35220 Embryo, 8 wee	9.51e+00
C	394	16	1.6	555 22	C07148	similar to insulin 1.	3.92e-01	C	467	15	1.5	204 9	T77882	yd20d07.s1 Homo sapien	9.51e+00
C	395	16	1.6	556 21	B27940	ze85h09.s1 Soares feta	3.92e-01	C	468	15	1.5	206 16	AA055181	zf20d07.r1 Soares feta	9.51e+00
C	396	16	1.6	563 22	AA115663	similar to glia-derlve	3.92e-01	C	469	15	1.5	208 17	AA174802	mt13b11.r1 Soares mous	9.51e+00
C	397	16	1.6	564 22	C06914	mg83g09.r1 Stratagene	3.92e-01	C	470	15	1.5	208 9	T59648	yc13d12.s1 Homo sapien	9.51e+00
C	398	16	1.6	564 16	AA025822	F.rubripes GSS sequenc	3.92e-01	C	471	15	1.5	211 20	HS067XA9	H.sapiens DNA segment	9.51e+00
C	399	16	1.6	568 22	C05975	SMEST0325 schistosoma	3.92e-01	C	472	15	1.5	215 16	AA209150	zd58c10.r1 Stratagene	9.51e+00
C	400	16	1.6	574 17	AA125071	F.rubripes GSS sequenc	3.92e-01	C	473	15	1.5	219 18	AA329889	EST33572 Embryo, 12 we	9.51e+00
C	401	16	1.6	576 21	FR0022372	CIT-HSP-345111.TP CIT	3.92e-01	C	474	15	1.5	222 10	R10761	yf32g08.s1 Homo sapien	9.51e+00
C	402	16	1.6	579 9	T24127	Yd08c10.s1 Homo sapien	3.92e-01	C	475	15	1.5	224 20	G04713	human STS WI-4876.	9.51e+00
C	403	16	1.6	583 21	B54513	mv26g11.r1 Guaywoodfor	3.92e-01	C	476	15	1.5	227 23	AA512493	vj17g04.r1 Barstead mo	9.51e+00
C	404	16	1.6	583 23	AA467314	mu83h05.r1 Stratagene	3.92e-01	C	477	15	1.5	228 18	AA347554	EST53879 Fetal heart I	9.51e+00
C	405	16	1.6	584 16	AA214998	zp23g03.s1 Stratagene	3.92e-01	C	478	15	1.5	228 11	M77985	EST01569 Homo sapiens	9.51e+00
C	406	16	1.6	587 16	AA176131	F.rubripes GSS sequenc	3.92e-01	C	479	15	1.5	233 11	T27616	EST101209 Homo sapiens	9.51e+00
C	407	16	1.6	588 21	FR0011370	Yd08c10.s1 Homo sapien	3.92e-01	C	480	15	1.5	235 10	R50701	yj60g12.s1 Homo sapien	9.51e+00
C	408	16	1.6	588 10	R39054	mv26g11.r1 Guaywoodfor	3.92e-01	C	481	15	1.5	237 23	C24922	Rice cDNA, partial seq	9.51e+00
C	409	16	1.6	591 17	AA230508	zp41d01.r1 Stratagene	3.92e-01	C	482	15	1.5	243 22	CELK006A4F	C.elegans cDNA clone y	9.51e+00
C	410	16	1.6	595 16	AA180962	CIT-HSP-2023021.TR CIT	3.92e-01	C	483	15	1.5	248 18	AA345297	EST51559 Gall bladder	9.51e+00
C	411	16	1.6	597 21	B66083	mj11d02.r1 Soares mous	3.92e-01	C	484	15	1.5	253 19	AA033802	zk19h12.r1 Soares preg	9.51e+00
C	412	16	1.6	600 14	AA050410	mj18e01.r1 Stratagene	3.92e-01	C	485	15	1.5	256 12	AA327842	EST31230 Embryo, 12 we	9.51e+00
C	413	16	1.6	601 16	AA105934	F.rubripes GSS sequenc	3.92e-01	C	486	15	1.5	257 18	H84068	ys94b11.r1 Homo sapien	9.51e+00
C	414	16	1.6	603 21	FR0016200	me80b10.r1 Soares mous	3.92e-01	C	487	15	1.5	260 18	HSPD01099	H.sapiens EST sequence	9.51e+00
C	415	16	1.6	603 15	W82950	mq09e08.r1 Barstead MP	3.92e-01	C	488	15	1.5	261 18	AA319360	EST21573 Adrenal gland	9.51e+00
C	416	16	1.6	608 17	AA122594	mq09h07.r1 Barstead MP	3.92e-01	C	489	15	1.5	261 23	RICS2108A	Rice cDNA, partial seq	9.51e+00
C	417	16	1.6	609 17	AA122639	mc84a10.r1 Soares mous	3.92e-01	C	490	15	1.5	261 11	T28704	EST52396 Homo sapiens	9.51e+00
C	418	16	1.6	609 13	W47910	mt52a02.r1 Stratagene	3.92e-01	C	491	15	1.5	262 9	T39149	ya01b10.r2 Homo sapien	9.51e+00
C	419	16	1.6	612 17	AA184420	va97a03.r1 Stratagene	3.92e-01	C	492	15	1.5	263 23	AA444191	ve34c02.r1 Ko mouse em	9.51e+00
C	420	16	1.6	612 17	AA268193	ms66c06.r1 Stratagene	3.92e-01	C	493	15	1.5	264 22	HUM00TB025	Human Hepg2 3'-directe	9.51e+00
C	421	16	1.6	613 17	AA167997	vi97f02.r1 Barstead mo	3.92e-01	C	494	15	1.5	264 23	AA317271	yj27c09.r1 Soares mous	9.51e+00
C	422	16	1.6	614 23	AA500275	m10d02.r1 Soares mous	3.92e-01	C	495	15	1.5	266 12	AA511356	Yc03f02.r1 Homo sapien	9.51e+00
C	423	16	1.6	615 14	AA030625	me78d12.r1 Soares mous	3.92e-01	C	496	15	1.5	267 18	AA327319	EST30631 Colon I Homo	9.51e+00
C	424	16	1.6	616 14	W78285	mq02e08.r1 Soares mous	3.92e-01	C	497	15	1.5	269 18	HSPD01177	H.sapiens EST sequence	9.51e+00
C	425	16	1.6	616 14	W97809	vj54g01.r1 Knowles Sol	3.92e-01	C	498	15	1.5	270 19	AA361252	EST70552 T-cell lympho	9.51e+00
C	426	16	1.6	618 23	AA541868	F.rubripes GSS sequenc	3.92e-01	C	499	15	1.5	271 14	AA017271	ze36c03.r1 Soares reti	9.51e+00
C	427	16	1.6	619 21	FR0007535	F.rubripes GSS sequenc	3.92e-01	C	500	15	1.5	272 18	AA344949	EST50925 Gall bladder	9.51e+00
C	428	16	1.6	619 21	FR0022373	F.rubripes GSS sequenc	3.92e-01	C	501	15	1.5	273 19	AA385950	EST99654 Thyroid Homo	9.51e+00
C	429	16	1.6	619 21	FR0019372	ms25a05.r1 Stratagene	3.92e-01	C	502	15	1.5	274 23	AA355638	EST46065 Jurkat T-cell	9.51e+00
C	430	16	1.6	619 17	AA167925	zd77b07.s1 Soares feta	3.92e-01	C	503	15	1.5	275 19	RICR2587A	Rice cDNA, partial seq	9.51e+00
C	431	16	1.6	620 15	W74645	mh93b06.r1 Soares mous	3.92e-01	C	504	15	1.5	276 11	T29473	EST981189 Homo sapiens	9.51e+00
C	432	16	1.6	621 16	AA024369	mw26d09.r1 Soares mous	3.92e-01	C	505	15	1.5	276 14	MMTEST44	M.musculus expressed s	9.51e+00
C	433	16	1.6	621 17	AA242331	mx98f01.r1 Barstead mo	3.92e-01	C	506	15	1.5	278 14	HSC0NC021	H. sapiens partial cDN	9.51e+00
C	434	16	1.6	623 17	AA220088	zi06c12.s1 Soares feta	3.92e-01	C	507	15	1.5	278 18	AA008986	mg99e02.r1 Soares mous	9.51e+00
C	435	16	1.6	634 14	AA034016	66h5 Human retina cDNA	3.92e-01	C	508	15	1.5	280 10	R17354	EST19799 Retina II Hom	9.51e+00
C	436	16	1.6	635 13	W22409	347J12.TVB CIT978SKA1	3.92e-01	C	509	15	1.5	281 19	AA384025	EST97576 Thyroid Homo	9.51e+00
C	437	16	1.6	647 21	B17760	my15a12.r1 Barstead mo	3.92e-01	C	510	15	1.5	282 11	H21432	Yr76f08.r1 Homo sapien	9.51e+00
C	438	16	1.6	649 17	AA221400	T2E21-Sp6.1 TAMU Arabi	3.92e-01	C	511	15	1.5	284 22	HUM00TB037	Human Hepg2 3'-directe	9.51e+00
C	439	16	1.6	680 21	B08043	ms08c04.r1 Stratagene	3.92e-01	C	512	15	1.5	286 9	T01318	WES102039 Caenorhabdit	9.51e+00
C	440	16	1.6	724 17	AA142395	F1N21-Sp6.1 IGF Arabid	3.92e-01	C	513	15	1.5	287 22	HUM519B03B	Human placenta cDNA 5'	9.51e+00
C	441	16	1.6	736 21	B12537	mt63g09.r1 Soares 2NbM	3.92e-01	C	514	15	1.5	290 19	AA361255	EST70555 T-cell lympho	9.51e+00
C	442	16	1.6	770 17	AA189657	zr35b09.s1 Soares NhM	3.92e-01	C	515	15	1.5	293 17	AA078562	7P05E10 Chromosome 7 P	9.51e+00
C	443	16	1.6	788 22	AA195034	mx97c12.r1 Barstead mo	3.92e-01	C	516	15	1.5	294 12	H64992	Yu66c10.r1 Homo sapien	9.51e+00
C	444	16	1.6	821 17	AA220004	mx97d11.r1 Barstead mo	3.92e-01	C	517	15	1.5	296 18	AA313091	EST183888 Prostate gla	9.51e+00
C	445	16	1.6	827 17	AA220007	mf78g10.r1 Soares mous	3.92e-01	C	518	15	1.5	296 9	T73404	yc34g06.r1 Homo sapien	9.51e+00
C	446	16	1.6	943 14	W89520	T4P6-T7 TAMU Arabidops	3.92e-01	C	519	15	1.5	296 19	AA133385	zk96c08.r1 Soares preg	9.51e+00
C	447	16	1.6	1101 21	B08401	F19121-T7 IGF Arabidop	3.92e-01	C	520	15	1.5	297 19	AA380840	EST93859 Activated T-c	9.51e+00
C	448	16	1.6	1127 21	B11053	human STS WI-9078.	3.92e-01	C	521	15	1.5	297 19	AA377854	EST90482 Synovial sarc	9.51e+00
C	449	16	1.6	1236 20	G07106	Human brain cDNA, comp	3.92e-01	C	522	15	1.5	298 18	HSPD02736	H.sapiens EST sequence	9.51e+00
C	450	16	1.6	3076 23	HUMSUPY030	za13h05.r1 Soares feta	9.51e+00	C	523	15	1.5	300 22	C07684	C.elegans cDNA clone y	9.51e+00
C	451	15	1.5	74 14	N91232	F1-1137D 22 week old h	9.51e+00	C	524	15	1.5	301 9	T37751	EST102978 Saccharomyce	9.51e+00
C	452	15	1.5	80 14	R29617	mc63a02.r1 Soares mous	9.51e+00	C	525	15	1.5	301 9	T37751	zk85f01.s1 Soares preg	9.51e+00
C	453	15	1.5	100 15	AA052545			C	526	15	1.5	302 15	AA099176		

527	15	1.5	303	9	T10587	hbc455 Homo sapiens cd	9.51e+00	C	600	15	1.5	360	22	CElK101BZF	C.elegans cDNA clone Y	9.51e-00
528	15	1.5	303	19	HSPD06151	H.sapiens EST sequence	9.51e+00	C	601	15	1.5	360	22	C09430	C.elegans cDNA clone Y	9.51e+00
529	15	1.5	304	9	T81373	Yd24c10.s1 Homo sapien	9.51e+00	C	602	15	1.5	360	22	C13375	C.elegans cDNA clone Y	9.51e+00
530	15	1.5	304	10	R26732	Yh51f01.s1 Homo sapien	9.51e+00	C	603	15	1.5	361	14	W56983	md18e10.r1 Soares mous	9.51e+00
531	15	1.5	304	17	R03918	Pk13a12.s1 Caenorhabdi	9.51e+00	C	604	15	1.5	361	10	R21192	Yh20f03.r1 Soares sapien	9.51e+00
532	15	1.5	304	17	AA254064	Va10e07.r1 Soares mous	9.51e+00		605	15	1.5	362	12	N20859	Yx52b09.s1 Homo sapien	9.51e+00
533	15	1.5	305	18	AA300819	EST13767 Testis tumor	9.51e+00		606	15	1.5	362	19	AA400942	zu50b08.s1 Soares ovar	9.51e+00
534	15	1.5	307	23	AA447704	aa20b04.s1 Soares N4HM	9.51e+00		607	15	1.5	362	11	R86068	Y062d04.r1 Homo sapien	9.51e+00
535	15	1.5	307	20	G30052	human STS SHGC-36062.	9.51e+00		608	15	1.5	362	10	R03397	pk06d03.s1 Caenorhabdi	9.51e+00
536	15	1.5	307	16	HSC2ZB112	H. sapiens partial cDN	9.51e+00	C	609	15	1.5	363	16	AA211705	zq84f09.r1 Stratagene	9.51e+00
537	15	1.5	308	13	AA166358	mt75a05.r1 Soares mous	9.51e+00		610	15	1.5	365	14	W24669	Zb63d02.r1 Soares feta	9.51e+00
538	15	1.5	312	18	AA309678	EST180578 Jurkat T-cel	9.51e+00		611	15	1.5	365	14	N86137	J6643F Fetal heart, Ia	9.51e+00
539	15	1.5	314	22	C00065	HUMGS0004676, Human Ge	9.51e+00		612	15	1.5	365	15	W42674	zc22e11.s1 Soares sene	9.51e+00
540	15	1.5	316	15	W96396	ze10e11.r1 Soares feta	9.51e+00		613	15	1.5	365	17	AA223481	zr09e03.s1 Stratagene	9.51e+00
541	15	1.5	317	19	HSPD04747	H.sapiens EST sequence	9.51e+00	C	614	15	1.5	365	15	AA095150	CP3025.seq.F Fetal hea	9.51e+00
542	15	1.5	317	9	T94387	Yx35c06.s1 Homo sapien	9.51e+00		615	15	1.5	366	23	AA452556	zx35f11.s1 Soares tota	9.51e+00
543	15	1.5	318	10	R06620	Yf10h01.s1 Homo sapien	9.51e+00		616	15	1.5	367	13	R57037	F0312 Fetal heart Homo	9.51e+00
544	15	1.5	318	14	W85548	mf47c09.r1 Soares mous	9.51e+00	C	617	15	1.5	368	23	AA530207	Vj46g07.r1 Stratagene	9.51e+00
545	15	1.5	319	23	AA532125	TENF0189 T. cruzi epima	9.51e+00		618	15	1.5	369	14	W77405	me64a07.r1 Soares mous	9.51e+00
546	15	1.5	321	19	W90544	zh75d10.r1 Soares feta	9.51e+00		619	15	1.5	369	11	H18289	Yn48g08.r1 Homo sapien	9.51e+00
547	15	1.5	321	9	T37447	EST102572 Saccharomyce	9.51e+00		620	15	1.5	371	12	H63162	Yr50d02.r1 Homo sapien	9.51e+00
548	15	1.5	323	13	N98942	Yy71b01.r1 Homo sapien	9.51e+00		621	15	1.5	371	10	R09690	Yf23b11.r1 Homo sapien	9.51e+00
549	15	1.5	326	17	AA253795	mw03g03.r1 Soares mous	9.51e+00		622	15	1.5	373	15	AA115597	Zl05h09.s1 Soares preg	9.51e+00
550	15	1.5	327	23	R1CS4235A	Rice cDNA, partial seq	9.51e+00	C	623	15	1.5	373	22	HUMGS00579	Human HL60 3'/directed	9.51e+00
551	15	1.5	328	9	T06890	EST04779 Homo sapiens	9.51e+00		624	15	1.5	374	19	AA364047	EST74556 Pineal gland	9.51e+00
552	15	1.5	328	19	AA115741	Zk96b07.s1 Soares preg	9.51e+00		625	15	1.5	374	18	AA316545	EST188233 HCC cell lin	9.51e+00
553	15	1.5	331	19	AA365311	EST76039 Pineal gland	9.51e+00		626	15	1.5	375	17	AA174716	mt12h12.r1 Soares mous	9.51e+00
554	15	1.5	331	9	T94160	Yy28g11.r1 Homo sapien	9.51e+00	C	627	15	1.5	375	16	AA185853	SW3ICAI1956SK Brugia ma	9.51e+00
555	15	1.5	332	9	T59780	Yc13d12.r1 Homo sapien	9.51e+00		628	15	1.5	376	15	AA085722	zn53g06.s1 Stratagene	9.51e+00
556	15	1.5	332	12	H99055	Yv90d08.s1 Homo sapien	9.51e+00		629	15	1.5	377	18	AA340603	EST45864 Fetal kidney	9.51e+00
557	15	1.5	333	22	CElK076C2R	C.elegans cDNA clone Y	9.51e+00		630	15	1.5	380	15	AA103011	md16d10.r1 Life Tech m	9.51e+00
558	15	1.5	333	9	T94945	Yx38b06.r1 Homo sapien	9.51e+00	C	631	15	1.5	380	14	W59014	H. sapiens partial cDN	9.51e+00
559	15	1.5	334	11	T27762	EST15391 Homo sapiens	9.51e+00		632	15	1.5	381	13	HSC1DFT101	Yv46h08.r1 Homo sapien	9.51e+00
560	15	1.5	335	9	T02531	0144C3 Plasmodium falc	9.51e+00		633	15	1.5	381	11	N76915	EST01292 Homo sapiens	9.51e+00
561	15	1.5	337	19	AA383732	EST97152 Testis I Homo	9.51e+00		634	15	1.5	381	12	H79144	Yy79c11.s1 Homo sapien	9.51e+00
562	15	1.5	339	12	H56449	Yq98g10.s1 Homo sapien	9.51e+00	C	635	15	1.5	381	10	H78329	Yg11b01.s1 Homo sapien	9.51e+00
563	15	1.5	340	18	AA346234	EST52345 Greater oment	9.51e+00		636	15	1.5	383	10	R41724	Yn58d09.r1 Homo sapien	9.51e+00
564	15	1.5	341	13	N67367	YZ50g01.s1 Homo sapien	9.51e+00		637	15	1.5	383	11	H44210	mf77e02.r1 Soares mous	9.51e+00
565	15	1.5	342	18	AA329709	EST33379 Embryo, 12 we	9.51e+00	C	638	15	1.5	385	15	AA351728	EST59579 Infant brain	9.51e+00
566	15	1.5	342	9	T99455	Yx664b09.s1 Homo sapien	9.51e+00		639	15	1.5	385	19	AA351728	Yg33g06.r1 Homo sapien	9.51e+00
567	15	1.5	344	16	W85750	Zh55b06.r1 Soares feta	9.51e+00	C	640	15	1.5	386	10	R24590	Yh39a07.r1 Homo sapien	9.51e+00
568	15	1.5	344	19	AA099716	Zk86d09.r1 Soares preg	9.51e+00		641	15	1.5	387	10	R23451	Zl88a01.r1 Stratagene	9.51e+00
569	15	1.5	345	11	H27803	Yl58g08.r1 Homo sapien	9.51e+00		642	15	1.5	388	22	AA122403	HS-1051-A2-B04-MR.ab1	9.51e+00
570	15	1.5	346	18	HSPD03798	H.sapiens EST sequence	9.51e+00	C	643	15	1.5	388	22	AA122403	HS-1051-A2-B04-MR.ab1	9.51e+00
571	15	1.5	347	10	R34810	Yh87f03.r1 Homo sapien	9.51e+00		644	15	1.5	389	17	AA267354	mc91b12.r1 Soares mous	9.51e+00
572	15	1.5	347	18	C24311	Citrus cDNA, partial s	9.51e+00	C	645	15	1.5	389	15	AA111954	mc74a05.r1 Soares mous	9.51e+00
573	15	1.5	348	18	AA317393	EST19366 Retina II Hom	9.51e+00		646	15	1.5	391	13	W41159	mc74a05.r1 Soares mous	9.51e+00
574	15	1.5	349	19	AA365285	EST76007 Pineal gland	9.51e+00	C	647	15	1.5	391	17	AA098210	mc74a05.r1 Soares mous	9.51e+00
575	15	1.5	349	9	T09707	0296m7 Plasmodium falc	9.51e+00		648	15	1.5	392	17	T66345	Yc78b11.r1 Homo sapien	9.51e+00
576	15	1.5	350	17	AA118862	mp55g07.r1 Soares 2NbM	9.51e+00	C	649	15	1.5	392	13	W44082	mq58b09.r1 Soares 2NbM	9.51e+00
577	15	1.5	350	17	AA233748	Zr48g07.s1 Soares N4HM	9.51e+00		650	15	1.5	392	13	H48037	Yp79e10.r1 Homo sapien	9.51e+00
578	15	1.5	350	11	R86949	Yq31e08.s1 Homo sapien	9.51e+00	C	651	15	1.5	393	11	H59986	Yr16h06.r1 Homo sapien	9.51e+00
579	15	1.5	351	9	T68955	Yc30g01.r1 Homo sapien	9.51e+00		652	15	1.5	394	14	AA311024	EST181795 Jurkat T-cel	9.51e+00
580	15	1.5	351	13	HSC36C111	H. sapiens partial cDN	9.51e+00		653	15	1.5	396	18	AA311024	EST181795 Jurkat T-cel	9.51e+00
581	15	1.5	351	17	AA255246	mz77g03.r1 Soares mous	9.51e+00	C	654	15	1.5	396	11	H22696	Ym49a02.r1 Homo sapien	9.51e+00
582	15	1.5	351	12	H88001	Yw18h01.r1 Homo sapien	9.51e+00		655	15	1.5	396	23	AA086192	zn46f08.s1 Stratagene	9.51e+00
583	15	1.5	351	23	AA447860	aa20b03.r1 Soares N4HM	9.51e+00		656	15	1.5	397	12	AA053704	Yr93d10.s1 Stratagene	9.51e+00
584	15	1.5	353	18	AA302423	EST10123 Adipose tissu	9.51e+00	C	657	15	1.5	397	22	H69141	Yr93d10.s1 Homo sapien	9.51e+00
585	15	1.5	355	16	AA211199	Zq87a07.r1 Stratagene	9.51e+00		658	15	1.5	397	9	T57831	Yc14f12.s1 Homo sapien	9.51e+00
586	15	1.5	355	14	AA013060	ze35f02.r1 Soares reti	9.51e+00	C	659	15	1.5	397	22	AA053616	Zl73g02.r1 Stratagene	9.51e+00
587	15	1.5	356	9	R02014	Yx82c12.r1 Homo sapien	9.51e+00		660	15	1.5	398	11	T299902	EST99693 Homo sapiens	9.51e+00
588	15	1.5	356	11	H42726	Y071a03.s1 Homo sapien	9.51e+00		661	15	1.5	400	10	R26849	Yh52b01.s1 Homo sapien	9.51e+00
589	15	1.5	357	12	H63611	Yr26f05.r1 Homo sapien	9.51e+00	C	662	15	1.5	401	15	W60498	Zb99e08.r1 Soares para	9.51e+00
590	15	1.5	358	21	B57550	CIT-HSP-2009P16.TR CIT	9.51e+00		663	15	1.5	401	17	AA224347	Zr16e04.s1 Stratagene	9.51e+00
591	15	1.5	358	22	HUM230A06B	Human aorta cDNA 5'-en	9.51e+00		664	15	1.5	402	23	AA505218	T4283 MYAT4 bloodstrea	9.51e+00
592	15	1.5	359	15	W68393	zd36b06.s1 Soares feta	9.51e+00		665	15	1.5	402	17	AA087763	mn98g09.r1 Stratagene	9.51e+00
593	15	1.5	359	14	AA050307	mj12b07.r1 Soares mous	9.51e+00		666	15	1.5	402	11	H15707	Ym28d01.s1 Homo sapien	9.51e+00
594	15	1.5	359	12	H66908	Yr71f01.r1 Homo sapien	9.51e+00	C	667	15	1.5	402	11	N63673	Za17h09.s1 Homo sapien	9.51e+00
595	15	1.5	360	16	AA021640	ze69b02.r1 Soares reti	9.51e+00		668	15	1.5	403	18	AA271136	Vb72b12.r1 Soares mous	9.51e+00
596	15	1.5	360	22	AA433938	Zw52f09.s1 Soares tota	9.51e+00	C	669	15	1.5	403	21	B22940	F24A2TF IGF Arabidopsi	9.51e+00
597	15	1.5	360	22	CElK119GZF	C.elegans cDNA clone Y	9.51e+00		670	15	1.5	404	17	AA105629	mm68d06.r1 Stratagene	9.51e+00
598	15	1.5	360	22	CElK072AXF	C.elegans cDNA clone Y	9.51e+00	C	671	15	1.5	404	10	R22816	Yh20g06.s1 Homo sapien	9.51e+00
599	15	1.5	360	22	CElK100DXF	C.elegans cDNA clone Y	9.51e+00		672	15	1.5	404	15	AA125091	mc37c01.r1 Life Tech m	9.51e+00

673	15	1.5	405	9	T68212	yc40b06.r1 Homo sapien	9.51e+00
674	15	1.5	405	15	AA116934	mn22f03.r1 Beddington	9.51e+00
675	15	1.5	405	21	FR0026122	F.rubripes GSS sequenc	9.51e+00
676	15	1.5	407	22	AA142927	z149c03.s1 Soares preg	9.51e+00
677	15	1.5	407	16	AA157736	zo34g08.r1 Stratagene	9.51e+00
678	15	1.5	407	13	HSAAADFLB	H. sapiens putatively	9.51e+00
679	15	1.5	408	9	T70939	yc49b05.r1 Homo sapien	9.51e+00
680	15	1.5	408	22	AA126087	z185b08.r1 Stratagene	9.51e+00
681	15	1.5	410	12	H72999	yu28f09.r1 Homo sapien	9.51e+00
682	15	1.5	410	16	AA157703	zo34d06.r1 Stratagene	9.51e+00
683	15	1.5	411	17	AA183694	mt20h04.r1 Soares mous	9.51e+00
684	15	1.5	411	21	B66415	CIT-HSP-2011B15.TFB CI	9.51e+00
685	15	1.5	412	11	H39085	yp65g11.r1 Homo sapien	9.51e+00
686	15	1.5	412	12	H63392	yr53b04.s1 Homo sapien	9.51e+00
687	15	1.5	412	16	N43212	SM3ICA1134SK Brugia ma	9.51e+00
688	15	1.5	412	12	N47629	yy54b05.r1 Homo sapien	9.51e+00
689	15	1.5	412	14	AA051775	mj54h12.r1 Soares mous	9.51e+00
690	15	1.5	413	20	G21142	human STS WI-11774.	9.51e+00
691	15	1.5	414	23	AA448393	zw68b10.r1 Soares test	9.51e+00
692	15	1.5	414	14	W24110	zb48h02.r1 Soares feta	9.51e+00
693	15	1.5	415	16	AA197211	zq11e12.s1 Stratagene	9.51e+00
694	15	1.5	415	9	T71700	yc64b04.r1 Homo sapien	9.51e+00
695	15	1.5	415	13	N62526	yz74g05.s1 Homo sapien	9.51e+00
696	15	1.5	416	17	AA218734	zg97h05.s1 Stratagene	9.51e+00
697	15	1.5	417	14	AA035540	ze24c01.s1 Soares feta	9.51e+00
698	15	1.5	417	9	T68143	yc28g02.r1 Homo sapien	9.51e+00
699	15	1.5	417	15	W47240	zc39d04.r1 Soares sene	9.51e+00
700	15	1.5	417	17	AA231091	mw11g09.r1 Soares mous	9.51e+00
701	15	1.5	418	17	AA223775	zr10c04.r1 Stratagene	9.51e+00
702	15	1.5	418	9	R02514	ye70b08.r1 Homo sapien	9.51e+00
703	15	1.5	419	20	HS284ZE5	H. sapiens (D3S1587) D	9.51e+00
704	15	1.5	419	17	AA200740	mu02f11.r1 Soares mous	9.51e+00
705	15	1.5	419	10	R63590	yi09g05.r1 Homo sapien	9.51e+00
706	15	1.5	420	22	HUM178D08B	Human fetal brain cDNA	9.51e+00
707	15	1.5	421	10	R18056	yg15c09.r1 Homo sapien	9.51e+00
708	15	1.5	421	23	AA459294	zx89b08.s1 Soares ovar	9.51e+00
709	15	1.5	421	11	M78870	EST01018 Homo sapiens	9.51e+00
710	15	1.5	421	15	AA013164	ze35e12.s1 Soares retl	9.51e+00
711	15	1.5	421	12	N24350	yx14a04.r1 Homo sapien	9.51e+00
712	15	1.5	423	15	W78044	zd72d02.r1 Soares feta	9.51e+00
713	15	1.5	423	19	HSPD04660	H.sapiens EST sequence	9.51e+00
714	15	1.5	423	15	W51830	zc37e02.s1 Soares sene	9.51e+00
715	15	1.5	424	15	AA126890	z116f02.s1 Soares preg	9.51e+00
716	15	1.5	424	16	AA080206	nm34g08.r1 Stratagene	9.51e+00
717	15	1.5	424	18	AA273921	vb99c03.r1 Soares mous	9.51e+00
718	15	1.5	425	17	AA224247	zr15g11.s1 Stratagene	9.51e+00
719	15	1.5	425	11	H21515	yl13a10.s1 Homo sapien	9.51e+00
720	15	1.5	426	10	R08878	yf21f06.s1 Homo sapien	9.51e+00
721	15	1.5	426	22	AA406421	zv10c01.r1 Soares NhHM	9.51e+00
722	15	1.5	427	13	N66594	yy69h01.s1 Homo sapien	9.51e+00
723	15	1.5	428	23	AA505216	T4280 MYAT4 bloodstrea	9.51e+00
724	15	1.5	428	20	G10179	human STS CHLC.ATCC6C03	9.51e+00
725	15	1.5	428	9	T60083	yb68b01.s1 Homo sapien	9.51e+00
726	15	1.5	428	22	AA404373	zw36h04.s1 Soares tota	9.51e+00
727	15	1.5	428	16	AA025823	ze85h10.s1 Soares feta	9.51e+00
728	15	1.5	428	15	AA037104	zc51a10.r1 Soares sene	9.51e+00
729	15	1.5	429	14	N88454	K3433F Fetal heart, Ia	9.51e+00
730	15	1.5	429	23	AA500939	vg01g01.r1 Soares mous	9.51e+00
731	15	1.5	431	15	W82700	mf07d03.r1 Soares mous	9.51e+00
732	15	1.5	431	9	T50411	yb30d01.s1 Homo sapien	9.51e+00
733	15	1.5	432	12	N31298	yx66f05.r1 Homo sapien	9.51e+00
734	15	1.5	432	20	G30467	human STS SHGC-37116.	9.51e+00
735	15	1.5	432	19	AA131911	z139c12.s1 Soares preg	9.51e+00
736	15	1.5	433	11	HA2471	yo64b02.s1 Homo sapien	9.51e+00
737	15	1.5	433	12	N30229	yw64c06.s1 Homo sapien	9.51e+00
738	15	1.5	434	22	AA437330	zw30a06.r1 Soares ovar	9.51e+00
739	15	1.5	434	15	AA091317	cch2660.seq.F Fetal h	9.51e+00
740	15	1.5	434	13	W45354	zc80b10.s1 Pancreatitc	9.51e+00
741	15	1.5	435	12	N49098	yy79f02.s1 Homo sapien	9.51e+00
742	15	1.5	435	18	AA340312	EST45500 Fetal brain I	9.51e+00
743	15	1.5	436	12	N47449	yy89b12.s1 Homo sapien	9.51e+00
744	15	1.5	437	14	W62539	md63e06.r1 Soares mous	9.51e+00
745	15	1.5	438	12	N55698	J0618F Homo sapiens cD	9.51e+00

746	15	1.5	438	16	AA199554	mw40b03.r1 Soares mous	9.51e+00
747	15	1.5	438	12	H71879	yr82d07.s1 Homo sapien	9.51e+00
748	15	1.5	439	23	RIC83450A	Rice cDNA, partial seq	9.51e+00
749	15	1.5	439	14	AA051063	mg73c11.r1 Soares mous	9.51e+00
750	15	1.5	440	17	AA226817	mr20a03.r1 Stratagene	9.51e+00
751	15	1.5	440	11	H29226	ym59b12.r1 Homo sapien	9.51e+00
752	15	1.5	440	10	R72285	yj89b05.s1 Homo sapien	9.51e+00
753	15	1.5	440	13	N66599	yy770a01.s1 Homo sapien	9.51e+00
754	15	1.5	441	16	AA099739	zd78b06.r1 Soares feta	9.51e+00
755	15	1.5	441	15	R24306	ze82e08.s1 Soares feta	9.51e+00
756	15	1.5	441	10	AA187406	yg32c05.r1 Homo sapien	9.51e+00
757	15	1.5	441	17	AA230981	mw30b04.r1 Soares mous	9.51e+00
758	15	1.5	442	11	H02797	yp69f04.r1 Homo sapien	9.51e+00
759	15	1.5	442	16	AA187406	mr24d04.r1 Stratagene	9.51e+00
760	15	1.5	443	17	AA163843	mf02b12.r1 Soares mous	9.51e+00
761	15	1.5	443	15	W82105	mf02b12.r1 Soares mous	9.51e+00
762	15	1.5	443	15	W56183	zd14b10.r1 Soares feta	9.51e+00
763	15	1.5	443	14	W30458	mc20c11.r1 Soares mous	9.51e+00
764	15	1.5	443	15	W78004	zd78b06.s1 Soares feta	9.51e+00
765	15	1.5	444	17	AA111136	mp65g12.r1 Soares 2Nm	9.51e+00
766	15	1.5	444	10	R80279	yi92c01.r1 Homo sapien	9.51e+00
767	15	1.5	444	10	R82626	yp19h09.r1 Homo sapien	9.51e+00
768	15	1.5	444	17	AA110949	mp56f10.r1 Soares 2Nm	9.51e+00
769	15	1.5	444	10	R36011	yg69a02.r1 Homo sapien	9.51e+00
770	15	1.5	445	15	AA136178	zk93f05.r1 Soares preg	9.51e+00
771	15	1.5	445	17	AA242288	mx12d10.r1 Soares mous	9.51e+00
772	15	1.5	445	15	W60969	zd31f05.s1 Soares feta	9.51e+00
773	15	1.5	446	14	W36380	mb83d09.r1 Soares mous	9.51e+00
774	15	1.5	446	12	N30233	yw64d02.s1 Homo sapien	9.51e+00
775	15	1.5	448	22	AA100479	z181e09.s1 Stratagene	9.51e+00
776	15	1.5	448	15	W74705	zd57e08.s1 Soares feta	9.51e+00
777	15	1.5	448	20	G23141	human STS WI-12652.	9.51e+00
778	15	1.5	449	14	AA007917	mg76e07.r1 Soares mous	9.51e+00
779	15	1.5	449	13	T26418	AB20068R Homo sapiens	9.51e+00
780	15	1.5	450	12	N40785	yw62a07.r1 Homo sapien	9.51e+00
781	15	1.5	450	18	ATU74163	Arabidopsis thaliana c	9.51e+00
782	15	1.5	450	18	AA277654	va80e04.r1 Soares mous	9.51e+00
783	15	1.5	450	10	R40502	yf72d05.s1 Homo sapien	9.51e+00
784	15	1.5	450	23	AA472873	vd59f05.r1 Knowles Sol	9.51e+00
785	15	1.5	451	18	AA285861	vb86a01.r1 Soares mous	9.51e+00
786	15	1.5	451	12	H98788	yx16f10.s1 Homo sapien	9.51e+00
787	15	1.5	451	21	B39564	HS-1049-B2-G08-MR.abi	9.51e+00
788	15	1.5	451	15	AA016257	ze33d01.s1 Soares retl	9.51e+00
789	15	1.5	452	10	R82864	yl25e10.r1 Homo sapien	9.51e+00
790	15	1.5	452	11	N51279	yz14e01.s1 Homo sapien	9.51e+00
791	15	1.5	452	12	H43949	yo70g02.r1 Homo sapien	9.51e+00
792	15	1.5	452	10	R34600	yh85f09.s1 Homo sapien	9.51e+00
793	15	1.5	452	10	R23647	yh35f01.r1 Homo sapien	9.51e+00
794	15	1.5	454	15	W69577	ye94b03.r1 Homo sapien	9.51e+00
795	15	1.5	454	15	R06173	zd47a04.r1 Soares feta	9.51e+00
796	15	1.5	455	13	N34509	yy55d02.s1 Homo sapien	9.51e+00
797	15	1.5	455	9	T60158	yc22c11.s1 Homo sapien	9.51e+00
798	15	1.5	455	10	R10278	yf36c11.r1 Homo sapien	9.51e+00
799	15	1.5	456	14	W97648	mf99f11.r1 Soares mous	9.51e+00
800	15	1.5	457	17	AA183812	mt21a02.r1 Soares mous	9.51e+00
801	15	1.5	457	15	AA123494	mn30c06.r1 Beddington	9.51e+00
802	15	1.5	458	16	AA192167	zg03a11.s1 Stratagene	9.51e+00
803	15	1.5	459	16	W86540	zhe2c01.r1 Soares feta	9.51e+00
804	15	1.5	459	16	N55180	yy44c08.s1 Soares feta	9.51e+00
805	15	1.5	459	12	N20491	yx40b09.s1 Homo sapien	9.51e+00
806	15	1.5	460	15	W95318	ze05h01.r1 Soares feta	9.51e+00
807	15	1.5	460	13	W17039	zbi7a01.r1 Soares feta	9.51e+00
808	15	1.5	460	13	AA24016	mx87g12.s1 Homo sapien	9.51e+00
809	15	1.5	461	17	AA238916	mx92c02.r1 Soares mous	9.51e+00
810	15	1.5	461	21	B58795	CIT-HSP-2014A10.TF CIT	9.51e+00
811	15	1.5	461	12	N25241	yx74c03.s1 Homo sapien	9.51e+00
812	15	1.5	461	14	W96387	ze10d09.r1 Soares feta	9.51e+00
813	15	1.5	462	17	AA199020	mu16h06.r1 Soares 2Nm	9.51e+00
814	15	1.5	463	23	AA474362	vd57a02.r1 Knowles Sol	9.51e+00
815	15	1.5	464	14	W31655	zb92c09.r1 Soares para	9.51e+00
816	15	1.5	464	13	W05284	za83e05.r1 Soares feta	9.51e+00
817	15	1.5	464	23	RICC2332A	Rice cDNA, partial seq	9.51e+00
818	15	1.5	465	14	AA034875	mi53a04.r1 Soares mous	9.51e+00

819	15	1.5	465	14	W98741	mg11g09.r1	Soares	mous	9.51e+00	892	15	1.5	526	16	AA051075	mj43c05.r1	Soares	mous	9.51e+00
820	15	1.5	465	18	AA315008	EST186815	HCC cell lin		9.51e+00	893	15	1.5	527	13	N79227	za12f12.r1	Homo	sapien	9.51e+00
821	15	1.5	466	11	N62462	zai1b10.s1	Homo sapien		9.51e+00	894	15	1.5	528	16	AA040307	zf05b04.r1	Soares	feta	9.51e+00
822	15	1.5	466	11	N05543	yl175a07.r1	Homo sapien		9.51e+00	895	15	1.5	529	18	AA275650	vc16e10.r1	Barstead	MP	9.51e+00
823	15	1.5	466	15	W68813	zd37e01.r1	Soares feta		9.51e+00	896	15	1.5	530	11	R99042	yg65a07.r1	Homo	sapien	9.51e+00
824	15	1.5	466	12	H77547	yu22b09.r1	Homo sapien		9.51e+00	897	15	1.5	531	14	W58840	md49a11.r1	Soares	mous	9.51e+00
825	15	1.5	466	12	N44963	yy35e11.r1	Homo sapien		9.51e+00	898	15	1.5	532	18	AA276960	vc43a11.r1	Soares	mous	9.51e+00
826	15	1.5	467	10	R32376	yh76a09.r1	Homo sapien		9.51e+00	899	15	1.5	533	21	B66140	CIT-HSP-2024C18.TF.CIT	Homo	sapien	9.51e+00
827	15	1.5	467	10	R72716	yy95c05.r1	Homo sapien		9.51e+00	900	15	1.5	533	9	T67689	yc27a11.s1	Homo	sapien	9.51e+00
828	15	1.5	468	16	AA215191	mu84g10.r1	Stratagene		9.51e+00	901	15	1.5	534	3	W23470	zb33d03.r1	Soares	para	9.51e+00
829	15	1.5	468	18	AA275349	vc07a04.r1	Soares mous		9.51e+00	902	15	1.5	535	23	AA114232	zn75h05.r1	Stratagene		9.51e+00
830	15	1.5	468	16	W86444	zh62c01.s1	Soares feta		9.51e+00	903	15	1.5	537	22	AA432480	vd72a03.r1	Beddington		9.51e+00
831	15	1.5	469	19	AA040020	zk45h03.r1	Soares preg		9.51e+00	904	15	1.5	538	18	AA313768	EST185632	Colon	carcin	9.51e+00
832	15	1.5	471	14	W30244	mc10f12.r1	Soares mous		9.51e+00	905	15	1.5	539	23	AA500809	vg01e10.r1	Soares	mous	9.51e+00
833	15	1.5	471	18	AA312884	EST183838	Pancreas tum		9.51e+00	906	15	1.5	540	17	AA207898	mw84e08.r1	GuayWoodfor		9.51e+00
834	15	1.5	471	23	AA497780	vi68g03.r1	Stratagene		9.51e+00	907	15	1.5	544	23	AA499848	vg05f08.r1	Soares	mous	9.51e+00
835	15	1.5	473	17	AA245642	my52g12.r1	Barstead mo		9.51e+00	908	15	1.5	545	18	AA275659	vc01h10.r1	Barstead	MP	9.51e+00
836	15	1.5	473	16	AA171327	ms58h05.r1	Life Tech m		9.51e+00	909	15	1.5	545	23	AA529101	vi32f02.r1	Barstead	mo	9.51e+00
837	15	1.5	474	12	H98761	yx13b10.s1	Homo sapien		9.51e+00	910	15	1.5	546	19	AA150239	zl07b08.s1	Soares	preg	9.51e+00
838	15	1.5	477	11	H38596	yp48d01.r1	Homo sapien		9.51e+00	911	15	1.5	547	13	N56842	yw83e01.r1	Homo	sapien	9.51e+00
839	15	1.5	477	17	AA267043	mz99h04.r1	Soares mous		9.51e+00	912	15	1.5	547	16	AA176792	zp36e11.r1	Stratagene		9.51e+00
840	15	1.5	477	12	H99292	yx22c03.s1	Homo sapien		9.51e+00	913	15	1.5	549	13	N78251	yp75f08.r1	Homo	sapien	9.51e+00
841	15	1.5	478	10	R21362	yg51a04.r1	Homo sapien		9.51e+00	914	15	1.5	550	16	AA180812	zp41c02.s1	Stratagene		9.51e+00
842	15	1.5	479	13	W03889	za61a01.r1	Soares feta		9.51e+00	915	15	1.5	550	19	T92196	ye17f10.s1	Homo	sapien	9.51e+00
843	15	1.5	480	12	N51093	yz03d08.s1	Soares sapien		9.51e+00	916	15	1.5	552	15	W44608	zc29c07.r1	Soares	sene	9.51e+00
844	15	1.5	480	20	G35293	human STS SHGC-37407.	human STS SHGC-37407.		9.51e+00	917	15	1.5	556	23	AA500042	vc15d04.r1	Barstead	MP	9.51e+00
845	15	1.5	481	9	T83395	yd44b02.r1	Homo sapien		9.51e+00	918	15	1.5	563	15	W44342	zc27b04.r1	Soares	sene	9.51e+00
846	15	1.5	481	23	R1CC2333A	Rice cDNA, partial seq		9.51e+00	919	15	1.5	563	14	W53500	md45e03.r1	Soares	mous	9.51e+00	
847	15	1.5	482	18	AA288288	vb12c02.r1	Soares mous		9.51e+00	920	15	1.5	563	23	C25720	Dictyostelium discoid			9.51e+00
848	15	1.5	482	16	AA041310	zf08g03.s1	Soares feta		9.51e+00	921	15	1.5	564	16	AA105837	mm02a11.r1	Stratagene		9.51e+00
849	15	1.5	484	11	R95127	yq44g10.r1	Homo sapien		9.51e+00	922	15	1.5	565	18	AA274729	vc015d04.r1	Barstead	MP	9.51e+00
850	15	1.5	484	10	R17600	yg14h09.r1	Homo sapien		9.51e+00	923	15	1.5	566	16	AA209432	zc035a03.r1	Stratagene		9.51e+00
851	15	1.5	484	11	H18774	yn52b03.r1	Homo sapien		9.51e+00	924	15	1.5	567	23	AA537117	vk45a12.r1	Soares	mous	9.51e+00
852	15	1.5	486	23	AA453392	zx47g06.r1	Soares test		9.51e+00	925	15	1.5	568	21	B24879	F22J13TF	IGF Arabidops		9.51e+00
853	15	1.5	486	14	N93333	zb69g06.s1	Soares feta		9.51e+00	926	15	1.5	570	23	AA4537350	vk46e10.r1	Soares	mous	9.51e+00
854	15	1.5	487	10	R78505	yi173f07.r1	Homo sapien		9.51e+00	927	15	1.5	570	23	AA455069	aa04d01.s1	Soares	NhHM	9.51e+00
855	15	1.5	488	14	W13956	mb30b09.r1	Soares mous		9.51e+00	928	15	1.5	572	23	AA082502	zn41e05.r1	Stratagene		9.51e+00
856	15	1.5	491	21	B40998	HS-1052-B2-C06-MF.abi	HS-1052-B2-C06-MF.abi		9.51e+00	929	15	1.5	573	16	AA195917	zp95g11.r1	Stratagene		9.51e+00
857	15	1.5	492	19	AA040610	zk61c06.r1	Soares preg		9.51e+00	930	15	1.5	576	23	AA516612	vh83e08.r1	Knowles	Sol	9.51e+00
858	15	1.5	493	17	AA168497	mr29e02.r1	Soares mous		9.51e+00	931	15	1.5	577	13	W03012	za02c03.r1	Soares	mela	9.51e+00
859	15	1.5	493	11	H45776	yp23d09.r1	Homo sapien		9.51e+00	932	15	1.5	577	9	T64964	yd11c08.s1	Homo	sapien	9.51e+00
860	15	1.5	494	10	R24311	yg32d02.r1	Homo sapien		9.51e+00	933	15	1.5	578	16	AA108210	ml63e10.r1	Stratagene		9.51e+00
861	15	1.5	495	13	N80367	zala4a12.r1	Homo sapien		9.51e+00	934	15	1.5	578	18	AA407684	EST178552	Colon	carcin	9.51e+00
862	15	1.5	495	20	G30594	human STS SHGC-37524.	human STS SHGC-37524.		9.51e+00	935	15	1.5	581	22	AA442550	zv75d03.r1	Soares	tota	9.51e+00
863	15	1.5	496	12	N27723	yx52h12.r1	Homo sapien		9.51e+00	936	15	1.5	584	21	FR0011086	vc94a09.r1	Barstead	MP	9.51e+00
864	15	1.5	497	15	W94920	ze14e04.s1	Soares feta		9.51e+00	937	15	1.5	585	19	AA388354	mr80g06.r1	Stratagene		9.51e+00
865	15	1.5	497	13	N92180	yz89e01.r1	Homo sapien		9.51e+00	938	15	1.5	587	17	AA144455	va88h06.r1	Soares	mous	9.51e+00
866	15	1.5	497	21	FR0007544	F.rubripes GSS sequenc		9.51e+00	939	15	1.5	588	17	AA260025	mv23f11.r1	GuayWoodfor		9.51e+00	
867	15	1.5	498	10	R70851	yi49f08.r1	Homo sapien		9.51e+00	940	15	1.5	589	17	AA241083	yv34h10.s1	Soares	feta	9.51e+00
868	15	1.5	499	16	AA009467	mp78a07.r1	Soares 2NmM		9.51e+00	941	15	1.5	592	16	N52921	CIT-HSP-2015P20.TFb	CIT		9.51e+00
869	15	1.5	500	23	HUMHBC4912	ze82h08.r1	Soares feta		9.51e+00	942	15	1.5	595	21	B66929	my33c03.r1	Barstead	mo	9.51e+00
870	15	1.5	500	17	AA254855	similar to none.		9.51e+00	943	15	1.5	596	17	AA238594	yv05a05.s1	Homo	sapien	9.51e+00	
871	15	1.5	501	12	N32510	mz75g09.r1	Soares mous		9.51e+00	944	15	1.5	597	12	H93078	zx59h06.r1	Soares	feta	9.51e+00
872	15	1.5	503	18	B40307	yy11c06.s1	Homo sapien		9.51e+00	945	15	1.5	597	16	AA203614	yy71a02.r1	Soares	feta	9.51e+00
873	15	1.5	503	21	AA307203	HS-1051-A2-B04-MF.abi		9.51e+00	946	15	1.5	597	16	N78013	F.rubripes GSS sequenc		9.51e+00		
874	15	1.5	503	18	AA307738	EST178107	Colon carcin		9.51e+00	947	15	1.5	599	21	FR0019748	F.rubripes GSS sequenc		9.51e+00	
875	15	1.5	504	18	AA307738	EST178600	Colon carcin		9.51e+00	948	15	1.5	600	22	HDM082B07A	Human fetal brain cDNA		9.51e+00	
876	15	1.5	506	11	T14848	crs295	Ricinus commun		9.51e+00	949	15	1.5	603	16	W35471	131 Mouse VM cDNA	libr		9.51e+00
877	15	1.5	508	12	N44537	yy32d10.r1	Homo sapien		9.51e+00	950	15	1.5	606	23	AA520956	TgESTz266e05.r1	TgME49		9.51e+00
878	15	1.5	510	17	R32324	yh68e06.s1	Homo sapien		9.51e+00	951	15	1.5	607	21	FR0021871	F.rubripes GSS sequenc		9.51e+00	
879	15	1.5	510	17	AA139626	mq40c07.r1	Barstead MP		9.51e+00	952	15	1.5	608	21	FR0027054	F.rubripes GSS sequenc		9.51e+00	
880	15	1.5	511	10	R13076	yf172e03.r1	Homo sapien		9.51e+00	953	15	1.5	609	23	AA520955	TgESTz266e04.r1	TgME49		9.51e+00
881	15	1.5	512	14	R84345	yg23f01.r1	Soares reti		9.51e+00	954	15	1.5	610	14	W92686	zd92f03.s1	Soares	feta	9.51e+00
882	15	1.5	512	10	R44626	yg24f10.s1	Homo sapien		9.51e+00	955	15	1.5	611	23	AA520970	TgESTz266e04.r1	TgME49		9.51e+00
883	15	1.5	513	13	W01267	za34b02.r1	Soares feta		9.51e+00	956	15	1.5	611	19	AA150386	zl07h04.r1	Soares	preg	9.51e+00
884	15	1.5	515	19	AA408801	ESTf03272	Mouse 7.5 dpc		9.51e+00	957	15	1.5	613	23	AA472521	vh02b11.r1	Soares	mous	9.51e+00
885	15	1.5	516	21	FR0020186	F.rubripes GSS sequenc		9.51e+00	958	15	1.5	613	19	AA156835	zl18d04.r1	Soares	preg	9.51e+00	
886	15	1.5	518	23	AA456617	zx75c07.s1	Soares ovar		9.51e+00	959	15	1.5	613	15	W20085	zk40f02.r1	Soares	para	9.51e+00
887	15	1.5	519	14	SSC20B11	S.scrofa mRNA; express		9.51e+00	960	15	1.5	615	13		mk02g12.r1	Soares	mous	9.51e+00	
888	15	1.5	519	15</															

C	965	15	1.5	642	16	AA107954	m199f10.r1	Stratagene	9.51e+00
	966	15	1.5	647	15	AA058940	z196c06.s1	Stratagene	9.51e+00
	967	15	1.5	647	14	AA003418	mg57h12.r1	Soares	9.51e+00
	968	15	1.5	650	17	AA222110	mw12h08.r1	Soares	9.51e+00
	969	15	1.5	668	22	AA152011	z149a09.r1	Soares	9.51e+00
	970	15	1.5	668	23	AA1520118	TgESTz38d04.r1	TgME49	9.51e+00
	971	15	1.5	679	15	AA147042	zo32b03.s1	Stratagene	9.51e+00
	972	15	1.5	700	13	W48130	mc85c11.r1	Soares	9.51e+00
	973	15	1.5	717	21	AG004752	Homo sapiens genomic D	9.51e+00	
	974	15	1.5	723	16	AA203188	zx55f07.r1	Soares	9.51e+00
	975	15	1.5	749	21	AG003107	Homo sapiens genomic D	9.51e+00	
	976	15	1.5	750	21	B02323	CSRL-151E4-u	CSRL flow	9.51e+00
	977	15	1.5	769	15	AA097531	mol5d05.r1	Life Tech m	9.51e+00
	978	15	1.5	773	21	B19318	F28D21-T7	IGF Arabidop	9.51e+00
	979	15	1.5	787	21	B08104	T6C4-T7	TAMU Arabidops	9.51e+00
	980	15	1.5	803	16	AA203385	zx57f10.r1	Soares	9.51e+00
	981	15	1.5	820	13	W23142	79C6 Human	retina cDNA	9.51e+00
	982	15	1.5	861	13	W29112	56e5 Human	retina cDNA	9.51e+00
	983	15	1.5	870	17	AA178598	mt17a06.r1	Soares	9.51e+00
	984	15	1.5	879	14	W41053	mc35d11.r1	Soares	9.51e+00
	985	15	1.5	891	21	B12630	F25A23-T7	IGF Arabidop	9.51e+00
	986	15	1.5	891	21	B12519	F19K5-Sp6	IGF Arabidop	9.51e+00
	987	15	1.5	894	21	B09406	T27L3-Sp6	TAMU Arabidop	9.51e+00
	988	15	1.5	898	21	B06830	CSRL-87A3-u	CSRL flow	9.51e+00
	989	15	1.5	944	14	W08052	mb38e11.r1	Soares	9.51e+00
	990	15	1.5	962	13	W28596	48b9 Human	retina cDNA	9.51e+00
	991	15	1.5	982	13	W28358	48e5 Human	retina cDNA	9.51e+00
	992	15	1.5	998	20	G26641	human STS	STS_U32315.	9.51e+00
	993	15	1.5	1135	20	G07072	human STS	WI-9003.	9.51e+00
	994	15	1.5	1142	21	B12549	F20O22-Sp6.1	IGF Arabi	9.51e+00
	995	15	1.5	1200	21	B10973	F12A21-T7	IGF Arabidop	9.51e+00
	996	15	1.5	1556	20	G26775	human STS	STS_L40392.	9.51e+00
	997	15	1.5	2378	20	AF015462	Plasmodium	falciparum	9.51e+00
	998	15	1.5	2398	20	G26768	human STS	STS_DI7532.	9.51e+00
	999	15	1.5	3588	20	HUMSWS3975	human	chromosome 7 STS	9.51e+00
	1000	15	1.5	3978	20	G10727	human	STS CHLC.UTR_006	9.51e+00

ALIGNMENTS

RESULT 1 R31984 153 bp mRNA EST 28-APR-1995
LOCUS yh62c10.r1 Homo sapiens cDNA clone 134322 5' similar to gb:L25119
DEFINITION MU-TYPE OPTOID RECEPTOR (HUMAN);.
R31984
ACCESSION g787827
NID
KEYWORDS
SOURCE human clone=134322 library=Soares placenta Nb2HP vector=PT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13RPI Rsite1=Not I Rsite2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5'
AACTGGAAGATTCGCGCGCCGACAGAAATTTTCTTTTCTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified PT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 153)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 120
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
source location/Qualifiers
1.153
/organism="Homo sapiens"
/clone="134322"
BASE COUNT 25 a 49 c 37 g 42 t
ORIGIN
Query Match 13.8%; Score 137; DB 10; Length 153;
Best Local Similarity 97.2%; Pred. No. 0.00e+00;
Matches 137; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 GCGTCTCATCTTTGCGCTTCGTGATGCCCTGTCCTCATCATCATCGTGTGCTACACCGCTGA 60
|||||
QY 529 GCGTCTCATCTTTGCGCTTCGTGATGCCCTGTCCTCATCATCATCGTGTGCTACACCGCTGA 588
Db 61 TGATCTCGCTTCACAGAGCGTCCGCGCTCTTCTGCGCTCCCGAGAGAAAGATCGCAACC 120
|||||
QY 589 TGATCTCGCTTCACAGANNGTCCGCGCTCTTCTGCGCTCCCGAGAGAAAGATNNCAACC 648
Db 121 TCGGTAGGATCACCAGACTGG 141
QY 649 TCGGTAGGATCACCAGACTGG 669

RESULT 2 R81583 183 bp mRNA EST 12-JUN-1995
LOCUS yj04b04.r1 Homo sapiens cDNA clone 147727 5' similar to gb:L25119
DEFINITION MU-TYPE OPTOID RECEPTOR (HUMAN);.
R81583
ACCESSION g858186
NID
KEYWORDS
SOURCE human clone=147727 library=Soares placenta Nb2HP vector=PT7T3D
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
resistant) primer=M13RPI Rsite1=Not I Rsite2=Eco RI Female placenta
obtained at birth (full term). 1st strand cDNA was primed with a
Not I - oligo(dT) primer [5'
AACTGGAAGATTCGCGCGCCGACAGAAATTTTCTTTTCTTTT 3'], double-stranded
cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the modified PT7T3
vector. Library went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 183)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT

Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the

ACCESSION	D75109
NID	G1120893
KEYWORDS	EST; EST(expressed sequence tag);
SOURCE	Caenorhabditis elegans (strain:N2) embryo Hermaphrodite embryo cDNA to mRNA, clone_lib:Yuji kohara unpublished cDNA.
ORGANISM	Caenorhabditis elegans
REFERENCE	Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE	1 (bases 1 to 360)
AUTHORS	Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and Nishigaki,A.
TITLE	Toward an expression map of the C.elegans genome
JOURNAL	Unpublished (1995)
REFERENCE	2 (bases 1 to 360)
AUTHORS	Kohara,Y.
TITLE	Direct Submission
JOURNAL	Submitted (23-AUG-1995) to the DDBJ/EMBL/GenBank databases. Yuji Kohara, National Institute of Genetics, Gene Library Lab; Yata 1111, Mishima, Shizuoka 411, Japan (E-mail:ykohara@lab.nig.ac.jp, Tel:0559-81-6854, Fax:0559-81-6855)
FEATURES	Location/Qualifiers
source	1. 360
	/organism="Caenorhabditis elegans"
	/strain="N2"
	/db_xref="taxon:6239"
	/clone_lib="Yuji kohara unpublished cDNA"
	/dev_stage="embryo"
	/sex="Hermaphrodite"
	/tissue_type="embryo"
BASE COUNT	98 a 120 c 64 g 74 t 4 others
ORIGIN	
Query Match	1.9%; Score 19; DB 22; Length 360;
Best Local Similarity	100.0%; Pred. No. 6.71e-06;
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	155 CCACCACCCAGGACGAG 173
Cp	684 CCACCACCCAGGACGAG 666
RESULT	5
LOCUS	M75869 415 bp mRNA EST 16-SEP-1992
DEFINITION	CEL06A11 Caenorhabditis elegans cDNA clone cm06a11 5'.
ACCESSION	M75869
NID	9275214
KEYWORDS	EST.
SOURCE	Nematodes clone=cm06a11 library=Chris Martin sorted cDNA library strain=Bristol N2 vector=lamdaphage SHLX2 host=MC1061 Mixed stage hermaphrodite cDNA library. Partially normalized by successively picking groups of clones that didn't hybridize to previously picked clones. Vector: lamdaphage SHLX2 (Lipshitz, D.H. et al., Gene 88:25-36 (1990)). Host: MC1061.
ORGANISM	Caenorhabditis elegans
REFERENCE	Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae.
AUTHORS	1 (bases 1 to 415)
	Waterston,R., Martin,C., Craxton,M., Huynh,C., Coulson,A., Hillier,L., Durbin,R.K., Green,P., Showkeen,R., Halloran,N., Hawkins,T., Wilson,R., Berks,M., Du,Z., Thomas,K., Thierry-Mieg,J. and Sulston,J.
TITLE	A survey of expressed genes in Caenorhabditis elegans
JOURNAL	Nature Genet. 1, 114-123 (1992)
COMMENT	Contact: Waterston R.H.(USA) and Sulston J.E.(UK) (USA) Dept. of Genetics or (UK) (USA) Washington Univ. School of Medicine or (UK) MRC Laboratory of Molecular Biology Box 8232,4566 Scott Ave.,St. Louis,MI 63110,USA,or,Hills Road,Cambridge CB2 2QH,UK Tel: (USA) (314)3627072 or (UK) (0223)248011 Fax: (USA) (314)3624137 or (UK) (0223)402008

```

Email: rwenematode.wustl.edu or jes@mcrc-lmb.cam.ac.uk.
FEATURES
    source
        1..415
            /organism="Caenorhabditis elegans"
            /clone="cm06a11"
            /strain="Bristol N2"
BASE COUNT    123 a    69 c    95 g    125 t    3 others
ORIGIN
Query Match    1.9%; Score 19; DB 9; Length 415;
Best Local Similarity 100.0%; Pred. No. 6.71e-06;
Matches    19; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
Db    78 CCTCATCATCATCGTCTGC 96
      |||
QY    560 CCTCATCATCATCGTCTGC 578

RESULT    7
LOCUS    AA447244    521 bp    mRNA    EST    03-JUN-1997
DEFINITION    zw93c04.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone
              784518 5'.
ACCESSION    AA447244
NID    g2159909
KEYWORDS    EST.
SOURCE    human.
ORGANISM    Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
            Homo.
REFERENCE    1 (bases 1 to 521)
AUTHORS    Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Maira,M., Martin,J.,
            Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
            WashU-Merck EST Project 1997
            Unpublished (1997)
TITLE    WashU-Merck EST Project 1997
JOURNAL
COMMENT
    Contact: Wilson RK
    WashU-Merck EST Project
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: est@watson.wustl.edu
    This clone is available royalty-free through LNL ; contact the
    IMAGE Consortium (info@image.llnl.gov) for further information.
    Seq primer: -28m13 rev2 ET from Amersham
    High quality sequence stop: 490.
    Location/Qualifiers
        1..521
            /organism="Homo sapiens"
            /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
            polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
            was prepared from mRNA obtained from pooled 8-9 week
            (total) fetus material with a Not I - oligo(dT) primer [5'
            TGTTACCAATCTGAAGTGGAGCGCGCTTAATTCTTTTCTTTTCTT 3'].
            Double-stranded cDNA was ligated to Eco RI adaptors
            (Pharmacia), digested with Not I and cloned into the Not I
            and Eco RI sites of the modified pT7T3 vector. Library
            went through one round of normalization, and was
            constructed by Bento Soares and M. Fatima Bonaldo."
            /db_xref="taxon:9606"
            /clone="784518"
            /clone_lib="Soares total fetus Nb2HF8 9w"
            /dev_stage="8-9 weeks"
            /lab_host="DH10B"
            <1..->521
            /db_xref="GDB:5982136"
BASE COUNT    142 a    128 c    127 g    124 t
ORIGIN
Query Match    1.9%; Score 19; DB 23; Length 521;

```


Best Local Similarity 100.0%; Pred. No. 6.71e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 498 CCTGCTGAGGCTCTGGG 516
| | | | | | | | | | | | | | | |
Qy 725 CCTGCTGAGGCTCTGGG 743

RESULT 8
LOCUS HSAADHHZ 187 bp RNA EST 31-JAN-1995
DEFINITION H. sapiens putatively transcribed partial sequence; UK-HGMP
sequence ID AAADHHZ; single read.

ACCESSION Z20996
NID g27739

KEYWORDS EST; cDNA sequence; putatively transcribed partial sequence;
transcribed sequence fragment; UK puts.

SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 187)

AUTHORS UK-HGMP.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-1992) MRC Human Genome Mapping Project Resource
Centre Clinical Research Centre, Watford Road, Harrow, Middx, HA1
3Uf, Email: biohelp@hgm.mrc.ac.uk

REFERENCE 2 (bases 1 to 187)

AUTHORS UK-HGMP.

TITLE The UK-HGMP cDNA program

JOURNAL Unpublished

COMMENT cloning vector is gtl1.
fully automatic.

FEATURES Location/Qualifiers
1..187

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="B, Human Liver tissue"

BASE COUNT 60 a 50 c 32 g 45 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 18; DB 13; Length 187;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 76 AAGAAGCAAAATCAGTAA 93
| | | | | | | | | | | | | | | |
Qy 1 AAGAAGCAAAATCAGTAA 18

LOCUS H74768 224 bp mRNA EST 31-OCT-1995

DEFINITION 313 Brassica napus cDNA clone DRP18R.
ACCESSION H74768
NID g1047973
KEYWORDS EST.

SOURCE rape clone=DRP18R primer=M13 reverse library=Deletion-treated
strain=L. cv Naehan vector=pUC19 host=E. coli DH5a Rsite1-Sma1
Rsite2-Sma1 ESTs were generated from the root cDNA library of
Brassica napus. The cDNAs were primed with oligo(dT) primer.
Before inserting the cDNAs into the pUC19 vector digested with
Sma1, we deleted approximately 200 nucleotides from both 5' and 3'
ends to remove some of the noncoding region of cDNAs. The Sma1 site
in pUC19 was destroyed by cloning.

ORGANISM Brassica napus

Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Dilleniidae;
Caprales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 224)

AUTHORS Park,Y.S., Kwak,J.M., Kwon,O.Y., Kim,Y.S., Lee,D.S., Cho,M.J.,
Lee,H.H. and Nam,H.G.

TITLE Generation of expressed sequence tags of random root cDNA clones of
Brassica napus by single-run partial sequencing

JOURNAL Plant Physiol. 103, 359-370 (1993)

COMMENT

Contact: Nam, HG
Plant Molecular Genetics Laboratory
Pohang University of Science and Technology
Dept. of Life Science, San31 Hyodang, Pohang Kyungbuk 790-784,
Korea
Tel: 825622792111
Fax: 825622792199
Email: nam@vision.postech.ac.kr.

FEATURES Location/Qualifiers
1..224
/organism="Brassica napus"
/clone="DRP18R"
/strain="L. cv Naehan"

BASE COUNT 70 a 36 c 38 g 80 t

ORIGIN

Query Match 1.8%; Score 18; DB 12; Length 224;
Best Local Similarity 100.0%; Pred. No. 3.21e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 168 AAGAAGAAAGAACATAG 185
| | | | | | | | | | | | | | | |
Cp 97 AAGAAGAAAGAACATAG 80

RESULT 10

LOCUS AA331167 261 bp mRNA EST 21-APR-1997
DEFINITION EST35211 Embryo, 8 week I Homo sapiens cDNA 5' end similar to
vasoactive intestinal peptide receptor RDCl.

ACCESSION AA331167

NID g1983628

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae;
Homo.

1 (bases 1 to 261)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstein,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligriano,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
96026280

COMMENT Other ESTs: EST35210 EST1179908 THC105954

Contact: Kerlavage, AR

Bioinformatics

The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850 USA

Tel: 3018699056

Fax: 3018699423

Email: arkerlav@tigr.org

For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers


```
source
1. .261
/organism="Homo sapiens"
/note="Organ: Embryo, 8 weeks; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):133016"
/db_xref="taxon:9606"
/clone_lib="Embryo, 8 week 1"
/dev_stage="embryo, 8 wks"
<1. .>261

BASE COUNT      59 a      90 c      54 g      56 t      2 others
ORIGIN

Query Match      1.8%; Score 18; DB 18; Length 261;
Best Local Similarity 100.0%; Pred. No. 3.21e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 205 ATGAGCGTGACCGCTAC 222
|||||
QY 297 ATGAGCGTGACCGCTAC 314

RESULT 11
LOCUS H38470 261 bp mRNA EST 16-AUG-1995
DEFINITION YP69b06.r1 Homo sapiens cDNA clone 192659 5'.
ACCESSION H38470
NID 9907969
KEYWORDS EST.
SOURCE human clone=192659 library=Soares adult brain N2b4HB55Y
vector=PT7T3D (Pharmacia) with a modified polylinker host=DH10B
(ampicillin resistant) primer=M13R1 Rsite1=Not I Rsite2=Eco RI
55-year old male, 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTTACCAATCTGAGTGGAGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI adapters
(Pharmacia), digested with Not I and cloned into the Not I and Eco
RI sites of a modified PT7T3 vector (Pharmacia). Library went
through one round of normalization to a Cot = 53. Library
constructed by Bento Soares and M.Fatima Bonaldo. The adult brain
RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18
hours after death which occurred in consequence of a ruptured
aortic aneurysm. RNA was prepared from a pool of tissues
representing the following areas of the brain: frontal, parietal,
temporal and occipital cortex from the left and right hemispheres,
subcortical white matter, basal ganglia, thalamus, cerebellum,
midbrain, pons and medulla.

ORGANISM Homo sapiens
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 261)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohlmann,P. and
Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 203
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
location/Qualifiers
1. .261
/organism="Homo sapiens"
FEATURES
source
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BASE COUNT      39 a      72 c      76 g      63 t      11 others
ORIGIN

Query Match      1.8%; Score 18; DB 11; Length 261;
Best Local Similarity 94.7%; Pred. No. 3.21e-04;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 153 GTCCTCATCATCATCGNCT 171
|||||
QY 558 GTCCTCATCATCATCGTCT 576

RESULT 12
LOCUS AA296456 316 bp mRNA EST 18-APR-1997
DEFINITION EST11038 Umbilical vein endothelial cells 11 Homo sapiens cDNA 5'
end similar to vasoactive intestinal peptide receptor RDC1.
ACCESSION AA296456
NID 91948859
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
Homo.
1 (bases 1 to 316)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palanges,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Saudak,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Yi,Y.,
Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns
JOURNAL based upon 83 million nucleotides of cDNA sequence
MEDLINE Nature 377 (6547 Suppl), 3-174 (1995)
COMMENT Other_ESTs: EST11039 EST183921 THC1055954
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
location/Qualifiers
1. .316
/organism="Homo sapiens"
/note="Organ: umbilical vein; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"
/db_xref="ATCC (inhost):194234"
/db_xref="taxon:9606"
/clone_lib="Umbilical vein endothelial cells 11"
/cell_type="endothelial cell"
/dev_stage="fetus"
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ORIGIN

MRNA
BASE COUNT      67 a      106 c      72 g      71 t
ORIGIN
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Query Match 1.8%; Score 18; DB 18; Length 316;
Best Local Similarity 100.0%; Pred. No. 3.21e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 230 ATGAGCGTGACCGCTAC 247
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QY 297 ATGAGCGTGACCGCTAC 314

RESULT 13
LOCUS AA361360 337 bp mRNA EST 21-APR-1997
DEFINITION EST70628 T-cell lymphoma Homo sapiens cDNA 5' end.
ACCESSION AA361360
NID 92013678
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae;
Homo.

REFERENCE 1 (bases 1 to 337)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,
Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr.,
Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A.,
He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,
Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H.,
Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
Fraser,C.M. and Venter,J.C.

TITLE Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT

Contact: Kerlavage, AR
Bioinformatics
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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
Seq primer: M13 Reverse.

FEATURES
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1..337
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/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
<1..>337
BASE COUNT 60 a 90 c 103 g 75 t 9 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.21e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 11 GTGACCGCTACATTGCC 28
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QY 303 GTGACCGCTACATTGCC 320

RESULT 14
LOCUS FR0019360 364 bp DNA GSS 10-DEC-1997
DEFINITION F.rubripes GSS sequence, clone 028B15aA7.
ACCESSION AL012252
NID 92678620
KEYWORDS GSS; genome survey sequence.
SOURCE Fugu rubripes.
ORGANISM Fugu rubripes
Eukaryotae; Metazoa; Chordata; Vertebrata; Actinopterygii;
Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformes; Tetraodontidae; Tetraodontidae; Fugu.

REFERENCE 1 (bases 1 to 364)
AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
TITLE Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource
JOURNAL Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
COMMENT Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
sequence.

FEATURES
source
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/clone_lib="cosmid 028B15"
/clone="028B15aA7"

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ORIGIN

Query Match 1.8%; Score 18; DB 21; Length 364;
Best Local Similarity 100.0%; Pred. No. 3.21e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 202 CATCGTCTGTACACCCCT 219
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QY 569 CATCGTCTGTACACCCCT 586

RESULT 15
LOCUS T01065 367 bp mRNA EST 10-NOV-1992
DEFINITION W6ST01786 Caenorhabditis elegans cDNA clone CEESM36.
ACCESSION T01065
NID 9277546
KEYWORDS EST.
SOURCE Nematodes clone=CEESM36 library=Early embryo, Stratagene (cat.
#937007) primer=M13 Forward.
ORGANISM Caenorhabditis elegans
Eukaryota; Animalia; Eumetazoa; Nematoda; Secernentea; Rhabditiida;
Rhabditiina; Rhabditiodea; Rhabditiidae.
REFERENCE 1 (bases 1 to 367)
AUTHORS McCombie,W.R., Kelley,J.M., Aubin,L., Goscoechea,M.,
Fitzgerald,M.G., Wu,A., Adams,M.D., Dubnick,M., Kerlavage,A.R.,
Venter,J.C. and Fields,C.A.
JOURNAL Unpublished (1993)
COMMENT

Contact: Kerlavage AR
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932 Clopper Road, Gaithersburg, MD 20878
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org

FEATURES
source
1..367
/organism="Caenorhabditis elegans"
/clone="CEESM36"
BASE COUNT 141 a 75 c 57 g 94 t
ORIGIN

Query Match 1.8%; Score 18; DB 9; Length 367;
Best Local Similarity 100.0%; Pred. No. 3.21e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 323 GCCCTTTCAGAGTACGGT 340
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QY 179 GCCCTTTCAGAGTACGGT 196

Search completed: Tue Apr 21 01:24:37 1998
Job time : 901 secs.